

Best Local Similarity:	77.46%	Mismatches:	12
Query Match:	76.04%	Indels:	8
DB:	14	Gaps:	2
US-08-728-463B-205 (1-403) x AAR41285 (1-142)			
QY	1	ATGAACACCTGTGGTTCTTCCTCTCTGTGGCAGCTCCAGATGGTCTGTGCCAG	60
DB	1	MetGluHisLeuTrpPheLeuLeuLeuValAlaProArgTrpValLeuSerGln	20
QY	61	GTGCACCTACACAGCTGGGGCCGAGCTGTTGAAGCTTCGGAGACCCCTCCCTCACC	120
DB	21	ValGlnLeuGlnIleSerGlyProGlyLeuValIysProSerGluThrLeuSerLeuThr	40
QY	121	TGCGCTGTCTATGTGGGTCTTCCTCAGTGGTCTACTTGGAGCTGGATCCGCCAGCCCCCA	180
DB	41	CysThrValSerGlyGlySerIleSerSerHisTyrTrpSerTrpIleArgGlnSerPro	60
QY	181	GGTAAGGGCTGAGTGGANTGGGAAATCAATCATAGTGAAGACCAACTACACCCG	240
DB	61	GlyLysGlyLeuGlnTrpIleGlyTyrIleTyrTrpSerGlySerThrAsnTyrSerPro	80
QY	241	TCCTCAAGAGTCGAGTCACCATATCAGTCACAGCTCCAGAACCAAGTTCCTCCCTGAAG	300
DB	81	SerLeuLysSerArgValThrIleSerValGluThrSerTyrAsnGlnPheSerLeuLys	100
QY	301	CTGAGCTCTGTGACCGCCGCGACACGCGTGTGTATTACTGTGCGAGA-----	348
DB	101	LeuThrSerMetThrAlaAlaAspThrAlaValTyrCysAlaArgGlyProValPro	120
QY	349	GTAATTAATTGG-----TTCGACCCCTGGGGCCAGGAACCCCTGGTCACCCGTC	396
DB	121	AlaValPheTyrGlyAspTyrArgLeuAspProTrpGlyGlnGlyThrLeuValThrVal	140
QY	397	TCCTCA 402	
DB	141	SerSer 142	
RESULT 15			
ID	AA64676	standard; Protein; 139 AA.	
XX	AA64676;		
AC			
XX			
DT	01-FEB-2000 (first entry)		
XX			
DE	Human 5' EST related polypeptide SEQ ID NO:837.		
XX			
KW	Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;		
KW	gene therapy; chromosome mapping; upstream regulatory sequence;		
KW	forensic; location; development; protein synthesis; stability;		
KW	regulation; identification.		
XX			
OS	Homo sapiens.		
XX			
FN	WO953051-A2.		
XX			
PD	21-OCT-1999.		
XX			
PF	09-APR-1999; 99WO-IB00712.		
XX			
PR	09-APR-1998; 98US-0057719.		
PR	28-APR-1998; 98US-0069047.		
XX			
FA	(GEST) GENSET.		
XX			
PI	Dumas Milne Edwards J, Duclert A, Giordano J;		
XX			
DR	WPI; 2000-038446/03.		
DR	N-PSDB; AA242290.		
XX			
PT	Novel secreted protein 5' expressed sequence tag sequences used in		
PT	diagnostic, forensic, gene therapy, and chromosome mapping procedures		

Claim 3; Page 605-606; 837pp; English.

XX PS
XX PS
CC AAZ42265 to AAZ43075 represent novel 5' expressed sequence tag (EST)
CC sequences, corresponding to human secreted proteins. AAY64651 to
CC AAY65438 represent the EST-related proteins corresponding to AAZ42265 to
CC AAZ43052. The 5' ESTs can be used for producing secreted human gene
CC products. They can be used to identify and isolate 5' untranslated
CC regions (UTRs) and upstream regulatory regions which control the
CC location, development stage, rate, and quantity of protein synthesis, as
CC well as stability of mRNA. The ESTs are also useful as probes for
CC chromosome mapping, and to obtain full length cDNA clones. The ESTs can
CC also be used in forensic procedures to identify individuals, or in
CC diagnostic procedures to identify individuals having genetic diseases
CC resulting from abnormal gene expression. The products may also be used in
CC gene therapy protocols. The nucleic acids encoding signal peptides can be
CC used for directing extracellular secretion of a polypeptide or the
CC insertion of a polypeptide into a membrane, or importing a polypeptide
CC into a cell. The proteins encoded by the EST sequences may be useful in
CC treating a variety of human conditions. Secreted proteins have
CC therapeutic value, and the identification of new secreted proteins is
CC valuable. AAZ42249 to AAZ42264 and AAY64644 to AAY64650 represent
CC sequences used in the exemplification of the present invention.

XX SQ Sequence 139 AA;

Alignment Scores:

Pred. No.:	2,6e-46	Length:	139
Score:	564.50	Matches:	111
Percent Similarity:	82.86%	Conservative:	5
Best Local Similarity:	79.29%	Mismatches:	14
Query Match:	75.98%	Indels:	10
DB:	21	Gaps:	1

US-08-728-463B-205 (1-403) x AAY64676 (1-139)

QY	1	ATGAAACACCTGTGGTTCTTCTCTCTGTGGCAGCTCCAGATGGGTCCTGTCCAG	60
DB	1	Met***HisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGin	20
QY	61	GTGCGACTACAGCTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCTGTCCCTCACC	120
DB	21	ValGlnLeuGlnGluSerGlyProGlyLeuValLysProSer***ThrLeuSerLeuThr	40
QY	121	TGCGCTGTCTATGTGGGTGCTCTCAGTGGTGTACTACTGAGCTGGATCCGCCAGCCCCA	180
DB	41	CysThrValSerGlyAspSerIleSerSerTyTrpSerTrpIleArgGlnProPro	60
QY	181	GTGAAGGGCTGGAGTGGATTGGGGAATCAATCATAGTGGAGACCAACTACAACCCG	240
DB	61	GlyLysGlyLeuGluTrpIleGlyTyTrpIleTyTrpSerGlySerThrAsnTyAsnPro	80
QY	241	TCCTTCAGAGTCGAGTCACATATCAGTCGACAGCTCCGAAGACCAAGTTCCTCCTGAAG	300
DB	81	SerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeuLys	100
QY	301	CTGAGCTCTGTGACCGCGCACACGCTGTGTATTACTGTGCGAGAGTAAT	354
DB	101	LeuSerSerValThrAlaAlaAspThrAlaValTyTrpCysAlaArg***Leu***Tyr	120
QY	355	-----AAVTGGTTCGACCCCTGGGGCCAGGGAACCTGGTCA	391
DB	121	TyrAspArgSerGlyTyrPheArgTyrPheAspTyrTrpGlyGlnGlyThrTrpSer	139

Search completed: June 3, 2003, 09:02:15
Job time : 29.2332 secs

Novel secreted protein 5' expressed sequence tag sequences used in PT diagnostic, forensic, gene therapy, and chromosome mapping procedures

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XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT Region 29..35 /label= CDR1
FT /note= "complementarity determining region"
FT Region 50..65 /label= CDR2
FT /note= "complementarity determining region"
FT Region 98..112 /label= CDR3
FT /note= "complementarity determining region"
FT
XX FR2724182-A1.
XX
XX 08-MAR-1996.
XX
XX 02-SEP-1994; 94FR-0010566.
XX
XX 02-SEP-1994; 94FR-0010566.
XX
XX (INSP ) INST PASTEUR.
XX (PROT-) PROTEINE PERFORMANCE.
XX
XX Chaabihi H, Edelman L, Kaczorek M, Margaritte C;
XX WPI; 1996-162018/17.
XX N-PSDB; AAT26870.
XX
XX Recombinant anti-rhesus D monoclonal antibody - expressed by
XX baculovirus-transformed insect cells and useful for preventing
XX haemolysis in new-born babies
XX
XX Example 1; Page 32; 46pp; French.
XX
XX The human monoclonal antibody D7C2, of isotype IgM, recognises a
XX 30-32 kD polypeptide on the membrane of rhesus positive red blood
XX cells. The antibody agglutinates rhesus positive cells but not
XX rhesus negative cells and is useful diagnostically and also for
XX preventing haemolysis in new-born rhesus positive babies.
XX Recombinant IGM-D7C2 can be produced by insect cells which have
XX been transformed by a baculoviral vector comprising a D7C2
XX expression cassette. The present sequence is that of the variable
XX region of the IGM-D7C2 heavy chain.
XX
XX SQ Sequence 123 AA;

Alignment Scores:
Pred. No.: 1.26e-47 Length: 123
Score: 578.00 Matches: 109
Percent Similarity: 90.24% Conservatives: 2
Best Local Similarity: 88.62% Mismatches: 4
Query Match: 77.79% Indels: 8
DB: 17 Gaps: 1

US-08-728-463B-205 (1-403) x AAW03757 (1-123)

QY 58 CAGGTGAGCTTACAGAGTGGCGGCGAGCTGTGAAGCTTCGGAGACCTGTCCCTC 117
Db 1 GlnValGlnLeuGlnGlnTrpGlyAlaGlyLeuLeuLysProSerGluThrLeuSerLeu 20

QY 118 ACCTGCGCTGTCTATGTGGTCCCTTCAGTGGTTACTACTGGAGCTGGATCCGCGACCCC 177
Db 21 ThrCysThrValTyrGlyGlySerPheSerGlyTyrTrpSerTrpIleArgGlnPro 40

QY 178 CCAGGTAAAGGGCTGGAGTGATGGGGAATCAATCATAGTGGAAACCACTACAAC 237
Db 41 ProGlyLysGlyLeuGluTrpIleGlyGluLeuAsnHisSerGlySerThrAsnTyrAsn 60

QY 238 CCGTCCCTCAGAGTCCGAGTCCACCATATCAGTCGACACGTCACAGACCTCCAGTCTCCCTG 297
Db 61 ProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeu 80

QY 298 AAGCTGAGCTCTGTGACCGCGCGGACACGGCTGTGTATTACTGTGCGAGAGTAATT--- 354
Db 81 LysLeuAenSerValThrAlaAlaAspThrAlaValTyr-Tyr-CysAlaArgAlaProGlu 100

QY 355 -----AATTGGTTCGACCCCTGGGGCCAGGGAACCTGTGTACCC 393
Db 101 TyrLysTrpLysTyrHisGlyAspTrpPheAspProTrpGlyGlnGlyThrThrValThr 120

QY 394 GTCCTCTCA 402
Db 121 ValSerSer 123

RESULT 14
AAR41285
ID AAR41285 standard; Protein; 142 AA.
XX
XX AAR41285;
XX
XX 01-NOV-1993 (first entry)
XX
XX F105 rearranged variable region heavy chain.
XX
XX Monoclonal antibody; MAb; envelope; glycoprotein; gp120; HIV; AIDS;
XX CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
XX chain; epitope; immune deficiency.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..19 /label= sig_peptide
XX Protein 20..142 /label= mat_protein
XX
XX W09312232-A.
XX
XX 24-JUN-1993.
XX
XX 10-DEC-1992; 92WO-US10928.
XX
XX 10-DEC-1991; 91US-0804652.
XX
XX (DAND ) DANA FARRER CANCER INST INC.
XX (NEW-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
XX
XX Haseltine WA, Marasco WA, Posner MR, Sodroski JG;
XX
XX WPI; 1993-214174/26.
XX N-PSDB; AAQ49154.
XX
XX DNA segments encoding monoclonal antibody - which binds to gp120
XX and neutralises HIV, for treating AIDS, and for diagnosing and
XX monitoring HIV infection
XX
XX Claim 9-10; Page 77; 109pp; English.
XX
XX mRNA from the known hybridoma F105 was converted to cDNA and this
XX subjected to PCR amplification using primers corresp. to appropriate
XX parts of the heavy or light chains and having restriction sites to
XX permit cloning. The extension prods. were isolated and sequenced.
XX The recombinant human monoclonal antibody (MAb) binds to a
XX discontinuous epitope on the HIV gp120 envelope glycoprotein, blocks
XX the binding of gp120 to the CD4 receptor, and neutralises a broad
XX range of HIV isolates. The MAb may be used to treat immune
XX deficiency, esp. at doses of 0.1-10 mg/kg.
XX
XX SQ Sequence 142 AA;

Alignment Scores:
Pred. No.: 2.33e-46 Length: 142
Score: 565.00 Matches: 110
Percent Similarity: 85.92% Conservatives: 12

```

CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.

XX SQ Sequence 249 AA;

Alignment Scores:
 Pred. No.: 1,37e-48 Length: 249
 Score: 588.50 Matches: 112
 Percent Similarity: 89.68% Conservative: 1
 Best Local Similarity: 88.89% Mismatches: 2
 Query Match: 79.21% Indels: 11
 DB: 23 Gaps: 1

US-08-728-463B-205 (1-403) x AAB45310 (1-249)

QY 58 CAGGTGACGTACAGCAGTGGGGCGCAGGACTGTTGAAGCTTCGGAGACCCCTGTCCTC 117
 DB 1 GlnValGlnLeuGlnGlnTrpGlyAlaGlyLeuLeuLysProSerGluThrLeuSerLeu 20
 QY 118 ACCTGCGCTGTCTATGTGGTCTCTTCACTGGTTACTGAGCTGGATCCGCCAGCCC 177
 DB 21 ThrCysAlaValTyrGlyGlySerPheSerGlyTyrTyrTrpSerTrpIleArgGlnPro 40
 QY 178 CCAGGTAAGGGCTGGAGTGGATTGGGAAATCAATCATATGTCGAGCACCACCACTACAAC 237
 DB 41 ProGlyLysGlyLeuGluTrpIleGlyGluLeuHisSerGlySerThrAsnTyrAsn 60
 QY 238 CCGTCCCTCAAGAGTCGAGTCACATATCATGTCGACACGTCCTCAAGAACCACTGTCCTCC 297
 DB 61 ProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeu 80
 QY 298 AAGCTGAGCTCTGTGACCGCGCGGACACGGCTGTGTATTACTGTCGAGA----- 348
 DB 81 LysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgGlyProArg 100
 QY 349 -----GTAATTAATTTGTTGACCCCTGGCGGCGCAGGAAAC 384
 DB 101 TyrTyrAspIleLeuThrGlyTyrArgTyrAsnTrpPheAspProTrpGlyArgGlyThr 120
 QY 385 CTGGTCACGTCCTCTCA 402
 DB 121 LeuValThrValSerSer 126

RESULT 12

AAB36206
 ID AAB36206 standard; protein; 473 AA.
 AC AAB36206;

XX 15-FEB-2001 (first entry)

XX Human immune system associated protein HISAP-4.

XX Human; immune system associated protein; HISAP-4; immune disorder;
 KW infection; autoimmune disease; cancer.

XX Homo sapiens.

XX US6135941-A.

XX 24-OCT-2000.

XX 27-MAR-1998; 98US-0049672.

XX 27-MAR-1998; 98US-0049672.

XX (INCY-) INCYTE PHARM INC.

XX Tang YT, Yue H, Lal P, Corley NC, Guégler KJ, Baughn MR;
 PI Hillman JL, Au-Young J;

XX WPI; 2001-030926/04.

XX N-PSDB; AAC66522.

XX New human immune system associated proteins (HISAP) and polynucleotides
 PT encoding the HISAP; useful for diagnosing, treating or preventing
 PT immune or cell proliferative disorders or infections

XX Claim 1; Column 53-56; 54pp; English.

XX The present invention provides the coding and protein sequences for a
 CC number of human immune system associated proteins (HISAPs). These can be
 CC used in the diagnosis and treatment of various autoimmune disorders,
 CC infections and cell proliferation diseases. The diseases include AIDS,
 CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
 CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
 CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
 CC erythematosus, arteriosclerosis, cirrhosis and cancer.

XX SQ Sequence 473 AA;

Alignment Scores:
 Pred. No.: 1,41e-47 Length: 473
 Score: 578.50 Matches: 118
 Percent Similarity: 86.01% Conservative: 5
 Best Local Similarity: 82.52% Mismatches: 11
 Query Match: 77.86% Indels: 9
 DB: 22 Gaps: 3

US-08-728-463B-205 (1-403) x AAB36206 (1-473)

QY 1 ATGAACACCTGTGGTTCTTCTCTCTGTGGCAGTCCAGATGGTCTGTCCAG 60
 DB 1 MetLysHisLeuTrpPheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20
 QY 61 GTGACGTACAGCAGTGGGGCGCAGGACTGTTGAAGCTTCGGAGACCCCTGTCCTCACC 120
 DB 21 ValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40
 QY 121 TGGCGTGTCTATGGTGGTCTCTTCAGT-----GTTACTAGTGGAGTGGATCCGCCAG 174
 DB 41 CysAlaValSerGlyGlySerIleThrSerGlyGlyTyrTyrTrpSerTrpIleArgGln 60
 QY 175 CCCCAGGTAAAGGGCTGGAGTGGATTGGGAAATCAATCATATGTAAGCACCACCACTAC 234
 DB 61 ProGlyLysGlyLeuGluTrpIleGlyTyrIleTyrTyrSerGlySerThrLeuTyr 80
 QY 235 AACCCGTCCTCAAGAGTCGAGTCACCATATCAGTCGACACAGCTCCAAAGACCACTCTCC 294
 DB 81 AsnProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSer 100
 QY 295 CTGAAGCTGAGCTCTGTGACCGCGGACACCGCTGTGTATTACTGTGGAGAGTAATT 354
 DB 101 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgAspAsp 120
 QY 355 -----AATTGG-----TTCACCCCTGGGGCGCAGGAAACCTGTGTCACC 393
 DB 121 ValGlyLeuArgGlyGlyAsnTyrGlyMetAspValTrpGlyGlnGlyThrLeuValThr 140
 QY 394 GTCTCTCTCA 402
 DB 141 ValSerSer 143

RESULT 13

AAB03757
 ID AAB03757 standard; Protein; 123 AA.

XX AAB03757;

XX 29-OCT-1996 (first entry)

XX Anti-rhesus D monoclonal antibody D7C2 heavy chain V region.

XX Human monoclonal antibody; immunoglobulin isotype IgM; agglutination;
 KW rhesus positive; rhesus negative; haemolysis; heavy chain;
 KW variable region; insect host cell; baculovirus; recombinant production.

CC and/or remedies for platelet reduction-associated blood diseases,
CC thrombocytopenia following cancer chemotherapy or leukaemia. The
CC antibody can act as a TPO signal transduction agonist by transducing a
CC signal into cells by crosslinking a TPO receptor to exert TPO agonism.
CC This is the amino acid sequence of a thrombopoietin (TPO) agonist
CC antibody associated protein.

XX

SQ Sequence 256 AA;

Alignment Scores:

Pred. No.:	5_65e-49	Length:	256
Score:	592.50	Matches:	115
Percent Similarity:	90.30%	Conservative:	6
Best Local Similarity:	85.82%	Mismatches:	12
Query Match:	79.74%	Indels:	1
DB:	23	Gaps:	1

US-08-728-463B-205 (1-403) x ABG35335 (1-256)

Qy 1 ATGAACACTGTGGTTCTTCCTCCTCGTGAGCACTCCAGATGGCTCCTGCCAG 60
Db 1 MetLysHisLeuTrpPhePheLeuLeuValAlaProArgTrpValLeuSerGln 20
Qy 61 GTGCAGCTACAGCACTGGGGCGCACGACTGTTGAAGCCTTCGGAGACCCTGCCAC 120
Db 21 ValGlnLeuGlnSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40
Qy 121 TGCGCTGTCATGTGGGTGCTTCAGTGGTTACTACTCGAGCTGGATCCGCCAGCCCCA 180
Db 41 CysThrValSerGlyAspSerIleSerSeryrTyrrTpSerTrpIleargGlnProPro 60
Qy 181 GGTAAAGGGCTGGAGTGGATGGGGAATCAATCATAGTGGAAAGCAACCACTACAACCG 240
Db 61 GlyLysGlyLeuGluTrpIleGlyTyrIleTyrSerGlySerThrAsnTyrAsnPro 80
Qy 241 TCCTCAAAGAGTCGAGTCACCATATCAGTCGACACGTCCAAGAACCAGTTCTCCTGAAG 300
Db 81 SerLeuLysSerArgValThrIleSerValAspThrSerLysSerGlnPheSerLeuLys 100
Qy 301 CTGAGCTCTGTACCGCGCGGACACGGCTGTGTATTACTGTCCGAGAGATAATTATGG 360
Db 101 LeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgGly---ArgTyr 119
Qy 361 TTCACCCCTGGGGCAGGGAACCTGTGTCACCGTCTCTCA 402 -
Db 120 PheaspValTrpGlyArgGlyThrmethValThrValSerSer 133

RESULT 9
ABG35336
ID ABG35336 standard; Protein; 266 AA.
AC ABG35336;
XX
DT 30-JUL-2002 (first entry)
XX
DE Thrombopoietin agonist antibody associated protein #29.
XX
KW Modified antibody; thrombopoietin; TPO; agonist;
KW TPO receptor; platelet reduction-associated blood disease;
KW thrombocytopenia; cancer chemotherapy; leukaemia; signal transduction.
XX
OS Synthetic.
XX
PN WO200233072-A1.
XX
PD 25-APR-2002.
XX
PF 22-OCT-2001; 2001WO-JP09259.
XX
PR 20-OCT-2000; 2000JP-0321821.
PR 17-APR-2001; 2001WO-JP03288.
PR 12-SEP-2001; 2001JP-0277314.
XX

(CHUS) CHUGAI SEIYAKU KK.

Tsuchiya M, Ohtomo T, Yabuta N, Tsunoda H, Orita T;
WPI; 2002-383513/41.
N-PSDB; ABK71414.

Degraded thrombopoietin agonist antibodies containing H and L chain V domains of monoclonal antibody, useful in preventives and/or remedies for blood diseases, thrombocytopenia following cancer chemotherapy or leukaemia -

Disclosure; Page 208-209; 213pp; Japanese.

The invention describes a modified antibody comprising at least 2 heavy chain variable domains and 2 or more light chain variable domains of an antibody, and exhibits thrombopoietin (TPO) agonistic effect by causing the TPO receptor to crosslink. The antibodies are useful in preventives and/or remedies for platelet reduction-associated blood diseases, thrombocytopenia following cancer chemotherapy or leukaemia. The antibody can act as a TPO signal transduction agonist by transducing a signal into cells by crosslinking a TPO receptor to exert TPO agonism. This is the amino acid sequence of a thrombopoietin (TPO) agonist antibody associated protein.

Sequence 266 AA;

Alignment Scores:

Pred. No.:	5.68e-49	Length:	266
Score:	592.50	Matches:	115
Percent Similarity:	90.30%	Conservative:	6
Best Local Similarity:	85.82%	Mismatches:	12
Query Match:	79.74%	Indels:	1
DB:	23	Gaps:	1

US-08-728-463B-205 (1-403) x ABG35336 (1-266)

Qy	1	ATGAAACACCTGTGGTTCTTCTCTCTCTGTGGCAGCTCCAGATGGTCTGTGCCAG	60
Db	1	MetlyshisLeuTrpPheLeuLeuLeuValAlaAlaProArgTrpValLeuSerGln	20
Qy	61	GTGAGCTACAGCAGTGCGGGCGAGGACTGTGAAGCCTTCGGAGACCTGTCCCTCAC	120
Db	21	ValGlnLeuGlnSerGlyProGlyLeuVallyysProSerGluThrLeuSerLeuThr	40
Qy	121	TGCCTCTATGTGTGGTCTTTCAGTGGTTACTGTAGAGCTGGATCCGCAGCCCCA	180
Db	41	CysThrValSerGlyAspSerIleSerSerTyrTrpSerTrpIleArgGlnProPro	60
Qy	181	GGTAAGGGCTGGAGTGGATTGGGGAATCAATCATAGTGAAGCACCACCTACAAACCG	240
Db	61	GlyysGlyLeuGluTrpIleGlyTrpIleTyrSerGlySerThrAsnTyrAsnPro	80
Qy	241	TCCCTCAAGAGTCGAGTCACCATATCAGTCACACGTCACCAAGACCACTTCTCCCTGAAG	300
Db	81	SerLeuLysserArgValThrIleSerValAspThrSerLysserGlnPheSerLeuLyss	100
Qy	301	CTGAGCTCTGTGACCCGGCGGACACCGCTGTGTATTACTGTGCGAGAGTAATTAATGG	360
Db	101	LeuSerSerValThrAlaAlaAspThrAlaValTyrTrpCysAlaArgGly---ArgTyr	119
Qy	361	TTTCACCCCTGGGGCCAGGACCCCTGGTCACCGCTCTCTCA	402
Db	120	PheAspValTrpGlyArgGlyThrMetValThrValSerSer	133

RESULT 10
AAY82628
ID AAY82628 standard; Protein; 139 AA.
XX AAY82628;
AC AAY82628;
XX
DY 02-AUG-2000 (first entry)
XX

Db 88 ILeSerValAspThrSerLysAsnGlnPheSerLeuLysLeuAsnSerValThrAlaAla 107
 QY 322 GACACGGCTGTATTACTGTGCGAGAGTAATT-----AAT 357
 Db 108 AspThrAlaValTyrTyrCysAlaAa-9AlaProGluTyrLysTyrHisGlyAsp 127
 QY 358 TGGTTCCGACCCCTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 402
 Db 128 TrpPheAspProTrpGlyGlnGlyThrThrValThrValSerSer 142

RESULT 7

ABG35331
 ID ABG35331 standard; Protein; 133 AA.

XX AC ABG35331;

DT 30-JUL-2002 (first entry)

XX Thrombopoietin agonist antibody associated protein #24.

XX Modified antibody; thrombopoietin; TPO; agonist;
 KW TPO receptor; platelet reduction-associated blood disease;
 KW thrombocytopenia; cancer chemotherapy; leukaemia; signal transduction.

XX Mus sp.

XX WO200233072-A1.

XX 25-APR-2002.

XX 22-OCT-2001; 2001WO-JP09259.

XX 20-OCT-2000; 2000JP-0321821.

XX 17-APR-2001; 2001WO-JP03288.

XX 12-SEP-2001; 2001JP-0277314.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Tauchiya M, Ohtomo T, Yabuta N, Tsunoda H, Orita T;

XX WPI; 2002-383513/41.

XX N-PSDB; ABK71396.

XX Degraded thrombopoietin agonist antibodies containing H and L chain V
 domains of monoclonal antibody, useful in preventives and/or remedies
 for blood diseases, thrombocytopenia following cancer chemotherapy or
 leukaemia

XX Disclosure; Page 196-197; 213pp; Japanese.

XX The invention describes a modified antibody comprising at least 2 heavy
 chain variable domains and 2 or more light chain variable domains of an
 antibody, and exhibits thrombopoietin (TPO) agonistic effect by causing
 the TPO receptor to crosslink. The antibodies are useful in preventives
 and/or remedies for platelet reduction-associated blood diseases,
 CC thrombocytopenia following cancer chemotherapy or leukaemia. The
 CC antibody can act as a TPO signal transduction agonist by transducing a
 CC signal into cells by crosslinking a TPO receptor to exert TPO agonism.
 CC This is the amino acid sequence of a thrombopoietin (TPO) agonist
 CC antibody associated protein.

XX Sequence 133 AA;

Alignment Scores:

Pred. No.:	5,08e-49	Length:	133
Score:	592.50	Matches:	115
Percent Similarity:	90.30%	Conservative:	6
Best Local Similarity:	85.82%	Mismatches:	12
Query, Match:	79.74%	Indels:	1
DB:	23	Gaps:	1

US-08-728-463B-205 (1-403) x ABG35331 (1-133)

QY 1 ATGAACACCTGTGTTCTTCTCTCTCTGTCGAGCTCCAGATGGGTCTGTCCACG 60
 Db 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20
 QY 61 GTGCAAGCTTACAGCAGTGGGGCCAGGAGCTTTGAAGCCTTCGGAGACCTGTCCCTCACC 120
 Db 21 ValGlnLeuGlnSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40
 QY 121 TCGCGTGTCTATGTGGTGGTCTTCACTGTGAGTGTACTGTGAGTGTGATCCGCGCCCA 180
 Db 41 CysThrValSerGlyAspSerIleSerSerTyrTyrTrpSerTrpIleargGlnProPro 60
 QY 181 GCTAAGGGCTCGAGTGGATTGGGAAATCAATCATAGTGAAGCACCACTACACCGG 240
 Db 61 GlyLysGlyLeuGluTrpIleGlyTyrIleTyrSerGlySerThrAsnTyrAsnPro 80
 QY 241 TCCCTCAAGAGTCGAGTCACCATATCATGTCAGTCAGACACGTCACCAAGACCTCTCCCTGAAG 300
 Db 81 SerLeuLysSerArgValThrIleSerValAspThrSerLysSerGlnPheSerLeuLys 100
 QY 301 CTGAGCTCTGTCACCGCCGCGACACGCGCTGTGTATTACTGTGCGAGAGTAATTAATTCG 360
 Db 101 LeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgGly---ArgTyr 119
 QY 361 TTCGACCCCTGGGGCCAGGAAACCTGTGTCACCGTCTCTCTCA 402
 Db 120 PheAspValTrpGlyArgGlyThrMetValThrValSerSer 133

RESULT 8

ABG35335
 ID ABG35335 standard; Protein; 256 AA.

XX AC ABG35335;

XX 30-JUL-2002 (first entry)

XX Thrombopoietin agonist antibody associated protein #28.

XX Modified antibody; thrombopoietin; TPO; agonist;
 KW TPO receptor; platelet reduction-associated blood disease;
 KW thrombocytopenia; cancer chemotherapy; leukaemia; signal transduction.

XX Synthetic.

XX WO200233072-A1.

XX 25-APR-2002.

XX 22-OCT-2001; 2001WO-JP09259.

XX 20-OCT-2000; 2000JP-0321821.

XX 17-APR-2001; 2001WO-JP03288.

XX 12-SEP-2001; 2001JP-0277314.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Tauchiya M, Ohtomo T, Yabuta N, Tsunoda H, Orita T;

XX WPI; 2002-383513/41.

XX N-PSDB; ABK71411.

XX Degraded thrombopoietin agonist antibodies containing H and L chain V
 domains of monoclonal antibody, useful in preventives and/or remedies
 for blood diseases, thrombocytopenia following cancer chemotherapy or
 leukaemia

XX Disclosure; Page 205-206; 213pp; Japanese.

XX The invention describes a modified antibody comprising at least 2 heavy
 chain variable domains and 2 or more light chain variable domains of an
 antibody, and exhibits thrombopoietin (TPO) agonistic effect by causing
 the TPO receptor to crosslink. The antibodies are useful in preventives

respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

Sequence 193 AA;

Alignment Scores:	2,21e-49	Length:	193
Pred. No.:	596.50	Matches:	117
Score:	84.62%	Conservative:	4
Percent Similarity:	81.82%	Mismatches:	13
Best Local Similarity:	81.82%	Indels:	9
Query Match:	20.28%	Gaps:	1
DB:	23		

US-08-728-463B-205 (1-403) x ABP43199 (1-193)

1	ATGAAACACCTCTGGTCTTCCTCTCTGTGGCAGCTCCACAGATGGGCTCTGTGCCAG	60
6	MetLysHisLeuTrpPhePheLeuLeuValAlaIaProArgTrpValLeuSerGln	25
61	GTGCACTACACAGCTGGGGCGCAGGACTGTTGAAGCTTCGGAGACCCTGTCCCTCAC	120
26	ValGlnLeuGlnIleSerGlyProGlyLeuValIysProSerGluThrLeuSerLeuThr	45
121	TCCGCTGTCTATGGTGGGTCCCTTCAGTGGTGTACTACTGGAGCTGGATCCGCCACGCCCA	180
46	CysThrValSerGlyGlySerIleSerSerTyrtyrtrpSertrpIleArgGlnProPro	65
181	GCTAAGGGCTGGAGTGGATGGGGAATCAATCATAGTCGAGACCACTACAACCCG	240
66	GlyLysGlyLeuGluIleGlyTyrIleTyrTrpSerGlySerThrAsnTyrAsnPro	85
241	TCCCTCAAGAGTCGAGTCACCATATCACTGCACACGTCCAAAGAACAGATTCTCCCTGAAG	300
86	SerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeuLys	105
301	CTGACCTCTGTGACCGCCGCGGACCGGCTGTGTATTACTGTGCGAGA	348
106	LeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgGlyProTyrSer	125
349	-----GTAATTAATTTGGTTCGACCCCTGGGGCCAGGAGACCCCTGTCTCAC	393
126	SerSerTrpTyrProArgAlaGluTyrPheGlnHisTrpGlyGlnGlyThrLeuValThr	145
394	GTCTCTCTCA	402
146	ValSerSer	148

RESULT 6

AA93166
ID AA93166 standard; Protein: 472 AA.

AC AAR93166;

30-OCT-1996 (first entry)

DE Anti-rhesus D recombinant antibody D7C2 heavy chain.

XX	Human monoclonal antibody; immunoglobulin isotype IgM; agglutination;
KW	rhesus positive; rhesus negative; haemolysis; gamma 1 heavy chain;
KW	variable region; insect host cell; baculovirus; recombinant production.
OS	Homo sapiens.
OS	Synthetic.

XX	Key	Location/Qualifiers	
FT	Peptide	1..19	
FT		/label= signal_peptide	
FT		/note= "mouse VH signal peptide sequence encoded by synthetic linker"	
FT	Protein	20..472	
FT		/label= heavy_chain	
FT		/note= "human gamma 1 chain constant region and the variable region from anti-rheus D antibody D7C2"	
FT			

FR2724182-A1.

08-MAR-1996.

02-SEP-1994: 94FR-0010566.

02-SEP-1994: 94FR-0010566

(TNSP) TNST PASTEUR

(PROT-) PROTEINE PERFORMANCE.

Chaabihi H, Edelman L, Kaczorek M, Margaritte C;

WPI; 1996-162018/17.

1

expressed by monoclonal antibody - baculovirus-transformed insect cells and useful for preventing haemolysis in new-born babies

Example 2; Page 35-37; 46pp; French.

The human monoclonal antibody D7C2, of isotype IgM, recognises a 30-32 kD polypeptide on the membrane of rhesus positive red blood cells. The antibody agglutinates rhesus positive cells but not rhesus negative cells and is useful diagnostically and also for preventing haemolysis in new-born rhesus positive babies.

Recombinant IgM-D7C2 can be produced by insect cells which have been transformed by a baculoviral vector comprising a D7C2 expression cassette. The present sequence is that of a recombinant IgM-D7C2 heavy chain fused downstream of a mouse VH signal peptide.

Sequence .472 AA;

Alignment Scores:

Pred. No.:	3.586-49	Length:	472
Score:	595.00	Matches:	115
Percent Similarity:	86.6%	Conservative:	2
Best Local Similarity:	85.1%	Mismatches:	10
Query Match:	80.0%	Indels:	8
DB:	17	Gaps:	1

US-08-728-463B-205 (1-403) x AAR93166 (1-472)

QY 22 CTCCTCCTGGTGGCAGCTCCACAGATGGGTCTGTCCACGGTGCCAGCTACAGCAGTGGGGC A1

8 Leuphe[euVa]A[atbhrA]athrg[v]a[Hi]sserG[nva]C[n]o[C]nG[n]t[rmC]v. 37

82 GCAGGACCTGTGAAGCCTTCGGAGACCCCTTCTCCTCAACTGCCATCGAACCCTGCCTCC
OV

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[illegible]

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87 valGlySerLeuLysSerArgValThr 87

FT XX /label= LH11238_antibody_heavy_chain_variable_region
 PN WO200032635-A2.
 XX 08-JUN-2000.
 XX 01-DEC-1999; 99WO-US28485.
 XX 02-DEC-1998; 98US-0203768.
 XX (IXSY-) IXSYS INC.
 XX Watkins JD, Huse WD;
 PI WPI; 2000-412293/35.
 XX DR N-PSDB; AAA52907.
 XX
 PT New tumor-specific human monoclonal antibody, useful for the treatment
 PT and diagnosis of cancer, comprises at least one complementarity
 PT determining region -
 XX
 PS Claim 1; Page 79-80; 84pp; English.
 XX
 CC The present sequence is the heavy chain variable region of a human
 CC tumour-specific monoclonal antibody. Neoplastic cells selectively express
 CC antigens which are not present on normal cells. Thus monoclonal
 CC antibodies can be produced that are specifically directed against
 CC tumour-specific antigens. The antibodies can be conjugated to cytotoxic
 CC or cytostatic agents and used to selectively target cancer cells for the
 CC elimination of tumours. They can also be linked to diagnostic moieties
 CC that allow the imaging of neoplastic cells. Nucleic acids encoding human
 CC tumour-specific monoclonal antibodies can be used to express the
 CC antibodies and can be recombinantly engineered to produced modified
 CC antibodies with higher affinity or higher selectivity for tumour cells.
 CC Tumour-specific antibodies were produced by hybridomas that were
 CC generated by in vitro immunisation of human spleen cell cultures with
 CC breast carcinoma cells. The nucleic acid encoding the monoclonal antibody
 CC was then isolated from the hybridoma by RT-PCR. The present sequence
 XX was produced by LH11238 hybridoma cell line.
 SQ Sequence 139 AA;

Alignment Scores:
 Pred. No.: 1.6e-57 Length: 139
 Score: 680.50 Matches: 130
 Percent Similarity: 94.24% Conservative: 1
 Best Local Similarity: 93.53% Mismatches: 3
 Query Match: 91.59% Indels: 5
 DB: 21 Gaps: 1

US-08-728-463B-205 (1-403) x AAY99556 (1-139)

QY 1 ATGAAACACCTGTGGTCTTCCTCCCTCGTGGCAGCTCCAGATGGTCTGTCCCAAG 60
 DB 1 MetLysHisLeuTrpPheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20
 QY 61 GTCACGCTACAGCTGGGCGCAGGACTGTTGAAGCCTTCGGAGACCTGTCCCTCAAC 120
 DB 21 ValGlnLeuGlnGlnTrpGlyAlaGlyLeuLeuLysProSerGlnThrLeuSerLeuThr 40
 QY 121 TGGCTGTCTATGGTGGGCTCTTCAGTGGTTACTACTGAGCTGGATCCGCGACCCCA 180
 DB 41 CysAlaValTrpGlyGlySerPheSerGlyTyTrpSerTrpIleArgGlnProPro 60
 QY 181 GGTAAAGGGCTGAGTGGATTGGGAAATCAATCATAGTGGAGACCACTACACCCG 240
 DB 61 GlyLeuGlyLeuGlnTrpIleGlyLeuLeuLeuHisSerGlySerThrAsnTrpAsnPro 80
 QY 241 TCCTCAAGAGTCCAGTACCATATCATGTCGACACGTCACAGACCAAGTCTCCCTGAAG 300
 DB 81 SerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeuLys 100
 QY 301 CTGAGCTCTGTGACCGCGCGACACGGCTGTGTATTACTGTCCGAGAGTAATT----- 354

Db 101 LeuSerSerValThrAlaAlaAspThrAlaValTrpCysAlaArgGluIleAlaAla 120
 QY 355 -----AATTGGTTCGACCCCTGGGGCCAGGAACCTGGTCAACCGTCTCTCTCA 402
 DB 121 ArgProHisArgTrpPheAspTrpTrpGlyGlnGlyThrLeuValThrValSerSer 139
 RESULT 2
 AAY96290
 ID AAY96290 standard; protein; 537 AA.
 XX
 AC AAY96290;
 XX
 DT 16-AUG-2000 (first entry)
 XX
 DE Human IGFAM-2 immunoglobulin.
 XX
 KW Human; immunoglobulin; IGFAM-2; IGFAM; immune disorder; cancer;
 KW infection; inflammation; haematopoiesis; AIDS; allergy.
 XX
 OS Homo sapiens.
 XX
 EH Key Location/Qualifiers
 FT Peptide 1..26
 FT /label= signal_peptide
 FT Protein 27..537
 FT /label= IGFAM-2
 FT Domain 41..128
 FT /label= Ig_domain
 FT Domain 174..239
 FT /label= Ig_domain
 FT Region 235..241
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 FT Domain 336..404
 FT /label= Ig_domain
 FT Domain 440..510
 FT /label= Ig_domain
 FT Region 444..466
 FT /label= Ig_signature
 FT Domain 486..536
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 FT Region 506..523
 FT /label= Ig_signature
 XX WO200029583-A2.
 PN 25-MAY-2000.
 PD 19-NOV-1999; 99WO-US27566.
 PF 19-NOV-1998; 99US-0113635.
 PR 22-DEC-1998; 98US-0113635.
 PR 07-APR-1999; 99US-0128194.
 XX (INCY-) INCYTE PHARM INC.
 XX
 PI Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;
 PI Lu DAM, Lal P, Hillman JL, Yang J;
 XX WPI; 2000-387796/33.
 DR N-PSDB; AAA27382.
 XX
 PT Immunoglobulin superfamily proteins, the agonist and antagonist of the
 PT protein is useful for preventing and treating disorders associated with
 PT altered levels of the protein such as cancer, immune system disorders
 PT
 PS Claim 1; Page 78-79; 105pp; English.
 XX
 CC The present sequence is the human immunoglobulin superfamily protein
 CC IGFAM-2. Its gene was isolated from a cDNA library of thyroid tissue. It
 CC is expressed in reproductive, gastrointestinal and haematopoietic and
 CC immune tissue, where cancer and inflammation are common. The

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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 08:56:21 ; Search time 26.0666 Seconds
(without alignments)
4120.219 Million cell updates/sec

Title: US-08-728-463B-205
Perfect score: 743
Sequence: 1 ATGAACACTGTGGTCTTT.....CTGTGTCACCGTCTCTCTCAG 403

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 1816940

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DBV=xlp
-Q=/cgn2.1/USPTO.spool/US08728463/runat_03062003_085613_16797/app.query.fasta_1.3690
-DB=A_Geneseq_101002 -OPMS=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A_Geneseq_101002.*
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18: /SID22/gcgdata/geneseq/geneseq-embl/AA1997.DAT.*
19: /SID22/gcgdata/geneseq/geneseq-embl/AA1998.DAT.*
20: /SID22/gcgdata/geneseq/geneseq-embl/AA1999.DAT.*
21: /SID22/gcgdata/geneseq/geneseq-embl/AA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseq-embl/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-embl/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	680.5	91.6	139	21	AA999556	Human LH11238 mono
2	650	87.5	537	21	AA996290	Human IGFAM-2 immu
3	646	86.9	462	21	AA268884	Human immunoglobul
4	622	83.7	116	16	AA66324	Human immunoglobul
5	596.5	80.3	193	23	ABP43199	Human ovarian anti
6	595	80.1	472	17	AA993166	Anti-thesus D reco
7	592.5	79.7	133	23	ABG35331	Thrombopoietin ago
8	592.5	79.7	256	23	ABG35335	Thrombopoietin ago
9	592.5	79.7	266	23	ABG35336	Thrombopoietin ago
10	590.5	79.5	139	21	AA982628	Human PTHP monocl
11	588.5	79.2	249	23	ABP45310	Human Blys binding
12	578.5	77.9	473	22	AA36206	Human immune syste
13	578	77.8	123	17	AAW03757	Anti-rhesus D mono
14	565	76.0	142	14	AA41285	F105 rearranged va
15	564.5	76.0	139	21	AA964676	Human 5' EST relat
16	560.5	75.4	244	20	AA921883	Amino acid sequenc
17	558	75.1	241	22	AA46061	Human TP anti-idio
18	555.5	74.8	249	23	ABP44946	Human Blys binding
19	554.5	74.6	132	22	AA62249	Human gene 4-encod
20	554.5	74.6	141	22	AA62249	Human gene 4-encod
21	551	74.2	136	18	AAW24536	Immunoglobulin rB6
22	551	74.2	476	18	AAW01822	Immunoglobulin rB6
23	551	74.2	476	19	AAW63765	Macaque primatized
24	551	74.2	476	23	AAU11646	Protein sequence o
25	550.5	74.1	139	21	AA956713	Amino acid sequenc
26	550	74.0	116	16	AA42689	Vh 71-4. Homo sap
27	550	74.0	116	16	AA42689	Human immunoglobul
28	548.5	73.8	487	23	AB90607	Human secreted pro
29	548.5	73.8	487	23	AB90607	Human albumin fusi
30	543	73.1	255	23	ABP45631	Human Blys binding
31	541	72.8	470	21	AA44721	Anti-human Rhd FOM
32	540.5	72.7	128	12	AA12269	Human immune syste
33	540	72.6	253	23	ABP45322	Human Blys binding
34	539.5	72.6	254	23	ABP45648	Human Blys binding
35	539.5	72.6	507	21	AA996304	Human IGFAM-16 imm
36	539	72.5	118	16	AA66348	Human immunoglobul
37	538	72.4	116	16	AA66298	Human immunoglobul
38	536	72.1	121	12	AA12270	Anti-human Rhd FOM
39	535.5	72.1	141	21	AA956728	Amino acid sequenc
40	535.5	72.1	250	23	ABP45402	Human Blys binding
41	535	72.0	120	22	AB62758	Human HIV-1 monocl
42	534	71.9	140	18	AAW2477	Anti-CD4 cynomolgu
43	534	71.9	140	19	AAW4340	Monkey anti-CD4 he
44	534	71.9	141	14	AA931948	Anti-CD4 VH peptid
45	534	71.9	467	18	AAW14927	Human gamma-4PE he

ALIGNMENTS

RESULT 1
AA999556
ID AA999556 standard; Protein; 139 AA.
XX
AC AA999556;
XX
DT 20-SEP-2000 (first entry)
XX
DE Human LH11238 monoclonal antibody heavy chain variable region.
XX
KW Human; LH11238 monoclonal antibody; hybridoma; tumour-specific; cancer;
KW cytotoxic; cytotoxic; heavy chain variable region.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Signal_peptide
FT Protein 20..139

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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 7.64116 Seconds

(without alignments)
4373.264 Million cell updates/sec

Title: US-08-728-463B-205

Perfect score: 743

Sequence: 1 ATGAACACCTGTGGTCTTT.....CTGGTCACCGTCTCTCTG 403

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 225784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USPTO.spool/US08728463/runat_03062003_085614_16804/app.query.fasta_1.3690
-DB=SwissProt 40 -OPMT=fastan -SUFFIX=rsp -MINMATCH=0.1 -LOOPCI=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08728463 @CNG 1.1.76 @runat_03062003_085614_16804 -NCPV=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	579	77.9	146	1 HV21 HUMAN	P06331 homo sapien
2	402	54.1	129	1 HV2F HUMAN	P01824 homo sapien
3	396	53.3	117	1 HV2G HUMAN	P01825 homo sapien
4	393.5	53.0	137	1 HV46 MOUSE	P01822 mus musculus
5	370	49.8	116	1 HV60 MOUSE	P18531 mus musculus
6	358	48.2	144	1 HV43 MOUSE	P01819 mus musculus
7	354	47.6	113	1 HV47 MOUSE	P01823 mus musculus
8	343	46.2	116	1 HV61 MOUSE	P18532 mus musculus
9	336	45.2	135	1 HV02 XENLA	P20957 xenopus lae
10	326.5	43.9	117	1 HV62 MOUSE	P18533 mus musculus
11	326.5	43.9	119	1 HV38 MOUSE	P01808 mus musculus
12	326	43.4	138	1 HV48 MOUSE	P03960 mus musculus
13	322.5	43.4	139	1 HV07 MOUSE	P01751 mus musculus
14	321	43.2	117	1 HV41 MOUSE	P01811 mus musculus
15	318.5	42.9	147	1 HV2H HUMAN	P04438 homo sapien
16	317.5	42.7	119	1 HV37 MOUSE	P01807 mus musculus
17	316	42.5	115	1 HV44 MOUSE	P01820 mus musculus
18	314.5	42.3	119	1 HV40 MOUSE	P01810 mus musculus

19	311.5	41.9	136	1 HV01 XENLA	P20956 xenopus lae
20	311	41.9	142	1 HV01 RAT	P01805 rattus norv
21	308.5	41.5	137	1 HV11 MOUSE	P01755 mus musculus
22	308	41.5	118	1 HV39 MOUSE	P01809 mus musculus
23	305	41.0	117	1 HV12 MOUSE	P01756 mus musculus
24	304	40.9	116	1 HV45 MOUSE	P01821 mus musculus
25	303.5	40.8	120	1 HV50 MOUSE	P06329 mus musculus
26	300	40.4	117	1 HV13 MOUSE	P01757 mus musculus
27	298.5	40.2	114	1 HV3B HUMAN	P01763 homo sapien
28	296.5	39.9	122	1 HV3G HUMAN	P01768 homo sapien
29	294	39.6	121	1 HV01 MOUSE	P01745 mus musculus
30	293.5	39.5	118	1 HV51 MOUSE	P06330 mus musculus
31	290.5	39.1	117	1 HV04 MOUSE	P01748 mus musculus
32	288.5	38.8	120	1 HV2B HUMAN	P01815 homo sapien
33	288.5	38.8	122	1 HV3A HUMAN	P01762 homo sapien
34	288	38.8	117	1 HV42 MOUSE	P01812 mus musculus
35	288	38.8	123	1 HV25 MOUSE	P01794 mus musculus
36	287.5	38.7	116	1 HV36 MOUSE	P01806 mus musculus
37	287	38.6	115	1 HV3D HUMAN	P01765 homo sapien
38	287	38.6	116	1 HV05 CARAU	P19181 carassius a
39	287	38.6	140	1 HV02 MOUSE	P01746 mus musculus
40	286	38.5	119	1 HV3I HUMAN	P01770 homo sapien
41	285	38.4	121	1 HV3J HUMAN	P01771 homo sapien
42	284	38.2	117	1 HV17 MOUSE	P01786 mus musculus
43	282.5	38.0	122	1 HV20 MOUSE	P01789 mus musculus
44	281.5	37.9	117	1 HV09 MOUSE	P01753 mus musculus
45	281.5	37.9	117	1 HV3C HUMAN	P01764 homo sapien

ALIGNMENTS

RESULT 1
HV21 HUMAN
ID HV21 HUMAN STANDARD; PRT; 146 AA.
AC P06331;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region ARH-77 precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85205332; PubMed=3922855;
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT 'A cloned human immunoglobulin heavy chain gene with a novel direct-
repeat sequence in 5' flanking region.';
RL Gene 33:181-189(1985).
DR PIR; A02101; GIHUH2.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 146 IG HEAVY CHAIN V-II REGION ARH-77.
FT DOMAIN 20 117 V SEGMENT.
FT DOMAIN 118 127 D SEGMENT.
FT DOMAIN 128 146 J SEGMENT.
FT DISULFID 42 115 BY SIMILARITY.
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;
Alignment Scores:
Pred. No.: 2.19e-47 Length: 146
Score: 579.00 Matches: 118
Percent Similarity: 83.67% Conservative: 5
Best Local Similarity: 80.27% Mismatches: 11
Query Match: 77.93% Indels: 14
DB: 1 Gaps: 3

US-08-728-463B-205 (1-403) x HV2I_HUMAN (1-146)

DB: 1 Gaps: 2

US-08-728-463B-205 (1-403) x HV2F_HUMAN (1-129)

QY 58 CAGGTGCAGCTACAGCAGTGGGGCGGCGAGCTGTTGAACCTTCGAGACCTGTCCTCCTC 117

Db 1 ArgLeuGlnLeuGlnSerGlyProGlyLeuValLysProSerGluThrLeuSerLeu 20

QY 118 ACTCTGCCTGCTCTATGCTGGTCCCTTC-----AGTGGTTACTACTGAGCTGGATCCGC 171

Db 21 ThrCysAlaValSerGlyGlyProLeuArgThrGlyTyrtTyrTrpGlyTrpLeuArg 40

QY 172 CAGCCCCCAGCTAAGCGCTCGAGTGGATTTGGGAAATCAATCATAGTGAAGACCAAC 231

Db 41 GlnProProGlyLeuGlnLeuGlnLeuGlnLeuGlnLeuGlnLeuGlnLeuGlnLeu 60

QY 232 TACAACCCCTCCCTCAAGAGTCGAGTCACCATATCAGTCGACAGCTCCCAAGACCACTTC 291

Db 61 TyrAsnProSerLeuArgGlyValThrIleSerValAspThrSerArgAsnGlnPhe 80

QY 292 TCCTGAAGCTGAGCTCTGTGACCCCGCGACACGGCTGTGTATTACTGTGCGAGA--- 348

Db 81 SerLeuAsnLeuArgSerMetSerAlaAlaAspThrAlaMetTyrTyrCysAlaArgGly 100

QY 349 -----GTAATTAATTGGTTCGACCCCTGGGGC 375

Db 101 AsnProProTyrTyrAspIleGlyThrGlySerAspGlyIleAspValTrpGly 120

QY 376 CAGGGAACCTGGTCCACCTCTCTCA 402

Db 121 GlnGlyThrThrValHisValSerSer 129

RESULT 3

HV2G_HUMAN STANDARD; PRT; 117 AA.

ID HV2G_HUMAN

AC P01825;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DE 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V-II region NEMM.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=77242302; PubMed=407927;

RA Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;

RT "Amino acid sequence of the VH region of a human myeloma immunoglobulin (IgG New).";

RL Biochemistry 16:3412-3420(1977).

RN [2]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.

RX MEDLINE=78066916; PubMed=618887;

RA Saul F.A., Anzel L.M., Poljak R.J.;

RT "Preliminary refinement and structural analysis of the Fab fragment from human immunoglobulin new at 2.0-A resolution.";

RL J. Biol. Chem. 253:585-597(1978).

CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA PROTEIN.

DR PIR; A02100; GIHUNM.

DR PDB; 7FAB; 31-JAN-94.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IgV; 1.

KW Immunoglobulin V-region; 3D-structure.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT STRAND 3 7

FT STRAND 11 12

FT TURN 14 15

FT STRAND 18 25

FT TURN 30 31

US-08-728-463B-205 (1-403) x HV2I_HUMAN (1-146)

QY 1 ATGAACACCTGTGTTCTTCT 56

Db 1 MetLysHisLeuTrpPheLeuLeuLeu-Leu-TrpCysGlnLeuProAspValGlyValLeuSe 20

QY 57 CCAGGTGCAGCTACAGCAGTGGGGCGGCGAGCTGTTGAACCTTCGAGACCTGTCCTCCT 116

Db 20 rGlnValGlnLeuGlnGlnTrpGlyAlaGlyLeuValLysProSerGluThrLeuSerLeu 40

QY 117 CACCTGCGCTGCTCTATGCTGGTCCCTTCAGTGGTCTACTGAGCTGGATCCGCAGCC 176

Db 40 uThrCysAlaValPheGlyGlySerPheSerGlyTyrtTyrTrpSerTrpIleArgGlnPr 60

QY 177 CCCAGGTAAGGGCTGAGTGGATTTGGGAAATCAATCATAGTGAAGACCACTACNA 236

Db 60 oProGlyArgGlyLeuGlnTrpIleGlyGlnLeuHisSerGlySerThrAsnTrpLys 80

QY 237 CCGTCCCTCAAGAGTCGAGTCACCATATCAGTCGACAGCTCCCAAGAACCTCTCCT 296

Db 80 sThrSerLeuLysSerArgValThrIleSerLeuAspThrSerLysAsnLeuPheSerLe 100

QY 297 GAAGCTGAGCTCTGTGACCCCGCGACACGGCTGTGTATTACTGTGCGAGTAATT-- 354

Db 100 uLysLeuSerSerValThrAlaAlaAspThrAlaValTyrCysAlaAaArgGlyLeuLe 120

QY 355 -----AATGG-----TTCCGACCCCTGGGCGCAGGGAAC 383

Db 120 uArgGlyGlyTrpAsnAspValAspTyrTyrTyrGlyMetAspValTrpGlyGlnGlyTh 140

QY 384 CTTGGTCCACCTCTCTCA 402

Db 140 rThrValThrValSerSer 146

RESULT 2

HV2F_HUMAN STANDARD; PRT; 129 AA.

ID HV2F_HUMAN

AC P01824;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DE 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V-II region WAH.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=82222235; PubMed=6806818;

RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;

RT "Complete amino acid sequence of the delta heavy chain of human immunoglobulin D.";

RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).

CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA PROTEIN.

DR PIR; A02099; D2HUWA.

DR HSSP; P01825; 7FAB.

DR GlycoSuiteDB; P01824;

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IgV; 1.

KW Immunoglobulin V region.

NON TER 129 129

SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Alignment Scores:

Pred. No.: 1.45e-30 Length: 129

Score: 402.00 Matches: 80

Percent Similarity: 72.87% Conservative: 14

Best-Local Similarity: 62.02% Mismatches: 21

Query Match: 54.10% Indels: 14

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FT STRAND 33 39
FT TURN 41 42
FT STRAND 46 51
FT TURN 53 54
FT STRAND 57 59
FT HELIX 61 63
FT TURN 64 66
FT STRAND 67 72
FT TURN 73 76
FT STRAND 77 82
FT HELIX 87 89
FT STRAND 91 98
FT STRAND 104 107
FT STRAND 111 115
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12790 MW; 2DA47B509562D237 CRC64;

Alignment Scores:
Pred. No.: 5 33e-30 Length: 117
Score: 396.00 Matches: 76
Percent Similarity: 81.20% Conservatives: 19
Best Local Similarity: 64.96% Mismatches: 20
Query Match: 53.30% Indels: 2
DB: 1 Gaps: 1

US-08-728-463B-205 (1-403) x HV2G_HUMAN (1-117)

QY 58 CAGGTGACAGTACAGCAGTGGCGGCGAGGACTGTTGAAGCTTCGGAGACCCCTGTCCCTC 117
Db 1 GlnValGlnLeuGlnSerGlyProGlyLeuValArgProSerGlnThrLeuSerLeu 20
QY 118 ACCTGGCTGTCTATGGTGGTCCCTCAGTGGTTACTACTGAGAGCTGGATCCGCCAGCCC 177
Db 21 ThrCysThrValSerGlySerThrPheSerAsnAspTyrThrTrpValArgGlnPro 40
QY 178 CCAGGTAAAGGGCTGGAGTGGTGGGAATCAATCATAGTAGTGAAGCACCACCACTACAAC 237
Db 41 ProGlyArgGlyLeuGlnTrpIleGlyTyrValPheTyrHisGlyThrSerAspThr 60
QY 238 CCCTCCCTCAAGAGTCCAGTCCACCATATCATGTCGACAGCTCCAGAACACCATGTTCTCCCTG 297
Db 61 ThrProLeuArgSerArgValThrMetLeuValAspThrSerIysAsnGlnPheSerLeu 80
QY 298 AAGCTGAGCTCTGTGACCGCGCGGACACGGCTGTGTATTAATCTGTCGAGA-----GTA 351
Db 81 ArgLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgAsnLeuIle 100
QY 352 ATTAATTTGGTTCCACCCCTGGGCGCCAGGACCCCTGTCACCGTCTCCCTCA 402
Db 101 AlaGlyCysIleAspValTrpGlyGlnGlySerLeuValThrValSerSer 117

RESULT 4
HV46 MOUSE STANDARD; PRT; 137 AA.
AC P01822;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig heavy chain V region MOPC 315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89238351; PubMed=2497341;
RA Rinfret A., Horne C., Dorrington K.J., Klein M.;
RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH
RT gene segment.";
RL Mol. Immunol. 26:431-434 (1989).
RN [2]
RP SEQUENCE OF 1-31.
RX MEDLINE=78094475; PubMed=414225;
```

```
RA Jilka R.L., Pestka S.;
RT "Amino acid sequence of the precursor region of MOPC-315 mouse
RT immunoglobulin heavy chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696 (1977).
RN [3]
RP SEQUENCE OF 1-21.
RX MEDLINE=79148758; PubMed=428562;
RA Schechter I., Wolf O., Zemell R., Burstein Y.;
RT "Structure and function of immunoglobulin genes and precursors.";
RL Fed. Proc. 38:1839-1845 (1979).
RN [4]
RP SEQUENCE OF 19-136.
RX MEDLINE=74170779; PubMed=4524622;
RA Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.;
RT "Amino-acid sequence of the variable region of the heavy (alpha)
RT chain of a mouse myeloma protein with anti-hapten activity.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127 (1974).
RN [5]
RP REVISION TO 53.
RX MEDLINE=77244979; PubMed=268248;
RA Hood L., Margolies M.N., Givol D., Zakut R.;
RL Unpublished results, cited by:
RL Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
RL Cold Spring Harb. Symp. Quant. Biol. 41:627-637 (1977).
CC -!- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; M27638; AAA61337.1; -
DR EMBL; X07880; CAA30727.1; -
DR PIR; P0102; AVMS35.
DR HSP; P01825; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 137 IG HEAVY CHAIN V REGION MOPC 315.
FT DOMAIN 19 48 FRAMEWORK-1.
FT DOMAIN 49 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 85 116 FRAMEWORK-3.
FT DOMAIN 117 126 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 127 137 FRAMEWORK-4.
FT DISULFID 40 114 BY SIMILARITY.
FT CONFLICT 15 15 G -> GG (IN REF. 1; CAA30727).
FT CONFLICT 15 15 G -> H (IN REF. 2).
FT CONFLICT 77 78 GV -> YG (IN REF. 4).
FT CONFLICT 102 102 N -> D (IN REF. 4).
FT CONFLICT 123 123 MISSING (IN REF. 4).
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15399 MW; FB3828304C2B81DC CRC64;

Alignment Scores:
Pred. No.: 9 36e-30 Length: 137
Score: 393.50 Matches: 82
Percent Similarity: 73.19% Conservatives: 19
Best Local Similarity: 59.42% Mismatches: 32
Query Match: 52.96% Indels: 5
DB: 1 Gaps: 3

US-08-728-463B-205 (1-403) x HV46_MOUSE (1-137)

QY 1 ATGAACACCTGTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCCAG 60
```

```

Db      1 MetLysValLeuSerLeuLeuTyrLeuLeuThrAlaIlePro---GlyIleMetSerAsp 19
      61 GTGAGCTACAGCAGTGGGGCGGAGCTGTGTGAGCCCTCGGAGACCCCTGCTCCCTCACC 120
      20 ValGlnLeuGlnSerGlyProGlyLeuValLysProSerGlnSerLeuLeuThr 39
      121 TGCCTGTCTATGTTGGTCTCTTC---AGTGGTTACTACTGGAGCTGGATCCGCCAGCCC 177
      40 CysSerValThrGlyTyrSerIleThrSerGlyTyrPheTyrPheTyrPheTyrPhe 59
      178 CCAGTAAGGGCTGGAGTGGGAAATCAATCATAGTGAAGCACCACCACTACAAC 237
      60 ProGlyAsnLysLeuGlnLysLeuGlyPheIleLysTyrAspGlySerAsnGlyTyrAsn 79
      238 CCGTCCCTCAAGAGTCGAGTCAACATATCAGTCGACAGCTGCAAGAACCCAGTCTCCCTG 297
      80 ProSerLeuLysAsnArgValSerIleThrArgAspThrSerGluAsnGlnPheLeu 99
      298 AAGCTGAGCTCTGTGACCGCGGACACGCTGTGTATTACTGTGCG-----AGA 348
      100 LysLeuAsnSerValThrGluAspThrAlaThrTyrTyrCysAlaGlyAspAsnAsp 119
      349 GTAATTATTCGTCGACCCCTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 402
      120 HisLeuTyrTyrPheAspTyrTrpGlyGlnGlyThrThrThrValSerSer 137

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RESULT 5

```

HV60 MOUSE
ID HV60 MOUSE STANDARD; PRT; 116 AA.
AC P18531.
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region M315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
DR PIR; JTO509; HVM531.
DR HSP; P01825; 7FAB.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 116 IG HEAVY CHAIN V REGION M315.
FT DOMAIN 19 48 FRAMEWORK-1.
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 54 67 FRAMEWORK-2.
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 85 116 FRAMEWORK-3.
FT DISULFID 40 114 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 13095 MW; 4562E03B53DC9E10 CRC64;

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Alignment Scores:

```

Pred. No.: 1.58e-27 Length: 116
Score: 370.00 Matches: 75
Percent Similarity: 76.92% Conservative: 15
Best Local Similarity: 64.10% Mismatches: 25
Query Match: 49.80% Indels: 2
DB: 1 Gaps: 2

```

```

US-08-728-463B-205 (1-403) x HV60_MOUSE (1-116).
QY      1 ATGAACACACTGGTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCCAG 60
      1 MetLysValLeuSerLeuLeuTyrLeuLeuThrAlaIlePro---GlyIleLeuSerAsp 19
      61 GTCAGCTACAGCAGTGGGGCGGAGCTGTGTGAGCCCTCGGAGACCCCTGCTCCCTCACC 120
      20 ValGlnLeuGlnSerGlyProGlyLeuValLysProSerGlnSerLeuLeuThr 39
      121 TGCCTGTCTATGTTGGTCTCTTC---AGTGGTTACTACTGGAGCTGGATCCGCCAGCCC 177
      40 CysSerValThrGlyTyrSerIleThrSerGlyTyrTyrTyrPheTyrPheTyrPhe 59
      178 CCAGTAAGGGCTGGAGTGGGAAATCAATCATAGTGAAGCACCACCACTACAAC 237
      60 ProGlyAsnLysLeuGlnLysLeuGlyPheIleLysTyrAspGlySerAsnGlyTyrAsn 79
      238 CCGTCCCTCAAGAGTCGAGTCAACATATCAGTCGACAGCTGCAAGAACCCAGTCTCCCTG 297
      80 ProSerLeuLysAsnArgIleSerIleThrArgAspThrSerLysAsnGlnPheLeu 99
      298 AAGCTGAGCTCTGTGACCGCGGACACGCTGTGTATTACTGTGCGGAGA 348
      100 LysLeuAsnSerValThrGluAspThrAlaThrTyrTyrCysAlaArg 116

```

RESULT 6

```

HV43 MOUSE
ID HV43 MOUSE STANDARD; PRT; 144 AA.
AC P01819.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ig heavy chain V region MOPC 141 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=81012133; PubMed=6774258;
RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT "Two types of somatic recombination are necessary for the generation
of complete immunoglobulin heavy-chain genes.";
RL Nature 286:676-683(1980).
CC -! MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC EMBL; V00768; CAA24149.1; -.
CC PIR; A02094; G2M314.
CC HSP; P01825; 7FAB.
CC InterPro; IPR003006; Ig MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGv; 1.
CC Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 144 IG HEAVY CHAIN V REGION MOPC 141.
FT NON_TER 144 144
SQ SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;

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Alignment Scores:

```

Pred. No.: 2.23e-26 Length: 144
Score: 358.00 Matches: 74
Percent Similarity: 66.67% Conservative: 22

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FT NON TER 117 117
SQ SEQUENCE 117 AA; 13223 MW; 1595517827F976BE CRC64;

Alignment Scores:
Pred. No.: 2,16e-23 Length: 117
Score: 326.50 Matches: 68
Percent Similarity: 70.34% Conservativeness: 15
Best Local Similarity: 57.63% Mismatches: 32
Query Match: 43.94% Indels: 3
DB: 1 Gaps: 2

US-08-728-463B-205 (1-403) x HV62_MOUSE (1-117)
QY 1 ATCAACACCTGGTTCCTCTCCTGCTGGCGAGCTCCAGATGGTCTGTCTCCAG 60
Dy 1 MetLysMetPheThrLeuLeuLeuLeuLeuValPro---GlyIleLeuSerAsp 19
QY 61 GTCAGCTACAGCAGTGGCGCGAGGACTGTTCAAGCTTTCGGAGACCCCTGCTCCCTCACC 120
Dy 20 ValGlnLeuGlnSerGlyProGlyLeuValLysProSerGlnSerIleAlaLeuThr 39
QY 121 TGGCTGTCTATGGTGGTCTCTTCACTG-----GGTTACTACTGGAGCTGGATCCGCCAG 174
Dy 40 CysThrValThrGlyIleSerIleThrThrGlyAsnFyrArgTrpSerTrpIleA-gGln 59
QY 175 CCCCCAGCTAAGGGCTGGAGTGGTGGGAATCAATCATAGTGAAGCACCACCACTAC 234
Dy 60 PheProGlyAsnLysLeuGluTrpIleGlyIleFyrIleFyrSerAlaIleThrSertyr 79
QY 235 AACCCGTCTCCTCAAGAGTGGAGTCCACATATAGTCGACACGCTCCAGAACACCACTCTCC 294
Dy 80 AsnProSerProLysSerArgThrThrIleThrArgAspThrSerLysAsnGlnPhePhe 99
QY 295 CTGAAGCTAGCTCTGTGACCGCGGACACAGCTGTGTATTACTGTGGAGA 348
Dy 100 LeuGluMetAsnSerLeuThrAlaGluAspThrAlaThrFyrCysAlaArg 117

RESULT 11
HV38_MOUSE
ID HV38_MOUSE STANDARD; PRT; 119 AA.
AC P01808;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region T601.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79223895; PubMed=111245;
RA Rao D.N., Rudikoff S., Kruttsch H., Potter M.;
RT "Structural evidence for independent joining region gene in
RT immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT its potential role in generating diversity in
RT complementarity-determining regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894 (1979).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC THAT BINDS GALACTAN.
DR PIR; A02078; AWMST6.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON TER 119
SQ SEQUENCE 119 AA; 13169 MW; BC38C84E6EA00E8 CRC64;

Alignment Scores:
Pred. No.: 2,16e-23 Length: 119
Score: 326.50 Matches: 65

US-08-728-463B-205 (1-403) x HV38_MOUSE (1-119)
QY 58 CAGGTGACGCTACAGCAGTGGGGCGGAGACTGTGTGAAGCCTTCGGAGACCCCTGTCCCTC 117
Dy 1 GluValLysLeuLeuLeuSerGlyGlyGlyLeuValGlnProGlyGlySerLeuLysLeu 20
QY 118 ACCTGGCTGTCTATGGTGGTCTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 177
Dy 21 SerCysAlaAlaSerGlyPheAspPheSerArgTrpMetSerTrpValArgGlnAla 40
QY 178 CCAGGTAAAGGGCTGGAGTGGGAAATCAATCATAGTGAAGACACC---AACTAC 234
Dy 41 ProGlyLysGlyLeuGluTrpIleGlyGluIleAsnProAspSerSerThrIleAsnTyr 60
QY 235 AACCCGTCTCCTCAAGAGTGGAGTCCACATATAGTCGACACGCTCCAGAACACCACTCTCC 294
Dy 61 ThrProSerLeuLysAspLysPheIleIleSerArgAspAsnAlaLysAsnThrLeuTyr 80
QY 295 CTGAAGCTAGCTCTGTGACCGCGGACACGGCTGTGTATTACTGTGGAGAGTA--- 351
Dy 81 LeuGlnMetSerLysValArgSerGluAspThrAlaLeuTyrFyrCysAlaArgLeuGly 100
QY 352 ---ATTAAATGTGTCACCCCTGGGCGGACGAGAACCCCTGCTCACCGCTCTCTCA 402
Dy 101 TyrTyrGlyTyrPheAspValTrpGlyAlaGlyThrThrValThrValSerSer 118

RESULT 12
HV48_MOUSE
ID HV48_MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region TEPC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RT delta in an Igd-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168 (1984).
DR PIR; A02033; HVMST7.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 1 138 IG HEAVY CHAIN V REGION TEPC 1017.
FT DOMAIN 21 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 128 138 FRAMEWORK-4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Alignment Scores:
Pred. No.: 2,44e-23 Length: 138

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DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin v region; Signal.
FT SIGNAL 1
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Alignment Scores:
Pred. No.: 5,26e-23 Length: 139
Score: 322.50 Matches: 65
Percent Similarity: 67.42% Conservative: 34
Best Local Similarity: 49.24% Mismatches: 28
Query Watch: 43.41% Indels: 5
DB: 1 Gaps: 2

US-08-728-463B-205 (1-403) x HV07_MOUSE (1-139)

Qy	22	CTCTCTGGTGGCGAGCTCCGACATGGGTCTGTGCCAGGTGCAGCTACAGCAGTGCGGC	81
Db	8	LeuPheLeuAlaAleThraLathrGlyValHisSerGlnValGlnLeuGlnProGly	27
Qy	82	GCAGGAGCTTCGAAGCCTTCGGAGACCCTGTCCTCACCTGCGCTGTCTATGGTGGGTCC	141
Db	28	AlaGlueValVallyProGlyAlaSerVallyLeuSerCysLySAlaSerGlyTyThr	47
Qy	142	TTCAGTGGTTACTATGGAGCTGGATCGCGAGCCCCAGGTAAAGGGCTGGAGTGATT	201
Db	48	PheThrSerTyTrpMetHisTrpVallyGlnArgProGlyArgGlyLeuGluTrpIle	67
Qy	202	GCGGAATCAAT--CATAGTGAAGACCAACAACCCGCTCCCTCAAGAGTCGAGTC	258
Db	68	GlyArgIleAspProAsnSerGlyGlyThrLysTyraSnGluLysPheLySerLySAla	87
Qy	259	ACCATATCAGTCACACAGCTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCC	318
Db	88	ThrLeuThrValAspLysProSerSerThrAlaTyMetGlnLeuSerSerLeuThrSer	107
Qy	319	GCGGACAGCGCTCTATTACTGTGCGAGACTA-----ATTATTCGTTCCGAC	366
Db	108	GluApSerAlaValTyTyCyAlaArgTyraPyrTyTyGlySerSerTyPheAsp	177
Qy	367	CCTCGGGCGCAGGAACCTGGTCACCGCTCTCTCA 402	
Db	128	TyrTrpGlyGlnGlyThrThrLeuThrValSerSer 139	

RESULT 14
HV41_MOUSE
ID HV41_MOUSE STANDARD; PRT; 117 AA.
AC P01811;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig heavy chain V region UPC10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83021113; PubMed=6181731;
RA Auffray C., Skorav J.L., Ollo R., Rougeon F.;
RT "Correlation between D region structure and antigen-binding
specificity: evidences from the comparison of closely related


```
RT immunoglobulin VH sequences";
RL Ann. Immunol. (Paris) 132D:77-88(1981).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IG GAMMA-2A MYELOMA
CC PROTEIN BINDING 2,6-LEVAN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M36631; AAA38078.1; --
CC PIR; A02081; G2MSUL.
CC HSSP; P01810; 2FBJ.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00047; Ig_1.
CC SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 117
FT SEQUENCE 117 AA; 13001 MW; B20A1074F8B99B7F CRC64;
Alignment Scores:
Pred. No.: 7.18e-23 Length: 117
Score: 321.00 Matches: 65
Percent Similarity: 68.91% Conservatives: 17
Best Local Similarity: 54.62% Mismatches: 31
Query Match: 43.20% Indels: 6
DB: 1 Gaps: 3
US-08-728-463B-205 (1-403) x HV41_MOUSE (1-117)
QY 58 CAGGTGAGTACAGAGTGGCGGAGGAGTCTTGAAGCTTCGGAGACCTGTCCCTC 117
DB 1 GluValysLeuLeuGluSerGlyGlyGlyLeuValGlnProGlySerLeuLysLeu 20
QY 118 ACTGCGCTGTCTATGGTGGGTCCTTCAGTGGTACTACTGGAGCTGGATCCGCCAGCCC 177
DB 21 SerCysAlaAlaSerGlyPheAspPheSerGlyTyr-TripMetSerTrpValArgGlnAla 40
QY 178 CCAGGTAAGGGCTGAGTGGATTTGGGAATCAATCATAGTGAAGACCC---AACTAC 234
DB 41 ProGlyLysGlyLeuGluTrpIleGlyGlyLeuAsnProAspSerThrIleAsnTyr 60
QY 235 AACCCGTCTCCTCAAGAGTCCAGTCCACATATCAGTCGACACGTCGAAGAACCCAGTTCTCC 294
DB 61 ThrProPheLeuLysAspLysPheIleIleSerArgAspAsnAlaLysAsnThrLeuPhe 80
QY 295 CTGAAGCTGAGCTCTGTGACCGCGCGGACACGGCTGTGTATTACTGTGCGAGAGTAATT 354
DB 81 LeuGlnMetSerLysValArgSerGluAspThrAlaLeuTyrPheCysAlaArg----- 98
QY 355 AATTGG-----TTGACCCCTGGGCGCCAGGAAACCTGTGTACCGTCTCCTCA 402
DB 99 AsnTrpAspValGlyPheAspTyrTrpGlyGlnValThrThrLeuThrValSerSer 117
RESULT 15
ID HV2H_HUMAN STANDARD; PRT; 147 AA.
AC P04438;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region SESS precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN NCBI_TaxID=9606;
RX MEDLINE=84298107; PubMed=6089186;
```

```
RA Takahashi N., Noma T., Honjo T.;
RT "Rearranged immunoglobulin heavy chain variable region (VH)
RT pseudogene that deletes the second complementarity-determining
RT region.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5194-5198(1984).
DR PIR; A02090; G2HUUS.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 147 IG HEAVY CHAIN V-II REGION SESS.
FT DOMAIN 20 118 V SEGMENT.
FT DOMAIN 119 132 D SEGMENT.
FT DOMAIN 133 147 J SEGMENT.
FT NON_TER 147
FT SEQUENCE 147 AA; 16323 MW; FCBDB3D00FB6666 CRC64;
Alignment Scores:
Pred. No.: 1.27e-22 Length: 147
Score: 318.50 Matches: 71
Percent Similarity: 62.41% Conservatives: 17
Best Local Similarity: 50.35% Mismatches: 39
Query Match: 42.87% Indels: 14
DB: 1 Gaps: 2
US-08-728-463B-205 (1-403) x HV2H_HUMAN (1-147)
QY 22 CTCCTCTGTGTGGAGCTCCAGAGTGGTCTGTCTCCAGGTGAGTACAGAGTGGGCG 81
DB 8 LeuLeuLeuLeuThrValProSerGlyValLeuSerGlnValAsnLeuArgGluSerGly 27
QY 82 CGAGGACTGTTCAAGCCTTCGGAGACCTGTCCCTCACCTGCGCTGTCTATGTGGTGC 141
DB 28 ProAlaLeuValLysAlaThrHisThrLeuThrLeuThrCysThrPheSerGlyLeuSer 47
QY 142 TTCAGT-----GGTTACTACTGGAGCTGGATCCGCCAGCCCCCAGGTAAAGGGCTGGAG 195
DB 48 ValAsnThrArgGlyMetSerValSerTrpIleArgGlnProProGlyLysAlaLeuGlu 67
QY 196 TGGATTGGGGAATCAATCATATAGTGAAGCACCACCACTACACCCGTCCTCAAGAGTCGA 255
DB 68 TrpLeuAlaAlaArgIleAspTrpAspAspLysTyrTyrGlyThrSerLeuGluThrArg 87
QY 256 GTCACCATATCAGTCGACACGTCGAAGACCAAGTTCCTCCCTGAAGCTGAGCTGTGACC 315
DB 88 LeuThrIleSerLysAspThrSerLysAsnGlnValValLeuLysValThrAsnMetAsp 107
QY 316 GCGCGGACACCGCTGTGTATTACTGTGCGAGAGTA----- 351
DB 108 ProAlaAspThrAlaThrTyrTyrCysAlaArgMetGlnValThrMetValArgGluVal 127
QY 352 -----ATTAAATTGGTTCCACCCCTGGGCGCCAGGAAACCTGTGTACCGTCTCCTCA 402
DB 128 MetIleThrSerAsnAlaPheAspIleTrpGlyGlnGlyThr-TripSerProSerLeuGly 147
QY 403 G 403
DB 147 n 147
Search completed: June 3, 2003, 09:04:01
Job time : 9.64416 secs
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Db 121 SerSer 122

RESULT 12

Q1X92

ID Q1X92 PRELIMINARY; PRT; 482 AA.

AC Q1X92, 2001 (T-EMBLrel. 19, Created)

DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)

DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)

DE Unknown (protein for MGC:18822).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=COLON;

RA Strausberg R.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC011181; AAH11181.1; -

DR InterPro; IPR003006; IG_MHC.

DR Pfam; PF00047; ig: 4.

DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.

SQ SEQUENCE 482 AA; 51865 MW; 312E01F9C1BC7F3C CRC64;

Alignment Scores:

Pred. No.:	1-09e-27	Length:	482
Score:	355.50	Matches:	75
Percent Similarity:	67.88%	Conservative:	18
Best Local Similarity:	54.74%	Mismatches:	41
Query Match:	47.85%	Indels:	3
DB:	11	Gaps:	1

US-08-728-4638-205 (1-403) x Q1X92 (1-482)

QY 1 ATGAACACCTGTGGTTCTTCTCTCTGTGGCAGCTCCAGATGGTCTGTCTCCAG 120

Db 1 MetAlaValLeuAlaLeuLeuLeuValThrPheProSerCysAlaLeuSerGln 20

QY 61 GTGCAGCTACACAGCTGGGGCCGAGGACTGTGAAGCTTCGGAGACCCTGTCCCTCACC 120

Db 21 ValGlnLeuLeuGluSerGlyProAspLeuAlaProSerGlnSerLeuSerIleThr 40

QY 121 TCGCGTGTCTATGTGGGTCTCTTACGTGGTGTACTGTGGAGCTGGACCGCCAGCCCCA 180

Db 41 CysThrValSerGlyPheAlaLeuThrSerTyrAlaIleSerTrpValArgGlnPro 60

QY 181 GGTAGGGGCTGGAGTGGGAATCAATCATAGTGGAGCACCACCTACACCCG 240

Db 61 GlyLeuGlyLeuGlnTrpLeuGlyValIleTrpThrGlyGlyValThrAsnTyrAsnSer 80

QY 241 TCCCTCAGAGTCGAGTACCATTATCAGTCAGCAGCTCCAGAACACAGTTCTCCCTGAAG 300

Db 81 AlaLeuLeuSerArgLeuSerIleSerIlyAspAsnSerIlySerGlnValPheLeuLeu 100

QY 301 CTGAGCTCTGTGACCGCGGACACGCGTGTGATTACTGTGGAGAGTAAATTAATTCG 360

Db 101 MetAsnSerLeuGlnThrAsnAspIleAlaArgTyrTyrCysAlaArgAspSerAsnTyr 120

QY 361 -----TTGACCCCTGGGGCAGGGAACCTGTGTACCTCACCCTCTCCCTCA 402

Db 121 GluGlyAlaMetAspTyrTrpGlyGlnGlyThrSerValThrValSerSer 137

RESULT 13

Q8VCX7

ID Q8VCX7 PRELIMINARY; PRT; 613 AA.

AC Q8VCX7;

DT 01-MAR-2002 (T-EMBLrel. 20, Created)

DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)

DE Hypothetical 67.9 kDa protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

US-08-728-463B-205 (1-403) x Q99M22 (1-479)

.....

Alignment Scores:

US-08-728-463B-205 (1-403) x 09UL75 (1-122)

•

```

Db      1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20
QY      61 GTGACGCTACAGCAGTGGGGCGCAGGACTGTGTGAAGCCTTCGGAGACCTGTCTCCCTACC 120
Db      21 LeuGlnLeuGlnGluSerGlyProGlyLeuValLysSerSerGluThrLeuSerLeuThr 40
QY      121 TGGCGTGTCTATGGTGGGTCTCTTC-----AGTGGTTACTACTGGAGCTGGATCCGCCAG 174
Db      41 CysThrValSerGlyGlySerIleSerSerSerSerTyrtTrpGlyTrpIleArgGln 60
QY      175 CCCCAGGTAAAGGGCTCGAGTGGATTGGGGAATCAATCATAGTGGAGCACCACCACTAC 234
Db      61 ProProGlyLysGlyLeuGluTrpIleAlaSerThrTyrtTrpSerGlyIleThrTyrtTr 80
QY      235 AACCGTCCCTCAAGAGTCGAGTCACCATATCAGTCGACACGTCACCAAGAACCACTCTCC 294
Db      81 AsnProSerLeuLysSerArgValThrIleSerValAlaSerThrSerLysAsnGlnLeuSer 100
QY      295 CTGAAGCTGAGCTCTGTGACCGCGCGGACACGGCTGTGTATTACTGTGGGAGA----- 348
Db      101 LeuLysValArgSerValThrAlaAlaAspThrAlaValTyrtPheCysAlaArgHisGly 120
QY      349 -----GTAATTAATTGGTTCCACCCCTGGGCGCAGGGAACCCCTGGTCACC 393
Db      121 TyrSerArgSerGlyArgThrGlyAlaIleAspTyrtTrpGlyGlnGlyThrLeuValThr 140
QY      394 GTCTCCTCA 402
Db      141 ValSerSer 143

```

RESULT 8

```

ID Q9UL73 PRELIMINARY; PRT; 119 AA.
AC Q9UL73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035041; AAD56277.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13219 MW; 1BD86B6420EA08E CRC64;

```

Alignment Scores:

```

Pred. No.: 1.19e-41 Length: 119
Score: 491.00 Matches: 95
Percent Similarity: 85.71% Conservative: 7
Best Local Similarity: 79.83% Mismatches: 13
Query Match: 66.08% Indels: 4
DB: 4 Gaps: 1

```

US-08-728-463b-205 (1-403) x Q9UL73 (1-119)

```

QY      58 CAGGTGACGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCTGTCTCCCTC 117

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```

Db      1 GlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeu 20
QY      118 ACCTGGCGTGTCTATGGTGGGTCTCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCC 177
Db      21 ThrCysThrValSerGlyGlySerIleCysSerSerTyrtTrpSerTrpIleArgGlnPro 40
QY      178 CCAGGTAAGGGCTCGAGTGGATTGGGGAATCAATCATAGTGAAGCACCACCACTACAAC 237
Db      41 ProGlyLysGlyLeuGluTrpIleGlyTyrtTrpIleTyrtTrpSerThrAsnTyrtTr 60
QY      238 CCGTCCCTCAAGAGTCGAGTCACCATATCAGTCGACACGTCACCAAGAACCACTGTCTCCCTG 297
Db      61 ProSerLeuLysSerArgValThrIleSerValAspArgSerLysAsnGlnPheSerLeu 80
QY      298 AAGCTGAGCTCTGTGACCGCGCGGACACGGCTGTGTATTACTGTGGAGAGTAATTAAT 357
Db      81 LysLeuThrSerLeuThrAlaAlaAspThrAlaValTyrtPheCysAlaArgLeuSerAsn 100
QY      358 TGG-----TTCGACCCCTGGGCGCAGGGAACCCCTGGTCACCCGTCTCTCA 402
Db      101 TrpGlyProTyrtTrpPheAspTyrtTrpGlyGlnGlyThrLeuValThrValSerSer 119

```

RESULT 9

```

ID Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 52.0 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

```

Alignment Scores:

```

Pred. No.: 1.75e-41 Length: 473
Score: 490.50 Matches: 97
Percent Similarity: 78.93% Conservative: 12
Best Local Similarity: 70.23% Mismatches: 24
Query Match: 66.02% Indels: 5
DB: 4 Gaps: 2

```

US-08-728-463b-205 (1-403) x Q8TC63 (1-473)

```

QY      1 ATGAACACCTGTGGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
Db      8 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerArg 27
QY      61 GTGACGCTACAGCAGTGGGGCGCAGGACTGTGTGAAGCCTTCGGAGACCTGTCTCCCTACC 120
Db      28 LeuGlnLeuGlnGluSerGlyProGlyLeuLysProSerValThrLeuSerLeuThr 47
QY      121 TGGCGTGTCTATGGTGGGTCTCTTC-----AGTGGTTACTACTGGAGCTGGATCCGCCAG 174
Db      48 CysThrValSerGlyAspSerValAlaSerSerSerTyrtTrpGlyTrpValArgGln 67
QY      175 CCCCAGGTAAAGGGCTCGAGTGGATTGGGGAATCAATCATAGTGGAGCACCACCACTAC 234
Db      68 ProProGlyLysGlyLeuGluTrpIleGlyThrIleAsnPheSerGlyAsnMetTyrtTr 87
QY      235 AACCGTCCCTCAAGAGTCGAGTCACCATATCAGTCGACACGTCACCAAGAACCACTCTCC 294
Db      88 SerProSerLeuArgSerArgValThrMetSerAlaAspMetSerGluAsnSerPheTyrt 107

```


DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 KW Hypothetical protein.
 SQ SEQUENCE 588 AA; 64438 MW; FC60DBAD82B39FD7 CRC64;

Alignment Scores:
 Pred. No.: 1.18e-57 Length: 588
 Score: 649.00 Matches: 125
 Percent Similarity: 86.81% Conservativity: 0
 Best Local Similarity: 86.81% Mismatches: 9
 Query Match: 87.35% Indels: 10
 DB: 4 Gaps: 1

US-08-728-463B-205 (1-403) x Q8WUX4 (1-588)

QY 1 ATGAACACCTGGTTCCTCTCTCTGGTGGCAGCTCCAGATGGGTCTGTCTCCAG 60
 |||||
 DB 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20
 |||||
 QY 61 GTGAGCTACAGAGTGGGGCGGAGGACTGTTGAAGCTTCGGAGACCCCTGTCTCCAC 120
 |||||
 DB 21 ValGlnLeuGlnTrpGlyAlaGlyLeuLeuLysProSerGluThrLeuSerLeuThr 40
 |||||
 QY 121 TGGCTGTCTATGGTGGTCTTCAGTGGTACTACTGGAGCTGGATCCGCCAGCCCCA 180
 |||||
 DB 41 CysGlyValTrpGlyGlySerPheSerGlyTrpTrpSerTrpIleArgGlnProPro 60
 |||||
 QY 181 GGTAAAGGGCTGGAGTGGGGAATCAATCATAGTGAAGCACCACCACTACAACCCG 240
 |||||
 DB 61 GlyLysGlyLeuGluTrpIleGlyGluLeuHisSerGlySerThrAsnTyrAsnPro 80
 |||||
 QY 241 TCCTCAAGAGTCGAGTCACATATAGTCGACACGCTCAAGACCAAGTCTCCCTGAAG 300
 |||||
 DB 81 SerLeuLysSerArgValThrIleSerValAspThrSerLysLysGlnLeuSerLeuLys 100
 |||||
 QY 301 CTGAGCTCTGACCGCGGACGCTGTATTACTGTCTGGAGTAAATTAAT--- 357
 |||||
 DB 101 LeuSerSerValAsnAlaAlaAspThrAlaValTyrCysAlaArgValIleThrArg 120
 |||||
 QY 358 -----TGGTTCGACCCCTGGGCGCAGGAAACCCCTGGTC 390
 |||||
 DB 121 AlaSerProGlyThrAspGlyArgTyrGlyMetAspValTrpGlyGlnGlyThrVal 140
 |||||
 QY 391 ACCGCTCTCTCA 402
 |||||
 DB 141 ThrValSerSer 144

RESULT 2

Q9BU10 PRELIMINARY; PRT; 597 AA.
 ID Q9BU10
 AC Q9BU10;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical 65.3 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LYMPH;
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC002963; AA02963.1; -;
 DR HSSP; P01825; 7FAB
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR003597; IG.c1.
 DR InterPro; IPR003600; IG like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; ig; 5.
 DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGc1; 4.
 DR SMART; SM00406; IGV; 1.
 DR SMART; SM00410; IG like; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 KW Hypothetical protein.
 SQ SEQUENCE 597 AA; 65274 MW; 2DAPAF8PB7E055851 CRC64;

Alignment Scores:
 Pred. No.: 1.18e-57 Length: 597
 Score: 649.00 Matches: 125
 Percent Similarity: 86.81% Conservativity: 0
 Best Local Similarity: 86.81% Mismatches: 9
 Query Match: 87.35% Indels: 10
 DB: 4 Gaps: 1

US-08-728-463B-205 (1-403) x Q9BU10 (1-597)
 QY 1 ATGAACACCTGGTTCCTCTCTCTGGTGGCAGCTCCAGATGGGTCTGTCTCCAG 60
 |||||
 DB 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20
 |||||
 QY 61 GTGAGCTACAGAGTGGGGCGGAGGACTGTTGAAGCTTCGGAGACCCCTGTCTCCAC 120
 |||||
 DB 21 ValGlnLeuGlnTrpGlyAlaGlyLeuLeuLysProSerGluThrLeuSerLeuThr 40
 |||||
 QY 121 TGGCTGTCTATGGTGGTCTCTCTCTCTGGTGGTACTACTGGAGCTGGATCCGCCAGCCCCA 180
 |||||
 DB 41 CysGlyValTrpGlyGlySerPheSerGlyTrpTrpSerTrpIleArgGlnProPro 60
 |||||
 QY 181 GGTAAAGGGCTGGAGTGGGGAATCAATCATAGTGAAGCACCACCACTACAACCCG 240
 |||||
 DB 61 GlyLysGlyLeuGluTrpIleGlyGluLeuHisSerGlySerThrAsnTyrAsnPro 80
 |||||
 QY 241 TCCTCAAGAGTCGAGTCACATATAGTCGACACGCTCAAGACCAAGTCTCCCTGAAG 300
 |||||
 DB 81 SerLeuLysSerArgValThrIleSerValAspThrSerLysLysGlnLeuSerLeuLys 100
 |||||
 QY 301 CTGAGCTCTGACCGCGGACGCTGTATTACTGTCTGGAGTAAATTAAT--- 357
 |||||
 DB 101 LeuSerSerValAsnAlaAlaAspThrAlaValTyrCysAlaArgValIleThrArg 120
 |||||
 QY 358 -----TGGTTCGACCCCTGGGCGCAGGAAACCCCTGGTC 390
 |||||
 DB 121 AlaSerProGlyThrAspGlyArgTyrGlyMetAspValTrpGlyGlnGlyThrVal 140
 |||||
 QY 391 ACCGCTCTCTCA 402
 |||||
 DB 141 ThrValSerSer 144

RESULT 3

Q96AA6 PRELIMINARY; PRT; 618 AA.
 ID Q96AA6
 AC Q96AA6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical 67.8 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LYMPH;
 RA Strausberg R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC017356; AA017356.1; -;
 DR InterPro; IPR003598; IG.c2.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; ig; 5.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 KW Hypothetical protein; Immunoglobulin domain.

GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 35.7747 Seconds
(without alignments)
4642.224 Million cell updates/sec

Title: US-08-728-463B-205

Perfect score: 743

Sequence: 1 ATGAACACCTGTGGTCTTCTGGTCACCTCTCTCTCAG 403

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1343160.

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-Q=/cgn2.1/USPTO_spool/US08728463/runat_03062003_085614_16815/app_query.fasta_1.3690
-DB=SPTREMBL_21 -QFMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40 cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08728463 @CNG 1.1.380 -runat_03062003_085614_16815 -NCPU=3
-NO MAP -LARGESQUERY -NEG SCORE=30 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp Vertebrate.*
14: sp Unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	649	87.3	588	4 Q8WUX4	Q8wux4 homo sapien

2	649	87.3	597	4	Q9BU10	Q9bu10 homo sapien
3	649	87.3	618	4	Q96AA6	Q96aa6 homo sapien
4	643	86.5	597	4	Q9BOB8	Q9bob8 homo sapien
5	573.5	77.2	613	4	Q96EY0	Q96ey0 homo sapien
6	553.5	74.5	150	4	Q95973	Q95973 homo sapien
7	524.5	70.6	496	4	Q96KX8	Q96kx8 homo sapien
8	491	66.1	119	4	Q967C3	Q967c3 homo sapien
9	490.5	66.0	473	4	Q8UL73	Q8ul73 homo sapien
10	430.5	57.9	479	11	Q99M22	Q99m22 mus musculus
11	363.5	48.9	122	4	Q9UL75	Q9ul75 mus musculus
12	355.5	47.8	482	11	Q91X92	Q91x92 mus musculus
13	353.5	47.6	613	11	Q8VCX7	Q8vcx7 mus musculus
14	343	46.2	298	11	Q9QYF0	Q9qyf0 mus musculus
15	336	45.2	168	11	Q8VDC9	Q8vdc9 mus musculus
16	330	44.4	473	11	Q9D8L4	Q9d8l4 mus musculus
17	326.5	43.9	613	4	Q8WUK1	Q8wuk1 mus musculus
18	323	43.5	140	11	Q924P8	Q924p8 mus musculus
19	322.5	43.4	278	11	Q921K1	Q921k1 mus musculus
20	316.5	42.6	471	4	Q8TC77	Q8tc77 mus musculus
21	314.5	42.3	494	4	Q96K68	Q96k68 mus musculus
22	313.5	42.2	121	11	Q9SNG4	Q9sng4 mus musculus
23	313.5	42.2	145	11	Q924R3	Q924r3 mus musculus
24	313	42.1	597	4	Q96BB9	Q96bb9 mus musculus
25	312	42.0	142	11	Q924Q1	Q924q1 mus musculus
26	311	41.9	118	4	Q9UL74	Q9ul74 mus musculus
27	310.5	41.8	488	11	Q91WR1	Q91wr1 mus musculus
28	310	41.7	146	11	Q924Q8	Q924q8 mus musculus
29	309.5	41.7	143	11	Q924Q5	Q924q5 mus musculus
30	309.5	41.7	143	11	Q924Q0	Q924q0 mus musculus
31	309.5	41.7	145	11	Q924Q7	Q924q7 mus musculus
32	309	41.6	146	11	Q924R8	Q924r8 mus musculus
33	308.5	41.5	143	11	Q924R7	Q924r7 mus musculus
34	308.5	41.5	143	11	Q91VA2	Q91va2 mus musculus
35	308.5	41.5	143	11	Q91V67	Q91v67 mus musculus
36	307.5	41.4	463	11	Q93LC4	Q93lc4 mus musculus
37	307	41.3	489	11	Q8VCX4	Q8vcx4 mus musculus
38	307	41.3	497	4	Q8WY24	Q8wy24 mus musculus
39	306.5	41.3	143	11	Q924P9	Q924p9 mus musculus
40	306.5	41.3	573	4	Q8WU38	Q8wu38 mus musculus
41	305	41.0	140	11	Q924R2	Q924r2 mus musculus
42	304.5	41.0	137	11	Q924R6	Q924r6 mus musculus
43	304.5	41.0	143	11	Q924R0	Q924r0 mus musculus
44	304	40.9	119	4	Q9UL94	Q9ul94 mus musculus
45	303	40.8	113	4	Q9UL90	Q9ul90 mus musculus

ALIGNMENTS

RESULT 1

ID	Q8WUX4	PRELIMINARY:	PRT:	588 AA.
AC	Q8WUX4;			
DT	01-MAR-2002 (Tremblrel. 20, Created)			
DT	01-MAR-2002 (Tremblrel. 20, Last sequence update)			
DT	01-JUN-2002 (Tremblrel. 21, Last annotation update)			
DE	Hypothetical 64.4 kDa protein.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUES=LYMPH;			
RA	Strausberg R.;			
RL	Submitted (DSC-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC019235; AAH19235.1; --			
DR	InterPro; IPR003599; IG_			
DR	InterPro; IPR003597; IG_			
DR	InterPro; IPR003006; IG_MHC.			
DR	PFam; PF00047; IG_5.			
DR	SMART; SM00409; IG_2.			
DR	SMART; SM00407; IGc1; 4.			

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 09:04:15 ; Search time 17.1229 Seconds
(without alignments)
4764.744 Million cell updates/sec

Title: US-08-728-463B-205
Perfect score: 743
Sequence: 1 ATGAACACCTGGTGTCTT.....CTGGTCACCGTCTCTCTAG 403

Scoring table:

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Ygapop 6.0			0.5
Delop 6.0			7.0
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Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 767038

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published Applications AA -QMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100
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-XGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications AA:
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11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pcp:*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pcp:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	588.5	79.2	249	9 US-09-880-748-1321	Sequence 1321, Ap
2	555.5	74.8	249	9 US-09-880-748-957	Sequence 957, App
3	551	74.2	476	9 US-10-124-905-12	Sequence 12, Appl
4	551	74.2	476	9 US-09-948-429B-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-09-880-748-1321
; Sequence 1321, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1321
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1321

5	548.5	73.8	487.	10	US-09-880-729-145	Sequence 145, App
6	543	73.1	255	9	US-09-880-748-1642	Sequence 1642, Ap
7	540	72.7	253	9	US-09-880-748-1333	Sequence 1333, Ap
8	539.5	72.6	254	9	US-09-880-748-1659	Sequence 1659, Ap
9	535.5	72.1	250	9	US-09-880-748-1413	Sequence 1413, Ap
10	534	71.9	467	9	US-10-211-357-8	Sequence 8, Appli
11	534	71.9	467	9	US-10-211-357-10	Sequence 10, Appl
12	534	71.9	476	9	US-10-211-357-12	Sequence 12, Appl
13	534	71.9	476	9	US-10-124-905-4	Sequence 4, Appli
14	534	71.9	476	9	US-09-948-429B-4	Sequence 4, Appli
15	530	71.3	117	10	US-09-864-761-44315	Sequence 44315, A
16	530	71.3	139	9	US-10-211-357-2	Sequence 2, Appli
17	530	71.3	139	10	US-09-850-165-17	Sequence 17, Appl
18	523.5	70.5	252	9	US-09-880-748-1326	Sequence 1326, Ap
19	518	69.7	97	9	US-10-194-975-40	Sequence 40, Appl
20	515	69.3	250	9	US-09-880-748-993	Sequence 993, App
21	512	68.9	253	9	US-09-880-748-954	Sequence 954, App
22	511.5	68.8	251	9	US-09-880-748-1316	Sequence 1316, Ap
23	509	68.5	97	9	US-10-194-975-49	Sequence 49, Appl
24	505	68.0	253	9	US-09-880-748-1602	Sequence 1602, Ap
25	504	67.8	255	9	US-09-880-748-1626	Sequence 1626, Ap
26	495.5	66.7	250	9	US-09-880-748-1645	Sequence 1645, Ap
27	494	66.5	119	9	US-10-125-687-5	Sequence 5, Appli
28	494	66.5	119	12	US-10-025-687-5	Sequence 5, Appli
29	486.5	65.5	254	9	US-09-880-748-1578	Sequence 1578, Ap
30	485.5	65.3	250	9	US-09-880-748-1548	Sequence 1548, Ap
31	472.5	63.6	252	9	US-09-880-748-1329	Sequence 1329, Ap
32	471	63.4	130	9	US-09-925-299-971	Sequence 971, App
33	471	63.4	130	10	US-09-925-299-971	Sequence 971, App
34	468	63.0	253	9	US-09-880-748-1339	Sequence 1339, Ap
35	466.5	62.8	248	9	US-09-880-748-1360	Sequence 1360, Ap
36	464	62.4	251	9	US-09-880-748-990	Sequence 990, App
37	463	62.3	97	9	US-10-194-975-50	Sequence 50, Appl
38	461	62.0	253	9	US-09-880-748-1619	Sequence 1619, Ap
39	461	62.0	255	9	US-09-880-748-841	Sequence 841, App
40	460.5	62.0	256	9	US-09-880-748-1607	Sequence 1607, Ap
41	459	61.8	105	10	US-09-864-761-44573	Sequence 44573, A
42	457.5	61.6	119	9	US-10-078-958-3	Sequence 3, Appli
43	457.5	61.6	247	9	US-09-880-748-1651	Sequence 1651, Ap
44	453.5	61.0	244	12	US-10-039-785-44	Sequence 44, Appl
45	450.5	60.6	252	9	US-09-880-748-1994	Sequence 1994, Ap

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-124-905-12

Alignment Scores:
Pred. No.: 4,23e-43 Length: 476
Score: 551.00 Matches: 111
Percent Similarity: 81.51% Conservative: 8
Best Local Similarity: 76.03% Mismatches: 15
Query Match: 74.16% Indels: 12
DB: Gaps: 4

US-08-728-463B-205 (1-403) x US-10-124-905-12 (1-476)

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QY 1 ATGAACACCTGTGGTTCCTCTCTCTGGTGGCAGCTCCACAGTGGTCTGTCTCCAG 60
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Db 1 MetLysHisLeuTrpPheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20

QY 61 GTGCAGCTACAGCAGTGGGGCGCAGACTGTGAAACCTTCGAGACCTGTCTCCAC 120
   |||||
Db 21 ValGlnLeuGlnSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40

QY 121 TCGCTGTCTATGTCGGTCTCTCAGT---GGTTACTTGGAGCTCCGACGCCC 177
   |||||
Db 41 CysAlaValSerGlySerIleSerGlyGlyTrpGlyTrpIleArgGlnPro 60

QY 178 CAGGTAAGGGCTGAGTGGGCTCTCAGT---AATCATAGTGGAAATC---AATCATAGTGGAAATC 234
   |||||
Db 61 ProGlyLysGlyLeuGluTrpIleGlySerPheTyrSerSerGlyAsnThrTyrTyr 80

QY 235 AACCCCTCCCTCAAGAGTCGAGTCACATATCAGTCGACACGTCGACGACCAAGTCTCC 294
   |||||
Db 81 AsnProSerLeuLysSerGlnValThrIleSerThrAspThrSerLysAsnGlnPheSer 100

QY 295 CTGAAGCTGAGCTCTGACCGCGGCGGACACGCTGTGTATTACTGTGCGAGA----- 348
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Db 101 LeuLysLeuAsnSerMetThrAlaAlaAspThrAlaValTyrTyrCysValArgAspArg 120

QY 349 -----GTAATT-----AATTGGTTCGACCCCTGGGCGCAGGGAAC 384
   |||||
Db 121 LeuPheSerValValGlyMetValTyrAsnAsnTrpPheAspValTrpGlyProGlyVal 140

QY 385 CTGGTCACCGTCTCTCTCA 402
   |||||
Db 141 LeuValThrValSerSer 146
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RESULT 4

US-09-948-429B-12
; Sequence 12, Application US/09948429B
; Patent No. US20020177689A1

GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/948,429B
; FILING DATE:

;
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-948-429B-12

Alignment Scores:
Pred. No.: 4,23e-43 Length: 476
Score: 551.00 Matches: 111
Percent Similarity: 81.51% Conservative: 8
Best Local Similarity: 76.03% Mismatches: 15
Query Match: 74.16% Indels: 12
DB: Gaps: 4

US-08-728-463B-205 (1-403) x US-09-948-429B-12 (1-476)

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QY 1 ATGAACACCTGTGGTTCCTCTCTCTGGTGGCAGCTCCACAGTGGTCTGTCTCCAG 60
   |||||
Db 1 MetLysHisLeuTrpPheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20

QY 61 GTGCAGCTACAGCAGTGGGGCGCAGACTGTGAAACCTTCGAGACCTGTCTCCAC 120
   |||||
Db 21 ValGlnLeuGlnSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40

QY 121 TCGCTGTCTATGTCGGTCTCTCAGT---GGTTACTTGGAGCTCCGACGCCC 177
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Db 41 CysAlaValSerGlySerIleSerGlyGlyTrpGlyTrpIleArgGlnPro 60

QY 178 CAGGTAAGGGCTGAGTGGGAAATC---AATCATAGTGGAAATC---AATCATAGTGGAAATC 234
   |||||
Db 61 ProGlyLysGlyLeuGluTrpIleGlySerPheTyrSerSerGlyAsnThrTyrTyr 80

QY 235 AACCCCTCCCTCAAGAGTCGAGTCACATATCAGTCGACACGTCGACGACCAAGTCTCC 294
   |||||
Db 81 AsnProSerLeuLysSerGlnValThrIleSerThrAspThrSerLysAsnGlnPheSer 100

QY 295 CTGAAGCTGAGCTCTGTGACCGCGGCGGACACGCTGTGTATTACTGTGCGAGA----- 348
   |||||
Db 101 LeuLysLeuAsnSerMetThrAlaAlaAspThrAlaValTyrTyrCysValArgAspArg 120

QY 349 -----GTAATT-----AATTGGTTCGACCCCTGGGCGCAGGGAAC 384
   |||||
Db 121 LeuPheSerValValGlyMetValTyrAsnAsnTrpPheAspValTrpGlyProGlyVal 140

QY 385 CTGGTCACCGTCTCTCTCA 402
   |||||
Db 141 LeuValThrValSerSer 146
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RESULT 5

US-09-800-729-145
; Sequence 145, Application US/09800729
; Patent No. US20020068319A1

GENERAL INFORMATION:

; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: PZ044PI
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08

;; PRIOR APPLICATION NUMBER: PCT/US00/26013
;; PRIOR FILING DATE: 2000-09-22
;; PRIOR APPLICATION NUMBER: 60/155,709
;; PRIOR FILING DATE: 1999-09-24
;; NUMBER OF SEQ ID NOS: 217
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 145
;; LENGTH: 487
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-800-729-145

Alignment Scores:
Pred. No.: 7,26e-43 Length: 487
Score: 548.50 Matches: 110
Percent Similarity: 80.95% Conservative: 9
Best Local Similarity: 74.83% Mismatches: 15
Query Match: 73.82% Indels: 13
DB: 10 Gaps: 2

US-08-728-463B-205 (1-403) x US-09-800-729-145 (1-487)

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Db 21 ValGlnLeuGlnUserGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40
QY 121 TGGCTGTCTATGTGGTCTCTCAGT-----GGTTACTACGGAGCTGGATCCGCCAG 174
Db 41 CysThrValSerGlyGlySerLeuSerGlyGlyHisTrpSerTrpIleArgGln 60
QY 175 CCCCAGGTAAAGGGCTGGAGTGGGGAATCAATCATAGTGAAGCACCACCACTAC 234
Db 61 HisProGlyLysGlyLeuGluTrpIleGlyTrpSerTrpAsnGlyValThrTyrTyr 80
QY 235 AACCGTCCCTCAAGAGTCAGTCAGTCACCATATCAGTCAGCAGCTGCAAGAACCACTCTCC 294
Db 81 AsnProSerLeuLysSerArgValThrIleSerValAspThrSerGlnAsnGlnPheSer 100
QY 295 CTGAAGCTGAGCTCTGTGACCGCGGACACGCTGTGTATTACTGTGCGAGA-----348
Db 101 LeuArgLeuSerSerValThrAlaAlaAspThrAlaValTyrCysAlaLysAspHis 120
QY 349 -----GTAATTAAATTGGTTCGACCCCTGGGGCCAGGGA 381
Db 121 ArgAlaThrArgAspGlyTyrGlnLeuGluTyrArgGlyPheAspTyrTrpGlyGlnGly 140
QY 382 ACCTGTGTCACCTCTCCTCA 402
Db 141 IleLeuValThrValSerSer 147

RESULT 6

US-09-880-748-1642
; Sequence 1642, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499

;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1642
;; LENGTH: 255
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-1642

Alignment Scores:
Pred. No.: 2.12e-42 Length: 255
Score: 543.00 Matches: 105
Percent Similarity: 84.50% Conservative: 4
Best Local Similarity: 81.40% Mismatches: 6
Query Match: 73.08% Indels: 14
DB: 9 Gaps: 1

US-08-728-463B-205 (1-403) x US-09-880-748-1642 (1-255)

QY 58 CAGGTGCAGCTACAGCAGTGGGGCGCAGACTGTGAGCCCTTCGAGACCCCTGTCCCTC 117
Db 1 GlnValGlnLeuGlnTrpGlyAlaGlyLeuLeuLysProSerGluThrLeuSerLeu 20
QY 118 ACTGCGCTGTCTATGTGGTCTCTTCACTGTGCTTACTGTGAGTGGATCCGCCAGCCC 177
Db 21 ThrCysAlaValTyrGlyGlySerPheSerGlyTyrTyrTrpSerTrpIleArgGlnSer 40
QY 178 CCAGGTAAAGGGCTGAGTGGGATGGGGAATCAATCATAGTGGAGACCACTACAC 237
Db 41 ProGlyLysGlyLeuGluTrpIleGlyLeuAsnHisGlyGlySerThrAsnTyrAsn 60
QY 238 CCGTCCCTCAAGAGTCGAGTCACCATATCAGTCGACACGTCCAGAACCCAGTTCCTCCCTG 297
Db 61 ProSerLeuLysSerArgValThrIleSerValAspAlaSerLysAsnGlnPheSerLeu 80
QY 299 AAGCTGAGCTCTGTGACCGCGGACACGCTGTGTATTACTGTGCGAGAGTAATTAAT 357
Db 81 LysLeuSerSerValThrAlaAlaAspThrAlaValTyrCysAlaArgGluArgSer 100
QY 358 TGGTTC-----GACCCCTGGGGC 375
Db 101 TyrTyrAspIleLeuThrGlyTyrSerProArgSerLysTyrGlyMetAspValTrpGly 120
QY 376 CAGGAACCCCTGTGTCACCGCTCTCCTCA 402
Db 121 ArgGlyThrLeuValThrValSerSer 129

RESULT 7

US-09-880-748-1333
; Sequence 1333, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1333
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-880-748-1333

Alignment Scores:

Pred. No.: 4,026-42 Length: 253
Score: 540.00 Matches: 107
Percent Similarity: 85.8% Conservative: 2
Best Local Similarity: 84.2% Mismatches: 6
Query Match: 72.68% Indels: 12
DB: 9 Gaps: 1

US-08-728-463B-205 (1-403) x US-09-880-748-1333 (1-253)

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QY 118 ACCTGCGCTGTATGTTGGTGGTTCCTTCACTGAGTGGTACTGAGTGGATCCGCCAGGCC 177
DB 21 ThrCysAlaValTyrGlyGluSerPheSerGlyTyrTyrTrpSerTrpIleArgGlnPro 40
QY 178 CCAGTAAGGGCTCGAGTGGATTGGGAAATCAATCATAGTGGAGCAACCAACTACAAC 237
DB 41 ProGlyLysGlyLeuGluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsn 60
QY 238 CGTCCCTCAAGTCCGAGTCCACCATATCAGTCCGACACGCTCCAAAGACCACTCCCTG 297
DB 61 ProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeu 80
QY 298 AAGCTGAGCTCTGTGACCGCCGACACGCGCTGTATTACTGTGCGAGA----- 348
DB 81 LysLeuSerSerValThrAlaAlaAspThrAlaPheTyrTyrCysAlaArgGlySerLeu 100
QY 349 -----GTAATTAATTGTTCCGACCCCTCGAGCCCTGGGGCCAGGGA 381
DB 101 TyrTyrAspIleLeuThrGlyTyrTyrIleGlyAsnAlaPheAspIleTrpGlyArgGly 120
QY 382 ACCCTGGTCACCGTCTCTCTCA 402
DB 121 ThrLeuValThrValSerSer 127

RESULT 8

US-09-880-748-1659
; Sequence 1659, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1659
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1659

Alignment Scores:

Pred. No.: 4,48e-42 Length: 254
Score: 539.50 Matches: 106
Percent Similarity: 85.18% Conservative: 3
Best Local Similarity: 82.81% Mismatches: 6

Query Match: 72.61% Indels: 13
DB: 9 Gaps: 1

US-08-728-463B-205 (1-403) x US-09-880-748-1659 (1-254)

QY 58 CAGGTGACAGTACAGAGTGGGGCCGACGACTGTTGAAGCCTTCGGAGACCTGTCCTC 117
DB 1 GlnValGlnLeuGlnGlnSerGlyProGlyLeuLeuLysProSerGluThrLeuSerLeu 20
QY 118 ACCTGCGCTGTATGTTGGTGGTTCCTTCACTGAGTGGTACTGAGTGGATCCGCCAGGCC 177
DB 21 ThrCysAlaValTyrGlyGlySerPheSerGlyTyrTyrTrpSerTrpIleArgGlnPro 40
QY 178 CCAGTAAGGGCTCGAGTGGATTGGGAAATCAATCATAGTGGAGCAACCAACTACAAC 237
DB 41 ProGlyLysGlyLeuGluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsn 60
QY 238 CGTCCCTCAAGTCCGAGTCCACCATATCAGTCCGACACGCTCCAAAGACCACTCCCTG 297
DB 61 ProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeu 80
QY 298 AAGCTGAGCTCTGTGACCGCCGACACGCGCTGTATTACTGTGCGAGAGTAATTAAT 357
DB 81 LysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgGlyArg 100
QY 358 TGGTTC-----GACCCCTGGGGCCAG 378
DB 101 TyrTyrAspIleLeuThrGlyTyrSerLeuGlyArgGlyGluMetAspValTrpGlyArg 120
QY 379 GGAACCTGGTCACCGTCTCTCTCA 402
DB 121 GlyThrLeuValThrValSerSer 128

RESULT 9

US-09-880-748-1413
; Sequence 1413, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1413
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1413

Alignment Scores:

Pred. No.: 1.05e-41 Length: 250
Score: 535.50 Matches: 103
Percent Similarity: 86.29% Conservative: 4
Best Local Similarity: 83.06% Mismatches: 8
Query Match: 72.07% Indels: 9
DB: 9 Gaps: 1

US-08-728-463B-205 (1-403) x US-09-880-748-1413 (1-250)

QY 58 CAGGTGACAGTACAGAGTGGGGCCGACGACTGTTGAAGCCTTCGGAGACCTGTCCTC 117
DB: 9 Gaps: 1

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
 TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 STREET: 699 Prince Street
 CITY: Alexandria
 STATE: VA
 COUNTRY: USA
 ZIP: 22314
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/124,905
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/383,916
 FILING DATE:
 APPLICATION NUMBER: US 08/487,550
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Teskin, Robin L.
 REGISTRATION NUMBER: 35,030
 REFERENCE/DOCKET NUMBER: 012712-131
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-836-6620
 TELEFAX: 703-836-2021
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 476 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-10-124-905-4

Alignment Scores:	
Pred. No.:	1.62e-41
Score:	534.00
Percent Similarity:	73.08%
Best Local Similarity:	73.29%
Query Match:	71.87%
DB:	9
Length:	476
Matches:	107
Conservative:	7
Mismatches:	20
Indels:	13
Gaps:	3

US-08-728-463B-205 (1-403) x US-10-124-905-4 (1-476)

QY	1	ATGAAACACCTGTGTTCTCTCTCTGTGGCAGCTCCACATGGGCTCTGTCCAG	60
Db	1	MetLysHisLeuTrpPheLeuLeuValAlaLaProArgTrpValLeuSerGln	20
QY	61	GTGCAGCTACACAGCTGGGGCGCAGGACTGTGAAGCCTTCGGAGACCCGTGCTCCAC	120
Db	21	ValLysLeuGlnGlnTrpGlyGluGlyLeuLeuGlnProSerGluThrLeuSerArgThr	40
QY	121	TCGCGTGTATGTGGGGTCTTCAGTGGT--TACTACTGGAGCTGGATCCGCCAGCCC	177
Db	41	CysValValSerGlyGlySerIleSerGlyTyrrTyrrTrpThrTrpIleArgGlnThr	60
QY	178	CCAGTAAGGGCTGGAGTGGATGGGGAAATCAATCATAGTGA---AGCACCAACTAC	234
Db	61	ProGlyArgGlyLeuGluTrpIleGlyHisIleTyrrGlyAsnGlyAlaThrThrAsnTyrr	80
QY	235	AACCGTCCCTCAGAGTCCGAGTCCCATATCATGTGCACACGTCCCAAGAACCAAGTTCCTC	294
Db	81	AsnProSerLeuLysSerArgValThrIleSerLysAspThrSerLysAsnGlnPhePhe	100
QY	295	CTGAAGCTGAGCTCTGTGACCCGCGGACACGCGTGTGTATTACTGTGGGAGA-----	348
Db	101	LeuAsnLeuAsnSerValThrAspAlaAspThrAlaValTyrrCysAlaArgGlyPro	120

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QY 349 -----GTAATAANTGTTCCGACCCCTGGGGCCAGGAAACC 384
Db 121 ArgProAspCysThrThrIleCysTyrGlyTTPvalAspValTPGlyProGlyAasp 140
QY 385 CTGTCACCGTCCTCCCTCA 402
Db 141 LeuValThrValSerSer 146

RESULT 14
US-09-948-429B-4
; Sequence 4, Application US/09948429B
; Patent No. US20020177689A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/948.429B

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1 CLASSIFICATION:
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: 09/383,916
4 FILING DATE:
5 APPLICATION NUMBER: US 08/487,
6 FILING DATE: 07-JUN-1995
7 ATTORNEY/AGENT INFORMATION:
8 NAME: Teskin, Robin L.
9 REGISTRATION NUMBER: 35,030
10 REFERENCE/DOCKET NUMBER: 01271
11 TELECOMMUNICATION INFORMATION:
12 TELEPHONE: 703-836-6620
13 TELEFAX: 703-836-2021
14 INFORMATION FOR SEQ ID NO: 4:
15 SEQUENCE CHARACTERISTICS:
16 LENGTH: 476 amino acids
17 TYPE: amino acid
18 TOPOLOGY: linear
19 MOLECULE TYPE: protein
20 US-09-948-429B-4

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Alignment Scores:		
Pred. No.:	1.628-41	Length:
Score:	534.00	Matches:
Percent Similarity:	78.08%	Conservative:
Best Local Similarity:	73.2%	Mismatches:
Query Match:	71.87%	Indels:
DB:	9	Gaps:
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		107
		20
		12
		3

US-08-728-463B-205 (1-403) x US-09-948-429B-4 (1-476)

QY	1	ATGAACACCTGTGGTTCCTCTCTCTGTGGTGCAGCTCCACAGATGGGTCCTGTCCCAG	60
DB	1	MetLysHisLeutrpPheLeuLeuLeuValaalaProArgTrpValLeuSerGin	20
QY	61	GTGCAGCTPACAGCAGTGGGGCGCAGGACTCTTGAAGCCTTCGAGAGCCCTGTCCCTCACC	120
DB	21	ValLysLeuGlnGlnTrpGlyGluGlyLeuLeuGlnProSerGluThrLeuSerArgThr	40

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INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-809A-118

Alignment Scores:
Pred. No.: 4, 01e-60 Length: 116
Score: 622.00 Matches: 116
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 83.71% Indels: 0
DB: 3 Gaps: 0

US-08-728-463B-205 (1-403) x US-08-545-809A-118 (1-116)

Qy 1 ATGAACACCTGGTTCCTCTCCTGGTGGCAGCTCCAGATGGGTCTGTGCCAG 60
Db 1 MetLysHisLeuTrpPheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20
Qy 61 GTCGAGCTACGAGTGGGGCGGAGGACTCTTGAAGCCTTCGAGACCCCTGTCCTCACC 120
Db 21 ValGlnLeuGlnTrpGlyAlaGlyLeuLysProSerGluThrLeuSerLeuThr 40
Qy 121 TGGCTCTCTATGGTGGTCTCTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCCCA 180
Db 41 CysAlaValTyrglyGlySerPheSerGlyTyrrTrpSerTrpIleArgGlnProPro 60
Qy 181 GGTAAGGGCTGGAGTGGGAAATCAATCATAGTGGAGCCCAACTACACCCG 240
Db 61 GlyLysGlyLeuGluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrrAsnPro 80
Qy 241 TCCTCAAGTGGAGTCCACCATCATCTAGTGGAGCTCCAGACCTCCAGACCTCTCCCTGAAG 300
Db 81 SerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeuLys 100
Qy 301 CTGAGCTCTGTACCGCGCGGACACCGCTGTGTATTACTGTGGAGA 348
Db 101 LeuSerSerValThrAlaAlaAspThrAlaValTyrrCysAlaArg 116

RESULT 2

US-08-793-450-8
Sequence 8, Application US/08793450
Patent No. 6312690
GENERAL INFORMATION:
APPLICANT: EDELMAN, LENA
APPLICANT: MARGARITTE, CHRISTEL
APPLICANT: KACZOREK, MICHEL
APPLICANT: CHAABIHI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: FR 94/10566

FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-793-450-8

Alignment Scores:
Pred. No.: 1,27e-56 Length: 472
Score: 592.00 Matches: 114
Percent Similarity: 86.67% Conservative: 3
Best Local Similarity: 84.44% Mismatches: 10
Query Match: 79.68% Indels: 8
DB: 4 Gaps: 1

US-08-728-463B-205 (1-403) x US-08-793-450-8 (1-472)

Qy 22 CTCCTCCTGGTGGCAGCTCCAGATGGGTCTGTCCAGTGCAGCTACAGCAGTGGGC 81
Db 8 LeuPheLeuValAlaThrAlaThrGlyValHisSerGlnValGlnLeuGlnTrpGly 27
Qy 82 GCAGGACTGTGAAGCCTTCGAGACCCCTGTCCCTCACCTCGCTCTCTATGGTGGTCC 141
Db 28 AlaGlyLeuLysProSerGluThrLeuSerLeuThrCysThrValTyrrGlyGlySer 47
Qy 142 TTCAGTGGTCTACTCTGAGCTGGATCCGCCAGCCCGAGTGAAGGCTGGAGTCGATT 201
Db 48 PheSerGlyTyrrTrpSerTrpIleArgGlnProGlyLysGlyLeuGluTrpIle 67
Qy 202 GGGGAATCAATCATAGTGGAGCAGCAACTACAAACCCCTCCCTCAAGAGTCCAGTCACC 261
Db 68 GlyGluIleAsnHisSerGlySerThrAsnTyrrAsnProSerLeuLysSerArgValThr 87
Qy 262 ATATCAGTCGACACGTCCTCAAGAACACAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCGC 321
Db 88 IleSerValAspThrSerLysAsnGlnPheSerLeuLysLeuAsnSerValThrAlaAla 107
Qy 322 GACACGGCTGTATTACTGTGCGAGAGTAATT-----AAT 357
Db 108 AspThrAlaValTyrrCysAlaArgAlaProGluTyrrLysTrpLysTyrrHisGlyAsp 127
Qy 358 TGGTTCGACCCCTGGGGCCAGGAGAACCTGGTCACCGTCTCTCTCA 402
Db 128 TrpPheAspProTrpGlyGlnGlyThrValThrValSerSer 142

RESULT 3

US-09-049-672A-4
Sequence 4, Application US/09049672A
Patent No. 6135941
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto

GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 09:02:35 ; Search time 9.17299 Seconds
(without alignments)
2585.294 Million cell updates/sec

Title: US-08-728-463B-205
Perfect score: 743
Sequence: 1 ATGAACACCTGTGTTCTT.....CTGTGTCACCGTCTCTCAG 403

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 525148

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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-DB=Issued Patents AA -QPMT=faatan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=BITS -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
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2	592	79.7	472	4 US-08-793-450-8
3	578.5	77.9	473	4 US-09-049-672A-4
4	578	77.8	123	4 US-08-793-450-4
5	565	76.0	142	2 US-08-480-774A-2
6	551	74.2	476	3 US-08-487-550-12
7	550	74.0	116	3 US-08-545-809A-140
8	539	72.5	118	3 US-08-545-809A-142
9	538	72.4	116	3 US-08-545-809A-92
10	534	71.9	467	4 US-08-523-894-8
11	534	71.9	467	4 US-08-523-894-10
12	534	71.9	467	4 US-08-523-894-12

13	534	71.9	476	3	US-08-487-550-4	Sequence 4, Appl
14	530	71.3	134	1	US-08-259-372A-6	Sequence 6, Appl
15	530	71.3	134	1	US-08-468-671-6	Sequence 6, Appl
16	530	71.3	139	1	US-08-478-039-108	Sequence 108, App
17	530	71.3	139	1	US-08-476-349A-108	Sequence 108, App
18	530	71.3	139	4	US-08-523-894-2	Sequence 2, Appl
19	527	70.9	118	3	US-08-545-809A-123	Sequence 123, App
20	521	70.1	118	3	US-08-545-809A-116	Sequence 116, App
21	514	69.2	120	3	US-08-545-809A-137	Sequence 137, App
22	507.5	68.3	118	4	US-09-025-769B-25	Sequence 25, Appl
23	499.5	67.2	117	3	US-08-545-809A-114	Sequence 114, App
24	494	66.5	119	4	US-09-025-769B-39	Sequence 39, Appl
25	494	66.5	119	4	US-09-025-769B-65	Sequence 65, Appl
26	491.5	66.2	244	4	US-08-518-148-79	Sequence 79, Appl
27	490.5	66.0	119	2	US-08-428-197-16	Sequence 16, Appl
28	490.5	66.0	119	5	PCT-US93-10555-16	Sequence 16, Appl
29	461.5	62.1	122	1	US-08-360-125-11	Sequence 11, Appl
30	461.5	62.1	122	2	US-08-450-578-11	Sequence 11, Appl
31	461.5	62.1	122	2	US-09-017-628-11	Sequence 11, Appl
32	461.5	62.1	122	2	US-09-014-880-11	Sequence 11, Appl
33	461.5	62.1	122	4	US-08-450-363-11	Sequence 11, Appl
34	454	61.1	119	2	US-08-652-818A-10	Sequence 10, Appl
35	451.5	60.8	278	4	US-09-260-527-3	Sequence 3, Appl
36	450.5	60.6	116	1	US-08-478-039-79	Sequence 79, Appl
37	450.5	60.6	116	1	US-08-476-349A-79	Sequence 79, Appl
38	448	60.3	119	1	US-08-360-125-5	Sequence 5, Appl
39	448	60.3	119	2	US-08-450-578-5	Sequence 5, Appl
40	448	60.3	119	2	US-09-017-628-5	Sequence 5, Appl
41	448	60.3	119	2	US-09-014-880-5	Sequence 5, Appl
42	448	60.3	119	4	US-08-450-363-5	Sequence 5, Appl
43	438	59.0	121	1	US-08-478-039-80	Sequence 80, Appl
44	438	59.0	121	1	US-08-476-349A-80	Sequence 80, Appl
45	434.5	58.5	137	2	US-08-621-751A-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1

US-08-545-809A-118
; Sequence 118, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154

CONTAINING THE SAME

[illegible]

ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows95
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/545,809A
 FILING DATE: 27-MAR-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP93/00603
 FILING DATE: 10-MAY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Freeman, John W.
 REGISTRATION NUMBER: 29,066
 REFERENCE/DOCKET NUMBER: 06501/004001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-542-5070
 TELEFAX: 617-542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 92:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 116 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-545-809A-92

Alignment Scores:
 Pred. No.: 6,28e-51 Length: 116
 Score: 538.00 Matches: 103
 Percent Similarity: 91.38% Conservative: 3
 Best Local Similarity: 88.79% Mismatches: 10
 Query Match: 72.41% Indels: 0
 DB: 3 Gaps: 0

US-08-728-463B-205 (1-403) x US-08-545-809A-92 (1-116)
 QY 1 ATGMAACCTGTGGTCTCTCTCTCTGGTGCAGCTCCAGATGGGTCTGTCCAG 60
 Db 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20
 QY 61 GTGCACTACAGCAGTGGGGCGAGGAGCTGTGAAGCCTTCGGAGACCCCTGTCCCTCAC 120
 Db 21 ValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40
 QY 121 TCGGCTGTCTATGGTGGTCTCTCAGTGGTGTACTACTGGAGCTGGATCCGCCAGCCCCA 180
 Db 41 CysThrValSerGlyGlySerIleSerSerTyrTyrTrpSerTrpIleArgGlnProAla 60
 QY 181 GGTAAAGGGCTGGAGTGGATTGGGGAATCAATCATAGTGGAGCACCACCACTACAACCCG 240
 Db 61 GlyLysGlyLeuGluTrpIleGlyArgIleTyrThrSerGlySerThrAsnTyrAsnPro 80
 QY 241 TCCCTCAAGAGTCGAGTCACCATATAGTCGACGACGTCGAAGAACAGTTCTCCCTGAAG 300
 Db 81 SerLeuLysSerArgValThrMetSerValAspThrSerLysAsnGlnPheSerLeuLys 100
 QY 301 CTGACCTGTGACGGCGCGGACACGGCTGTATTACTGTGCGAGA 348
 Db 101 LeuSerSerValThrAlaAlaAspThrAlaValTyrCysAlaArg 116

RESULT 10
 US-08-523-894-8
 ; Sequence 8, Application US/08523894
 ; Patent No. 6136310
 ; GENERAL INFORMATION:
 ; APPLICANT: Hanna, Nabil
 ; APPLICANT: Newman, Roland A.
 ; APPLICANT: Reff, Mitchell E.
 ; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
 ; TITLE OF INVENTION: Therapy
 ; NUMBER OF SEQUENCES: 59

C;Keywords: heterotetramer; immunoglobulin
F;31-105/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	3.36e-43	Length:	125
Score:	573.00	Matches:	110
Percent Similarity:	93.44%	Conservative:	4
Best Local Similarity:	90.16%	Mismatches:	8
Query Match:	82.09%	Indels:	0
DB:	2	Gaps:	0

US-08-728-463B-206 (1-388) x S40316 (1-125)

Qy	22	CAGCTCCTGGGCTCCTGCTCTGCTGTTCCAGGTTCCAGATGCGACATCCAGATGACC	81
Db	1	GlnLeuLeuGlyLeuLeuLeuLeuTrpPheProGlySerArgCysAspIleGlnLeuThr	20
Qy	82	CAGTCTCCATCTTCGGTCTCGCATCTGTAGGAGACAGATCACCATCACTTGTTCGGGCG	141
Db	21	GlnSerProSerSerValSerAlaSerValGlyAspArgValThrIleThrCysArgAla	40
Qy	142	AGTCAGGATATTAGCAGCTGGTTCAGCTGGTATCAGCATAAACACGAGGAAAGCCCTAAG	201
Db	41	SerGlnGlyIleSerSerTrpPheuAlaTrpYrGlnGlnLysProGlyLysAlaProAsn	60
Qy	202	CTCCTGATCTATGCTGCATCCAGTATTGCAAGTGGGGTCCCATCAAGGTTTCAGCGCAGT	261
Db	61	LeuLeuIleTyrHisIleSerSerLeuGlnThrGlyValProSerArgPheSerGlySer	80
Qy	262	GGATCTGGGACAGATTTCACTCTCACATCAGCAGCCCTGCAGCTGAAGATTTTGCACCT	321
Db	81	GlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPheAlaIle	100
Qy	322	TACTATTGTCAACAGGCTAATAGTTTCCGTCACACTTTTGGCCAGGGGACCAAGCTGGAG	381
Db	101	TyrTyrcysGlnGlnAlaAspSerPheProLeuThrPheGlyGlyThrLysValGlu	120
Qy	382	ATCAAA 387	
Db	121	IleLys 122	

RESULT 6

S40369

Ig kappa chain - human

C;Species: Homo sapiens (man)

C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accession: S40369

F;Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Accession: S40369

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-129 <KLE>

A;Cross-references: EMBL:X74279; NID:g441426; PIDN:CAA51147.1; PID:g441427

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;37-111/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	5.03e-43	Length:	129
Score:	571.00	Matches:	112
Percent Similarity:	92.19%	Conservative:	6
Best Local Similarity:	87.50%	Mismatches:	10
Query Match:	81.81%	Indels:	0
DB:	2	Gaps:	0

US-08-728-463B-206 (1-388) x S40369 (1-129)

Qy	4	GACATGATGTTCCCGCTCAGCTCTCGGGCTCTGCTGCTCTGTTCCAGTTCAGATCCAGA	63
Db	1	AspMetArgValLeuAlaGlnLeuLeuGlyLeuLeuLeuCysPheProGlyAlaArg	20

QY	64	TGGCAGCATCCAGATGACCCAGCTTCCTCACTCTTCCGTGTCTGCATCTGTGTAGGAGACAGATGC	123
Db	21	CysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgVal	40
QY	124	ACCATCACCTGTTCGGCGCAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAA	183
Db	41	ThrIleThrCysArgAlaSerHisValIleSerAsnHisLeuValTrpPheGlnGlnLys	60
QY	184	CCAGGGAAAGCCCTTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAGTGGGGTCCCA	243
Db	61	ProGlyLysAlaProLysSerLeuIleTyAlaAlaSerSerLeuGlnSerGlyValPro	80
QY	244	TCAAGGTTCCAGCGGCAGTGGAGTCCTGGGACAGATTCTCTCACCATCAGCAGCCTTGAG	303
Db	81	SerLysPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGln	100
QY	304	CCTGAAGATTGTGCACCTACTATTCTCAACAGGCTAATAGTTTCCCGTACACTTTTGGC	363
Db	101	ProGluAspPheAlaThrTyfTyfCysGlnGlnTyfAsnSerTyfProTyfThrPheGly	120
QY	364	CAGGGGACCAAGCTGGAGATCAAA	387
Db	121	GlnGlyThrLysLeuGluIleLys	128

QY 241 CCATCAAGTTTCAGCGGCAGTGAGTCTGGGACAGATTTCACTCCACCATCAGCAGCTG 300
|||
Db |||

83 ProSerArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerCysLeu 102
|||
|||

QY 301 CAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAAGTTTCCGTACACTTTT 360
|||
Db |||

103 GinSerGluaspPheAlaThr-Tyr-TyrCysGlnItyrTySerTyrProArgThrPhe 122
|||
|||

QY 361 GCCCAGGGGACCAGCTGGAGATCAA 387
|||
Db |||

123 GlyGlnGlyThrLysValGluIleLys 131

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Job time : 18.412 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 7.35964 Seconds
(without alignments)
4373.264 Million cell updates/sec

Title: US-08-728-463B-206

Perfect score: 698

Sequence: 1 ATGGACATGATGTCCTCCCGC.....GACCAAGCTGGAGATCAAC 388

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 225784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DRV=xlp
-O=/cgn2.1/USPTO/spool/US08728463/runat_03062003_085614_16804/app_query.fasta_1.3690
-DB=SwissProt 40 -QFMT=faetan -SUFFIX=rsp -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US08728463 @CGN 1.1 76 @runat_03062003_085614_16804 -NCPU=3
-NO MAP -LARGEQUERY -NEG SCORE=0 -WAIT -DSBLOCK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	560	80.2	129	1 KVIW HUMAN	P04431 homo sapien
2	542	77.7	117	1 KVIJ HUMAN	P01602 homo sapien
3	534	76.5	117	1 KVIH HUMAN	P01601 homo sapien
4	519	74.4	129	1 KVIK HUMAN	P04432 homo sapien
5	479	68.6	108	1 KVIS HUMAN	P01611 homo sapien
6	473	67.8	128	1 KVSE MOUSE	P01637 mus musculus
7	467.5	67.0	107	1 KVID HUMAN	P01596 homo sapien
8	467	66.9	108	1 KVIH HUMAN	P01600 homo sapien
9	466	66.8	108	1 KVIH HUMAN	P04430 homo sapien
10	465	66.6	108	1 KVIH HUMAN	P01594 homo sapien
11	464	66.5	108	1 KVIH HUMAN	P01598 homo sapien
12	460	65.9	108	1 KVIH HUMAN	P01607 homo sapien
13	458	65.6	108	1 KVIH HUMAN	P01610 homo sapien
14	457	65.5	108	1 KVIH HUMAN	P01599 homo sapien
15	453	64.9	108	1 KVIH HUMAN	P01594 homo sapien
16	452	64.8	108	1 KVIH HUMAN	P01606 homo sapien
17	448.5	64.3	129	1 KV3M HUMAN	P18136 homo sapien
18	447.5	64.1	129	1 KV3L HUMAN	P18135 homo sapien

19	447	64.0	108	1 KVIH HUMAN	P01597 homo sapien
20	446	63.9	108	1 KVIH HUMAN	P01605 homo sapien
21	445	63.8	108	1 KVIH HUMAN	P01608 homo sapien
22	443	63.5	130	1 KV5G MOUSE	P01639 mus musculus
23	440	63.0	108	1 KVIH HUMAN	P01595 homo sapien
24	440	63.0	108	1 KVIH HUMAN	P01632 homo sapien
25	437.5	62.7	129	1 KVIH HUMAN	P04207 homo sapien
26	437	62.6	108	1 KVIH HUMAN	P01593 homo sapien
27	436	62.5	108	1 KVIH HUMAN	P01603 homo sapien
28	432	61.9	108	1 KVIH HUMAN	P01609 homo sapien
29	430	61.6	115	1 KV5F MOUSE	P01638 mus musculus
30	430	61.6	128	1 KV3K HUMAN	P06311 homo sapien
31	417	59.7	134	1 KV4C HUMAN	P06314 homo sapien
32	414	59.3	115	1 KVIH HUMAN	P04433 homo sapien
33	408.5	58.5	109	1 KVIH HUMAN	P01612 homo sapien
34	406	58.2	131	1 KV3I MOUSE	P01661 mus musculus
35	405	58.0	108	1 KV5K MOUSE	P01644 mus musculus
36	404	57.9	115	1 KV5C MOUSE	P01635 mus musculus
37	402	57.6	117	1 KV5H MOUSE	P01641 mus musculus
38	402	57.6	132	1 KV3F MOUSE	P01658 mus musculus
39	401.5	57.5	116	1 KV3J HUMAN	P04434 homo sapien
40	400	57.3	108	1 KV5L MOUSE	P01645 mus musculus
41	400	57.3	108	1 KV5O MOUSE	P01648 mus musculus
42	400	57.3	108	1 KV5P MOUSE	P01649 mus musculus
43	399.5	57.2	133	1 KV4B HUMAN	P06313 homo sapien
44	397	56.9	108	1 KV5D MOUSE	P01636 mus musculus
45	395	56.6	108	1 KV5M MOUSE	P01646 mus musculus

ALIGNMENTS

RESULT 1

ID	KVIW HUMAN	STANDARD;	PRT;	129 AA.
AC	P04431			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DE	Ig kappa chain V-I region Walker precursor.			
DE	Ig kappa chain V-I region Walker precursor.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85014148; PubMed=6091049;			
RA	Klobeck H.G., Combriato G., Zachau H.G.;			
RT	"Immunoglobulin genes of the kappa light chain type from two human			
RT	lymphoid cell lines are closely related.";			
RL	Nucleic Acids Res. 12:6995-7006(1984).			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; X00965; CAA25477.1; ALT_TERM.			
DR	PIR; A01883; KIHUWK.			
DR	HSSP; P01607; IREI.			
DR	InterPro; IPR003006; Ig MHC.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; ig_1.			
DR	SMART; SM00406; Igv; 1.			
DR	Immunoglobulin V region; Signal.			
KW	SIGNAL	1	22	
FT	CHAIN	23	129	IG KAPPA CHAIN V-I REGION WALKER.
FT	DOMAIN	23	45	FRAMEWORK-1
FT	DOMAIN	46	56	COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN	57	71	FRAMEWORK-2.
FT	DOMAIN	72	78	COMPLEMENTARITY-DETERMINING-2.

QY 181 AAACAGGGAAGCCCTAAGCTCTGATCTATGCTGATCCAGTTTCAAGTGGGTC 240
 Db 61 LysProGlyLysAlaProThrLeuLeuLeuLeuLeuLeuLeuLeuLeuValGlyVal 80
 QY 241 CCATCAAGTTTCAAGGCGAGTCTGGACAGATTTCACTCTCACCATCAGCAGCTG 300
 Db 81 ProSerArgPheSerGlySerGlyAlaGluPheThrLeuThrIleSerSerLeu 100
 QY 301 CAGCTGGAAGTTTGCACCTTACTATTGTCACAGGCTAATAGTTTCCCGTACACTTT 360
 Db 101 GlnProGluAspPheAlaThrTyrCysGlnGlnAsnTyrAsnPheThrPhe 120
 QY 361 GCCAGGAGCAAGCTGGAGATCAA 387
 Db 121 GlyGlyGlyThrLysValAspAsnLys 129

RESULT 5

KV15_HUMAN STANDARD; PRT; 108 AA.
 AC P01611;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-1 region Wes.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81092279; PubMed=6778806;
 RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
 RT "Preparative separation of the tryptic hydrolysate of a protein by
 RT high-pressure liquid chromatography. The primary structure of a
 RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
 RT Wes).";
 RL Hoppe-Sevler's Z. Physiol. Chem. 361:1591-1598(1980).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01877; KIHWS.
 DR HSSP; P80362; 1WTL.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1
 FT DOMAIN 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;

Alignment Scores:

Pred. No.: 6,56e-43 Length: 108
 Score: 479.00 Matches: 92
 Percent Similarity: 93.46% Conservative: 8
 Best Local Similarity: 85.98% Mismatches: 7
 Query Match: 68.62% Indels: 0
 DB: 1 Gaps: 0

US-08-728-463b-206 (1-388) x KV15_HUMAN (1-108)

QY 67 GACATCCAGATGACCCAGTCTCCATCTCCGTTCTGCTATCTAGGACAGAGTCACC 126
 Db 1 AspIleGlnMetThrGlnSerProSerValSerAlaSerValGlyAspArgValThr 20
 QY 127 ATCACTTGTGCGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACA 186

Db 21 IleThrCysArgAlaSerGlnAspIleSerHisTrpLeuAlaTrpTyrGlnGlnLysSer 40
 QY 187 GGAAGAGCCCTAAGCTCTGATCTATGCTGATCCAGTTTCAAGTGGGTCCTCCATCA 246
 Db 41 GlyLysAlaProLysLeuLeuLeuLeuLeuLeuLeuLeuLeuValProSer 60
 QY 247 AGTTTCAGGCGAGTCTGGACAGATTTCACTCTCACCATCAGCAGCTGAGCCT 306
 Db 61 ArgPheSerGlySerGlyThrGluPheThrLeuThrIleSerSerLeuGlnPro 80
 QY 307 GAAGATTTTGCACCTTACTATTGTCACAGGCTAATAGTTTCCCGTACACTTTTGGCCAG 366
 Db 81 GluAspPheAlaThrTyrPheCysGlnGlnAlaHisSerValProLeuThrPheGlyGly 100
 QY 367 GGAACCAAGCTGGAGATCAA 387
 Db 101 GlyThrThrValAspIleLys 107

RESULT 6

KV5E_MOUSE STANDARD; PRT; 128 AA.
 AC P01637;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-V region T1 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81052342; PubMed=6776411;
 RA Altenburger W., Steinmetz M., Zachau H.G.;
 RT "Functional and non-functional joining in immunoglobulin light chain
 RT genes of a mouse myeloma.";
 RL Nature 287:603-607(1980).
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 CC EMBL; V00772; CAA24150.1; -
 DR PIR; A01920; KVMST1.
 DR HSSP; P80362; 1WTL.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1
 FT CHAIN 20
 FT DOMAIN 21 128
 FT DOMAIN 21 43
 FT DOMAIN 44 54
 FT DOMAIN 55 69
 FT DOMAIN 70 76
 FT DOMAIN 77 108
 FT DOMAIN 109 117
 FT DOMAIN 118 127
 FT DISULFID 43 108
 FT NON TER 128 128
 SQ SEQUENCE 128 AA; 14385 MW; AFA556D31BB7E05 CRC64;

Alignment Scores:

Pred. No.: 2,89e-42 Length: 128
 Score: 473.00 Matches: 87
 Percent Similarity: 82.68% Conservative: 18
 Best Local Similarity: 68.50% Mismatches: 22

Query Match:	57.77%	Indels:	0
DB:	1	Gaps:	0
US-08-728-463B-206 (1-388) x KV5E_MOUSE (1-128)			
Qy	7	ATGATGTC	CCCGCTCAGCTCTCGGGCTCTGCTGCTCGTTCCTGGTCCAGGTTCCAGATGC 56
Db	1	MetArgThrProAlaGlnPhe	LeuGlyIleLeuLeuLeuThrPheProGlyIleLysCys 20
Qy	67	GACATCCAGATGACCCAGCTCCCATCTTC	CCGTCCTGCATCTGTAGGACACAGAGTCACC 126
Db	21	AspIleLysMetThrGlnSerProSerMetTyrAlaSerLeu	GlyGlnArgValThr 40
Qy	127	ATCACTTGTCGGGCGAGTCAGATATTAGCAGCTGGT	TAGCCTGGTATCAGCATAAACCA 186
Db	41	IleSerCysLysAlaSerGlnAspIleAsnSerTyrLeu	ThrTrpPheGlnGlnLysPro 60
Qy	187	GGGAAGCCCTTAAGCTCCTCATCTATCTGCATCCAGT	TTCCAAGTGGGTGCCCATCA 246
Db	61	GlyLysSerProLysThrLeuLeuTyrArgAlaAsnArgLeu	ValAspGlyValProSer 80
Qy	247	AGGTTTCAGCGCAGTGGATCTGGGACAGATTTCAC	TCTCACCATCAGCAGCTGCAGCCT 306
Db	81	ArgPheSerGlySerGlySerGlyGlnAspPheSerLeu	ThrIleSerSerLeuGluTyr 100
Qy	307	GAAGATTTTGCAACTTACTATTGTCAACGGCTAA	TAGTTTCCCGCTACACTTTTGGCCAG 366
Db	101	GluAspMetGlyIleTyrTyrCysLeuGlnTyrAsp	GluPheProLeuThrPheGlyAla 120
Qy	367	GGGACCAAGCTGGAGATCAAA	387
Db	121	GlyThrLysLeuGluLeuLys	127

RESULT	7
KVID	HUMAN
ID	-KVID HUMAN
AC	STANDARD; PRT; 107 AA.
P01596;	
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	Ig kappa chain V-I region CAR.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCHI_TaxID=9606;	
[1]	
SEQUENCE.	
RX	MEDLINE=75075135; PubMed=4216454;
RP	Milstein C.P.; Deverson E.V.;
RA	"Primary structure of kappa light chain from a human myeloma
RT	protein.";
RL	Eur. J. Biochem. 49:377-391(1974).
CC	-I- MISCLEANEUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC	MARKER.
CC	-I- MTSCELANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR	PIR: A01854; KIHUAR.
DR	HSPF; P80362; IWL.
DR	InterPro; IPR003006; Ig MHC.
DR	InterPro; IPR003596; Ig_V.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; IGv; 1.
KW	Immunoglobulin v region; Glycoprotein.
FT	CARBOHYD 28
FT	NON TER 107
SQ	SEQUENCE 107 AA; 11703 MW; ELBFD0F9844C3346 CRC64;

US-08-728-463B-206 (1-388) x KVID_HUMAN (1-107)

QY	67	GACATCCAGATGACCCAGTCTCCATCTTCGCTGTCTGCATCTGTAGGACAGAGTCACC	126
Db	1	AspIleGlnMetThrGlnSerProSerThrLeuSerAlaSerValGlyAspArgValAla	20
QY	127	ATCATTGTTCGGGGAGTCAGGATATTAGCAGCTGGTTAGCTGTGATCAGCATAAACCA	186
Db	21	IleThrCysArgAlaSerGlnAsnIleSerSerTrpLeuAlaIleTyrGlnGlnLysPro	40
QY	187	GGGAAAGCCCTTAAGCTCCTGATCTATGCTGCATCCAGTTTGGCAAAGTGGGTCCCATCA	246
Db	41	GlyIysAlaProIysValLeuIleTyrIysSerSerLeuGluSerGlyValProSer	60
QY	247	AGGTTACGGCGCAGTGGATCTGGCAGAGATTTCATCTCCACATCAGCAGCTGCAGCCT	306
Db	61	ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu**Pro	80
QY	307	GAAGATTTTCGAACTTACTATTGTCAACAGCTAATAGTTTCCCGTACACITTTGGCCAG	366
Db	81	*****PheAlaThrTyrTyrCysGlnGlnTyrAsnThrPhe---PheThrPheGlyPro	99
QY	367	GGGACCAAGCTGGAGATCAAA	387
Db	100	GlyThrIysValAspIleLys	106

RESULT 8

KV1H_HUMAN	STANDARD;	PRT;	108 AA.
ID	KV1H_HUMAN		
AC	P01600;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DE	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	Ig kappa chain V-I region Hau.		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE.		
RX	MEDLINE=71032830; PubMed=4097974;		
RA	Watanabe S., Hilschmann N.;		
RT	"The primary structure of a monoclonal kappa-type immunoglobulin L-		
RT	chain of subgroup I (Bence-Jones Protein Hau): subdivision within		
RT	subgroups.;"		
RL	Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295 (1970).		
CC	-I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.		
CC	-I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.		
DR	PIR; A01868; KIHUHU.		
DR	HSP; P80362; IWL.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	InterPro; IPR003596; Ig_V.		
DR	Pfam; PF00047; Ig; 1.		
DR	SMART; SM00406; IGV; 1.		
KW	Immunoglobulin v region; Bence-Jones protein.		
FT	DOMAIN 1 23		
FT	DOMAIN 24 34		
FT	DOMAIN 35 49		
FT	DOMAIN 50 56		
FT	DOMAIN 57 88		
FT	DOMAIN 89 97		
FT	DOMAIN 98 107		
FT	DISULFID 23 88		
FT	NON_TER 108 108		
SQ	SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;		

Alignment Scores:

Pred. No.:	1,23e-41	Length:	108
Score:	467.00	Matches:	91
Percent Similarity:	92.52%	Conservative:	8
Best Local Similarity:	85.05%	Mismatches:	8
Query Match:	66.91%	Indels:	0

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DB: 1 1 Gaps: 0
US-08-728-463B-206 (1-388) x KV1V_HUMAN (1-108)
QY 67 GACATCCAGATGACCCAGTCTCCATCTTCGGTCTGTCATCTCTAGAGACAGAGTCACC 126
Db 1 AsplleGlnLeuThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThr 20
QY 127 ATCACTTGTGCGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCA 186
Db 21 IleThrCysArgAlaSerGlnSerValTyraGntyrValatrrPheGlnGlnlyPro 40
QY 187 GGAAGAGCCCTAAGCTCTGATCTTATGCTGCATCCAGTTTGCAGAGTGGGTCCCATCA 246
Db 41 GlyLysAlaProGlnValLeuIleTyraAlaSerSerLeuProSerGlyValProSer 60
QY 247 AGGTTTCAGCGGCGAGTCGGGACAGATTTCATCTCCACATCAGCAGCCTCGAGCCT 306
Db 61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80
QY 307 GAAGATTTTGCACCTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAG 366
Db 81 GluAspPheAlaThrTyTy-CysGlnGlnAsnTyrrileThrProThrSerPheGlyGln 100
QY 367 GGGACCAAGCTGGAGATCAAA 387
Db 101 GlyThrArgValGluileLys 107

RESULT 9
KV1V_HUMAN STANDARD; PRT; 108 AA.
AC P04430.
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE IG kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240;
RA Dwulet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR PIR; A01878; KIHUBN.
DR HSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_V.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Amyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Alignment Scores:
Pred. No.: 1.56e-41 Length: 108
Score: 466.00 Matches: 87
Percent Similarity: 92.52% Conservative: 12
Best Local Similarity: 81.31% Mismatches: 8
Query Match: 66.76% Indels: 0
DB: 1 Gaps: 0

US-08-728-463B-206 (1-388) x KV1V_HUMAN (1-108)
QY 67 GACATCCAGATGACCCAGTCTCCATCTTCGGTCTGTCATCTCTAGAGACAGAGTCACC 126
Db 1 AsplleGlnLeuThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThr 20
QY 127 ATCACTTGTGCGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCA 186
Db 21 IleThrCysArgAlaSerGlnSerValTyraGntyrValatrrPheGlnGlnlyPro 40
QY 187 GGAAGAGCCCTAAGCTCTGATCTTATGCTGCATCCAGTTTGCAGAGTGGGTCCCATCA 246
Db 41 GlyLysAlaProGlnValLeuIleTyraAlaSerSerLeuProSerGlyValProSer 60
QY 247 AGGTTTCAGCGGCGAGTCGGGACAGATTTCATCTCCACATCAGCAGCCTCGAGCCT 306
Db 61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80
QY 307 GAAGATTTTGCACCTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAG 366
Db 81 GluAspPheAlaThrTyTy-CysGlnGlnAsnTyrrileThrProThrSerPheGlyGln 100
QY 367 GGGACCAAGCTGGAGATCAAA 387
Db 101 GlyThrArgValGluileLys 107

RESULT 10
KV1L_HUMAN STANDARD; PRT; 108 AA.
AC P01604;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-I region Kue.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE.
RX MEDLINE=79237924; PubMed=112021;
RA Eulitz M., Kley H.-P., Zeitler H.-J.;
RT "The primary structure of the Bence-Jones protein Kue. The amino acid
sequence of the variable part of a human L-chain of the kappa-type.";
RL Hoppe-Seyler's Z. Physiol. Chem. 360:725-734(1979).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR PIR; A01870; KIHUKU.
DR HSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 12127 MW; 906679A5D90E498 CRC64;

Alignment Scores:
Pred. No.: 2e-41 Length: 108
Score: 465.00 Matches: 87
Percent Similarity: 91.59% Conservative: 11
Best Local Similarity: 81.31% Mismatches: 9
Query Match: 66.62% Indels: 0
DB: 1 Gaps: 0

US-08-728-463B-206 (1-388) x KV1L_HUMAN (1-108)

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QY 67 GACATCCAGATGACCCAGTCTCCATCTTCGGTCTCGCATCTCTAGGACAGAGTCACC 126
 DB 1 AspIleGlnMetThrGlnSerProSerThrGlnProAlaSerValGlyAspArgValThr 20
 QY 127 ATCACTTGTTCGGCGAGTCCAGGATATTAGCAGCTGGTGTAGCCTGGTATCAGCATRAACCA 186
 DB 21 IleThrCysArgAlaSerGlnSerIleAsnIleThrPheLeuAlaThrPyrGlnGlnLysPro 40
 QY 187 GGGAAAGCCCTTAAGCTCTGATCTATGCTGATCCAGTTTGCAGAGTGGGTGCCATCA 246
 DB 41 GluLysAlaProLysLeuLeuIleThrLysAlaSerThrLeuGluThrGlyValProSer 60
 QY 247 AGTTTCAGCGGAGTCTGGACAGATTTCACTCTCAGCATCAGAGCCCTGCAGCCT 306
 DB 61 ArgPheSerGlySerGlyThrGluPheThrLeuThrIleAsnSerLeuGlnPro 80
 QY 307 GAAGATTTTGCACTTACTTATTCACAGGCTTAATAGTTTCCCGTACACTTTTGGCCAG 366
 DB 81 AspAspPheAlaThrTyrTyrCysGlnGlnTyrSerArgTyrProThrPheGlyGln 100
 QY 367 GGGACCAAGCTGGAGATCAA 387
 DB 101 GlyThrLysLeuAspIleLys 107

RESULT 11
 KVIF_HUMAN
 ID KVIF_HUMAN STANDARD; PRT; 108 AA.
 AC P01598;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region EU.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=71064023; PubMed=5489770;
 RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
 RT acid sequence of the light chain."
 RL Biochemistry 9:3155-3161(1970).
 RN [2]
 RP DISULFIDE BOND.
 RX MEDLINE=71064027; PubMed=4923144;
 RA Gall W.E., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. X.
 RT Intrachain disulfide bonds."
 RL Biochemistry 9:3188-3196(1970).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PIR; A01866; KIHUEU.
 DR HSP; P01607; IREI.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGv; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;

Alignment Scores:

Pred. No.: 2.55e-41

Length: 108

Score: 464.00 Matches: 88
 Percent Similarity: 91.59% Conservative: 10
 Best Local Similarity: 82.24% Mismatches: 9
 Query Match: 66.48% Indels: 0
 DB: 1 Gaps: 0

US-08-728-463b-206 (1-388) x KVIF_HUMAN (1-108)

QY 67 GACATCCAGATGACCCAGTCTCCATCTTCGGTCTCGCATCTCTAGGACAGAGTCACC 126
 DB 1 AspIleGlnMetThrGlnSerProSerThrLeuSerAlaSerValGlyAspArgValThr 20
 QY 127 ATCACTTGTTCGGCGAGTCCAGGATATTAGCAGCTGGTGTAGCCTGGTATCAGCATRAACCA 186
 DB 21 IleThrCysArgAlaSerGlnSerIleAsnIleThrPheLeuAlaThrPyrGlnGlnLysPro 40
 QY 187 GGGAAAGCCCTTAAGCTCTGATCTATGCTGATCCAGTTTGCAGAGTGGGTGCCATCA 246
 DB 41 GluLysAlaProLysLeuLeuIleThrLysAlaSerThrLeuGluThrGlyValProSer 60
 QY 247 AGTTTCAGCGGAGTCTGGACAGATTTCACTCTCAGCATCAGAGCCCTGCAGCCT 306
 DB 61 ArgPheIleGlySerGlyThrGluPheThrLeuThrIleSerSerLeuGlnPro 80
 QY 307 GAAGATTTTGCACTTACTTATTCACAGGCTTAATAGTTTCCCGTACACTTTTGGCCAG 366
 DB 81 AspAspPheAlaThrTyrTyrCysGlnGlnTyrAsnSerAspSerLysMetPheGlyGln 100
 QY 367 GGGACCAAGCTGGAGATCAA 387
 DB 101 GlyThrLysValGluValLys 107

RESULT 12

KVIF_HUMAN

ID KVIF_HUMAN STANDARD; PRT; 108 AA.

AC P01607;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-I region Rei.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=76023758; PubMed=809329;

RA Palm W., Hilschmann N.;

RT "The primary structure of a crystalline monoclonal immunoglobulin

RT kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation

RT and characterization of the tryptic peptides; the complete amino acid

RT sequence of the protein; a contribution to the elucidation of the

RT three-dimensional structure of antibodies, in particular their

RT combining site.";

RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).

RN [2]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RX MEDLINE=76039968; PubMed=1182131;

RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;

RT "The molecular structure of a dimer composed of the variable portions

RT of the Bence-Jones protein Rei refined at 2.0-A resolution.";

RL Biochemistry 14:4943-4952(1975).

CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)

CC MARKER.

CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

CC PIR; A01873; KIHURE.

DR PDB; IREI; 17-FEB-84.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGv; 1.

DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.

KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.

FT DOMAIN 1 23

FT FRAMEWORK-1.

FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88
 FT STRAND 4 7
 FT STRAND 10 13
 FT TURN 15 16
 FT STRAND 19 25
 FT STRAND 20 31
 FT TURN 30 35
 FT STRAND 33 38
 FT TURN 40 41
 FT STRAND 45 49
 FT TURN 50 52
 FT STRAND 53 54
 FT TURN 56 57
 FT TURN 60 61
 FT STRAND 62 67
 FT TURN 68 69
 FT STRAND 70 75
 FT HELIX 80 82
 FT STRAND 85 90
 FT STRAND 98 98
 FT STRAND 102 106
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Alignment Scores:
 Pred. No.: 6,76e-41 Length: 108
 Score: 460.00 Matches: 88
 Percent Similarity: 89.62% Conservative: 7
 Best Local Similarity: 83.02% Mismatches: 11
 Query Match: 65.90% Indels: 0
 DB: 1 Gaps: 0

US-08-728-463B-206 (1-388) x KV10_HUMAN (1-108)

QY 67 GACATCCAGATACCCAGTCTCCATCTCCGTCGTCTGTCATCTCTAGGAGACAGAGTCACC 126
 Db 1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
 QY 127 ATCACTGTGCGGAGTCAGGATATAGCAGCTGGTACCTGGTATCAGCATCAACCA 186
 Db 21 IleThrCysGlnAlaSerGlnAspIleIleLysrTyLeuAsnTrpTyGlnGlnThrPro 40
 QY 187 GGGAAAGCCCTAAGCTCTCTGATCTATGCTGCATCCAGTTTGCAGAGTGGGGTCCCATCA 246
 Db 41 GlyLysAlaProLysLeuLeuIleTyGluAlaSerAsnLeuGlnAlaGlyValProSer 60
 QY 247 AGTTTCAGCGCAGTGGATCTGGACAGATTTCACTCTCAACATCAGCAGCTGCAGCCT 306
 Db 61 ArgPheSerGlySerGlyThrAspTyThrPheThrIleSerSerLeuGlnPro 80
 QY 307 GAAGATTTGCACTTACTATTGTCACAGGCTAATAGTTTCCCGTACACTTTTGGCCAG 366
 Db 81 GluAspIleAlaThrTyTyCysGlnGlnTyGlnSerLeuProTyThrPheGlyGln 100
 QY 367 GGGACCAAGCTGGAGATC 384
 Db 101 GlyThrLysLeuGlnIle 106

RESULT 13

KV1R_HUMAN
 ID KV1R_HUMAN STANDARD; PRT; 108 AA.
 AC P01610;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region WEA.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=83273707; PubMed=6410398;
 RA Goni F., Frangione B.;
 RT "Amino acid sequence of the Fv region of a human monoclonal IgM
 (protein WEA) with antibody activity against 3,4-pyruvylated
 galactose in Klebsiella polysaccharides K30 and K33.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841 (1983).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
 AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
 WALDENSTROM'S MACROGLOBULINEMIA.

DR PIR; A01876; KIHUWE.
 DR HSP; P80362; IWLTL.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF000447; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR Immunoglobulin V region; Monoclonal antibody.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Alignment Scores:
 Pred. No.: 1.1e-40 Length: 108
 Score: 458.00 Matches: 88
 Percent Similarity: 90.65% Conservative: 9
 Best Local Similarity: 82.24% Mismatches: 10
 Query Match: 65.62% Indels: 0
 DB: 1 Gaps: 0

US-08-728-463B-206 (1-388) x KV1R_HUMAN (1-108)

QY 67 GACATCCAGATACCCAGTCTCCATCTCCGTCGTCTGTCATCTCTAGGAGACAGAGTCACC 126
 Db 1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
 QY 127 ATCACTGTGCGGAGTCAGGATATAGCAGCTGGTACCTGGTATCAGCATCAACCA 186
 Db 21 IleThrCysArgAlaSerGlnGlyIleArgAsnAspLeuThrTyGlnGlnLysPro 40
 QY 187 GGGAAAGCCCTAAGCTCTCTGATCTATGCTGCATCCAGTTTGCAGAGTGGGGTCCCATCA 246
 Db 41 GlyThrAlaProLysArgLeuIleTyGlyAlaThrSerLeuGlnSerGlyValProSer 60
 QY 247 AGTTTCAGCGCAGTGGATCTGGACAGATTTCACTCTCAACATCAGCAGCTGCAGCCT 306
 Db 61 ArgPheSerGlySerGlyThrAspTyThrPheThrIleSerSerLeuGlnPro 80
 QY 307 GAAGATTTGCACTTACTATTGTCACAGGCTAATAGTTTCCCGTACACTTTTGGCCAG 366
 Db 81 GluAspPheAlaThrTyTyCysLeuGlnTySerSerPheProThrPheGlyGln 100
 QY 367 GGGACCAAGCTGGAGATCAA 387
 Db 101 GlyThrLysValGluValLys 107

RESULT 14

KVIG_HUMAN
 ID KVIG_HUMAN STANDARD; PRT; 108 AA.
 AC P01599;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region GNL.

Db 81 GluAspIleAlaThrTyrTyrCysGlnGlnTyrAspTyrLeuProTrpThrPheGlyGln 100
QY 367 GGGACCAAGCTGGAGATCAAA 387
|||||:|||||
Db 101 GlyThrLysValGluIleLys 107

Search completed: June 3, 2003, 09:04:03
Job time : 9.35964 secs

OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX	NCB1_TaxID=9606;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=75059122; PubMed=4215718;
RA	Laure C.J., Watanabe S., Hilschmann N.;
RT	"The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal.), I. The amino acid sequence of the L-chain of kappa-type, subgroup I."
RL	Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504 (1973).
CC	- - MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC	- - MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.
DR	PIR; A01867; KIHUGL.
DR	HSP; P01607; IREI.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; ig; 1.
DR	SMART; SM00406; IGv; 1.
KW	Immunoglobulin v region.
FT	DOMAIN 1 23
FT	DOMAIN 24 34
FT	DOMAIN 35 49
FT	DOMAIN 50 56
FT	DOMAIN 57 88
FT	DOMAIN 89 97
FT	DOMAIN 98 107
FT	DISULFID 23 88
FT	NON TER 108 108
SQ	SEQUENCE 108 AA; 11814 MW; CIAD3CBOF600FF73 CRC64;

Alignment Scores:

Pred. No.:	1.4e-40	Length:	108
Score:	457.00	Matches:	89
Percent Similarity:	90.6%	Conservative:	8
Best Local Similarity:	83.18%	Mismatches:	10
Query Match:	65.4%	Indels:	0
DB:	1	Gaps:	0

US-08-728-463B-206 (1-388) x KVIG_HUMAN (1-108)

QY	67	GACATCCAGATGACCAGTCTCCATCTTCCTGGTGTCATCTGTAGGAGACAGAGTCACC	126
Dd	1	AspLeuGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr	20
QY	127	ATCACTTTGCGGCCAGTCAGCATATTAGCAGCTGGTTCACCTCGTATCAGCATAAACA	186
Dd	21	IleIleCysArgAlaSerGlnGlyIleArgAsnAspLeuThrTrpTyrGlnGlnLysPro	40
QY	187	GGGAAGCCCCAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGTCCCACATCA	246
Dd	41	GlyLysAlaProLysGluLeuIleTyrAlaAlaSerAsnLeuGlnSerGlyValProSer	60
QY	247	AGGTTTCAGGCGAGTGGATCTGGACAGATTCTACTCTCACATCAGCAGCTCGAGCCT	306
Dd	61	ArgPheSerGlySerGlyAlaGlyThrGluPheThrLeuThrIleSerSerLeuGlnPro	80
QY	307	GAAGAATTTTGCAACTTACTATTGTCAACAGCTAAATAGTTTCCCGTACACTTTGGCCAG	366
Dd	81	GluAspPheAlaThrTyrTyrCysLeuGlnGlnAsnSerTyrProArgSerPheGlyGln	100
QY	367	GGGACCAAGCTGGAGATCAAA	387
Dd	101	GlyThrLysValGluIleLys	107

RESULT 15

ID	KVIB_HUMAN
AC	P01594;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 34.4431 Seconds
(without alignments)
4642.224 Million cell updates/sec

Title: US-08-728-463B-206

Perfect score: 698

Sequence: 1 ATGGACATCATGCTCCCGC.....GACCAAGCTGGAGATCAAC 388

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1343160

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-Q=/cgn2.1/USPTO spool/US08728463/runat_03062003_085614.16815/app_query.fasta_1.3690
-DB=SPTREMBL_21 -QFWT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08728463 @CGN_1.1.380 @runat_03062003_085614.16815 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

SPTREMBL_21:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phase:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_virus:
16: sp_bacteriaph:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	481	68.9	108 4 Q9UL77	Q9UL77 homo sapien

2	473	67.8	108 4 Q9UL70	Q9UL70 homo sapien
3	470.5	67.4	107 4 Q96SA9	Q96SA9 homo sapien
4	470	67.3	234 11 Q8R062	Q8R062 mus musculus
5	463	66.3	234 11 Q91WF8	Q91WF8 mus musculus
6	462	66.2	234 11 Q8VCP0	Q8VCP0 mus musculus
7	456	65.3	108 4 Q9UL79	Q9UL79 homo sapien
8	445.5	63.8	107 4 Q9UL81	Q9UL81 homo sapien
9	439	62.9	127 11 Q925S9	Q925S9 mus musculus
10	431	61.7	233 11 Q91WS9	Q91WS9 mus musculus
11	414	59.3	116 4 Q96PF6	Q96PF6 homo sapien
12	402	57.6	214 11 Q9R1A5	Q9R1A5 mus musculus
13	394	56.4	108 4 Q9UL83	Q9UL83 homo sapien
14	393	56.3	109 11 Q920S6	Q920S6 mus musculus
15	392	56.2	298 11 Q9QYF0	Q9QYF0 mus musculus
16	390	55.9	108 11 Q8VIJ0	Q8VIJ0 mus musculus
17	383.5	54.9	239 4 Q8TCD0	Q8TCD0 homo sapien
18	383	54.9	107 11 Q9JL84	Q9JL84 mus musculus
19	382.5	54.8	109 4 Q9UL78	Q9UL78 homo sapien
20	379.5	54.4	109 4 Q9UL85	Q9UL85 homo sapien
21	378	54.2	238 11 Q99M37	Q99M37 mus musculus
22	377	54.0	111 11 Q920S9	Q920S9 mus musculus
23	364.5	52.2	109 4 Q9UL86	Q9UL86 homo sapien
24	362	51.9	238 11 Q8VC16	Q8VC16 mus musculus
25	357.5	51.2	241 11 Q921A6	Q921A6 mus musculus
26	354.5	50.8	134 11 Q8VDD0	Q8VDD0 mus musculus
27	350.5	50.2	239 11 Q8VC55	Q8VC55 mus musculus
28	347	49.7	107 11 Q9ER29	Q9ER29 mus musculus
29	342.5	49.1	106 5 Q9U410	Q9U410 schistosoma
30	340	48.7	234 11 Q8R028	Q8R028 mus musculus
31	337	48.3	99 11 Q9JL74	Q9JL74 mus musculus
32	334	47.9	101 11 Q9JL78	Q9JL78 mus musculus
33	327	46.8	103 11 Q9JL80	Q9JL80 mus musculus
34	321.5	46.1	235 11 Q9JL72	Q9JL72 mus musculus
35	318	45.6	97 11 Q9JL76	Q9JL76 mus musculus
36	305.5	43.8	104 11 Q9JL82	Q9JL82 mus musculus
37	304	43.6	114 4 Q9UL80	Q9UL80 homo sapien
38	294	42.1	109 6 Q9N0W5	Q9N0W5 cryptotolagus
39	265	38.0	130 4 Q9NFP29	Q9NFP29 homo sapien
40	262.5	37.6	233 4 Q8TBC9	Q8TBC9 homo sapien
41	250.5	35.9	237 4 Q8WTU6	Q8WTU6 homo sapien
42	246.5	35.3	237 4 Q8WUK4	Q8WUK4 homo sapien
43	231	33.1	107 4 Q9UL82	Q9UL82 homo sapien
44	230.5	33.0	107 4 Q9NSD6	Q9NSD6 homo sapien
45	225.5	32.3	236 4 Q96E61	Q96E61 homo sapien

ALIGNMENTS

RESULT 1

ID	Q9UL77	PRELIMINARY;	PRT;	108 AA.
AC	Q9UL77;			
DT	01-MAY-2000 (Tremblrel. 13, Created)			
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)			
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)			
DE	Myosin-reactive immunoglobulin light chain variable region (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98277139; PubMed=9614934;			
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,			
RA	Young D.C.;			
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."			
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).			
DR	EMBL; AF035037; AAD56273.1; -			
DR	HSSP; P01607; IREI.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_v.			

DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
FT NON_TER 1 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;
Alignment Scores:
Pred. No.: 6.14e-46 Length: 108
Score: 481.00 Matches: 94
Percent Similarity: 93.46% Conservative: 6
Best Local Similarity: 87.85% Mismatches: 7
Query Match: 68.91% Indels: 0
DB: 4 Gaps: 0
US-08-728-463B-206 (1-388) x Q9UL77 (1-108)
QY 67 GACATCCAGATGACCCAGTCTCCATCTCCGTCCTGCATCTGTAGAGACAGAGTCACC 126
Db 1 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
QY 127 ATCACTTTGTGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATATAACCA 186
Db 21 IleThrCysArgAlaSerGlnSerIleSerSerTyrlleuAsnTrpTyrlGlnGlnLysPro 40
QY 187 GGGAAAGCCCTTAAGCTCTGATCTGATCTGCTGATCTCCATCTCCGTCCTGCATCTGTAGAGACAGAGTCACC 246
Db 41 GlyLysAlaProAsnLeuLeuIleTyrlAlaAlaSerSerLeuGlnSerGlyValProSer 60
QY 247 AGTTTCAGCGCAGTCGATCTGATCTGATCTGATCTCCATCTCCGTCCTGCATCTGTAGAGACAGAGTCACC 306
Db 61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80
QY 307 GAAGATTTTGCACCTTACTTACTTCTCAACAGGCTTAATAGTTTCCCGTACACTTTTGGCCAG 366
Db 81 GluAspPheAlaThrTyrlCysGlnSerTyrlSerThrSerThrTrpThrPheGlyGlu 100
QY 367 GGGACCAAGCTGGAGATCAAA 387
Db 101 GlyThrLysValGluIleLys 107
RESULT 2
ID Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; RAD56280.1; -;
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
FT NON_TER 1 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
Alignment Scores:
Pred. No.: 4.97e-45 Length: 108
Score: 470.50 Matches: 95
Percent Similarity: 92.52% Conservative: 4
Best Local Similarity: 88.79% Mismatches: 7
Query Match: 67.41% Indels: 1
DB: 4 Gaps: 1
US-08-728-463B-206 (1-388) x Q96SA9 (1-107)
QY 67 GACATCCAGATGACCCAGTCTCCATCTTCGTCGTCTGATCTCTAGAGACAGAGTCACC 126
Db 1 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20


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RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA "Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035033; AAD56269.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 107 107
FT SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Alignment Scores:
Pred. No.: 6.6e-42 Length: 107
Score: 445.50 Matches: 89
Percent Similarity: 89.72% Conservative: 7
Best Local Similarity: 83.18% Mismatches: 10
Query Match: 63.83% Indels: 1
DB: 4 Gaps: 1

US-08-728-463B-206 (1-388) x Q9UL81 (1-107)

QY 67 GACATCCAGATGACCCAGTCCATCTCCGTGTCATCTGTAGGAGACAGTCACC 126
Db 1 MetArgAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCys 20
QY 127 ATCACTTGTGGCGGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAACCA 186
Db 21 IleThrCysArgAlaSerGlnSerIleSerAsnIleLeuAsnTrpIleGlnGlnLysPro 40
QY 187 GGGAAAGCCCTAAGCTCTGATCTGTCATCCAGCTGGTTGCAAGTGGGGTCCCATCA 246
Db 41 GlyLysAlaProAsnLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSer 60
QY 247 AGGTTACAGCGGAGTCGATCTGGAGAGATTTCACTCTACCATCAGCAGCTTCAGCCT 306
Db 61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerGlyLeuGlnAla 80
QY 307 GAAGATTTTGCAACTTACTATTGTCACAGGCTAATAGTTTCCCGTACACTTTTGGCCAG 366
Db 81 GluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSer---AlaLeuThrPheGlyPro 99
QY 367 GGGACCAAGCTGGAGATCAAA 387
Db 100 GlyThrLysValAspIleArg 106

RESULT 9
Q925S9 PRELIMINARY; PRT; 127 AA.
AC Q925S9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Immunoglobulin light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C;
RX MEDLINE=99306687; PubMed=10380019;
RA Tripathi P.K., Qin H., Bhattacharya-Chatterjee M., Ceriani R.L.,
RA Foon K.A., Chatterjee S.K.;
RT "Construction and characterization of a chimeric fusion protein
RT consisting of an anti-idiotype antibody mimicking a breast cancer-
RL associated antigen and the cytokine GM-CSF.";
RL Hybridoma 18:193-202 (1999).
DR EMBL; AF124721; AAK55120.1; -.

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DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 127 127
SQ SEQUENCE 127 AA; 13794 MW; 13FG1BBB8B981FA5 CRC64;

Alignment Scores:
Pred. No.: 3.69e-41 Length: 127
Score: 439.00 Matches: 88
Percent Similarity: 77.95% Conservative: 11
Best Local Similarity: 69.29% Mismatches: 28
Query Match: 62.89% Indels: 0
DB: 11 Gaps: 0

US-08-728-463B-206 (1-388) x Q925S9 (1-127)

QY 7 ATGATGGTCCCGCTCAGCTCTGGGGTCTGCTGCTGCTCCAGGTTCCAGATGC 66
Db 1 MetArgAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCys 20
QY 67 GACATCCAGATGACCCAGTCCATCTCCGTGTCATCTGTAGGAGACAGTCACC 126
Db 21 AsplieGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
QY 127 ATCACTTGTGGCGGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAACCA 186
Db 41 LeuThrCysArgAlaSerGlnAspIleGlyLeuLeuLeuHisTrpLeuGlnGlnGluPro 60
QY 187 GGGAAAGCCCTAAGCTCTGATCTGTCATCCAGCTGGTTGCAAGTGGGGTCCCATCA 246
Db 61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys 80
QY 247 AGGTTACAGCGGAGTCGATCTGGAGAGATTTCACTCTACCATCAGCAGCTTCAGCCT 306
Db 81 ArgPheSerGlySerArgSerGlySerAspIleThrLeuThrIleSerSerLeuGluSer 100
QY 307 GAAGATTTTGCAACTTACTATTGTCACAGGCTAATAGTTTCCCGTACACTTTTGGCCAG 366
Db 101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
QY 367 GGGACCAAGCTGGAGATCAAA 387
Db 121 GlyThrLysLeuGluIleLys 127

RESULT 10
Q91WS9 PRELIMINARY; PRT; 233 AA.
AC Q91WS9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 25.8 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RX Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013496; AAH13496.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 233 AA; 25781 MW; B1CL84DA149A16EB CRC64;

Alignment Scores:
Pred. No.: 3.24e-40 Length: 233
Score: 431.00 Matches: 84
Percent Similarity: 82.05% Conservative: 12
Best Local Similarity: 71.79% Mismatches: 21

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN NCBI_TaxID=10090;
RP [1]
RP SEQUENCE FROM N.A.

RC STRAIN=BALB/C; TISSUE=SPLEEN;
RX MEDLINE=20183931; PubMed=10706631;
RA Shinohara N., Demura T., Fukuda H.;
RT "Isolation of a vascular cell wall-specific monoclonal antibody
RT recognizing a cell polarity by using a phage display subtraction
RT method.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).

DR EMBL; AB036341; BAB8633.1; -;
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IG; 2.
SQ SEQUENCE 298 AA; 31867 MW; EOF96B8A17004317 CRC64;

Alignment Scores:

Pred. No.:	9e-36	Length:	298
Score:	392.00	Matches:	74
Percent Similarity:	81.98%	Conservative:	17
Best Local Similarity:	66.67%	Mismatches:	20
Query Match:	56.16%	Indels:	0
DB:	11	Gaps:	0

US-08-728-463B-206 (1-388) x Q9QYP0 (1-298)

QY	55	GGTTCAGATGCCACATCCAGATCCAGTCCATCTCCGTCTCGATCTGATCTGTAGGA	114
Db	169	GlyGlyGlySerAspIleGluThrGlnSerProAlaSerLeuSerAlaSerValGly	188
QY	115	GACAGAGTCACTCTGCGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGTAT	174
Db	189	GluThrValThrIleThrCysArgAlaSerGlyAsnIleHisAsnIleuAlaIleTyr	208
QY	175	CAGCATAAACCCAGGAAAGCCCTAAGCTCCTGATCTGATCTGATCCAGTTTGCAAGT	234
Db	209	GlnGlnLysGlnGlyLysSerProGlnLeuLeuValTyrAsnAlaLysThrLeuAlaAsp	228
QY	235	GGGTCCTCCATCAAGTTTCAGCGCAGTGGATCTGGGACAGATTTCATCTCACCATCAGC	294
Db	229	GlyValProSerArgPheSerGlySerGlyThrGlnTyrSerLeuLysIleAsn	248
QY	295	AGCTGCGAGCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTAC	354
Db	249	SerLeuGlnProGluAspPheGlySerTyrTyrCysGlnHisPheThrThrThrProTyr	268
QY	355	ACTTTGGCCAGGGACCAAGCTGGAGATCAAA	387
Db	269	ThrPheGlyGlyGlyThrLysLeuGluIleLys	279

Search completed: June 3, 2003, 09:15:49
Job time : 36.4431 secs

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Db 61 ArgPheSerGlySerGlyGlnAspTyrSerLeuThrIleSerLeuGluTyr 80
|||
307 GAAGATTTTGCACCTTACTTATGTCACAGGCTAAATAGTTTCCCGTACACTTTTGCCACG 366
|||
Db 81 GluAspMetGlyIleTyrTyrCysLeuGlnTyrAspGluPheProPheThrPheGlySer 100
|||
QY 367 GGGACCAAGCTGGAGATCAAA 387
|||
Db 101 GlyThrLysLeuGluIleLys 107
|||
RESULT 13
Q9UL83 PRELIMINARY; PRT; 108 AA.
AC Q9UL83;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
(Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035031; AAD56267.1; -.
DR HSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96BEA CRC64;
Alignment Scores:
Pred. No.: 4,66e-36 Length: 108
Score: 394.00 Matches: 72
Percent Similarity: 85.98% Conservative: 20
Best Local Similarity: 67.29% Mismatches: 15
Query Match: 56.45% Indels: 0
DB: 4 Gaps: 0
US-08-728-463b-206 (1-388) x Q9UL83 (1-108)
QY 67 GACATCCAGATGACCCAGTCTCCATCTCCGTGCTGTCATCTGTAGGACAGAGTCACC 126
|||
Db 1 GluIleValMetThrGlnSerProAlaThrLeuSerValSerProGlyGluArgAlaThr 20
|||
QY 127 ATCACTTGTGGCGAGTCAGGATATTAGCAGCTGGTGTAGCTGGTATCAGCATAAACCA 186
|||
Db 21 LeuSerCysArgAlaSerGlnSerValSerAsnLeuAlaTrpTyrGlnGlnLysPro 40
|||
QY 187 GGGAAAGCCCTTAAGCTCTGATCTATGTCATCCAGTTTGCNAAGTGGGTCCCATCA 246
|||
Db 41 GlyGlnAlaProArgLeuLeuIleTyrCysAlaSerThrArgAlaThrGlyIleProAla 60
|||
QY 247 AGGTTTCAGCGGAGTGGATCTGGACAGATTTTCATCTCCATCAGCAGCTGCAGCCT 306
|||
Db 61 ArgPheSerGlySerGlyThrGluPheThrLeuThrIleSerSerLeuGlnPhe 80
|||
QY 307 GAAGATTTTGCACCTTACTTATGTCACAGGCTAAATAGTTTCCCGTACACTTTTGCCACG 366
|||
Db 81 GluAspPheAlaValTyrTyrCysGlnHisTyrAsnAsnTyrProPheThrPheGlyPro 100
|||
QY 367 GGGACCAAGCTGGAGATCAAA 387
|||

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Db 101 GlyThrLysValAspIleLys 107
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RESULT 14
Q920E6 PRELIMINARY; PRT; 109 AA.
AC Q920E6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Pterin-mimicking anti-idiotope kappa chain variable region
(Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
in Mammalian Cells.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307938; AAL09422.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11943 MW; DAD3F98E05DD1501 CRC64;
Alignment Scores:
Pred. No.: 6,06e-36 Length: 109
Score: 393.00 Matches: 75
Percent Similarity: 84.11% Conservative: 15
Best Local Similarity: 70.09% Mismatches: 17
Query Match: 56.30% Indels: 0
DB: 11 Gaps: 0
US-08-728-463b-206 (1-388) x Q920E6 (1-109)
QY 67 GACATCCAGATGACCCAGTCTCCATCTCCGTGCTGTCATCTGTAGGACAGAGTCACC 126
|||
Db 1 AspIleGlnMetThrGlnSerProAlaSerLeuSerAlaSerValGlyGluThrValThr 20
|||
QY 127 ATCACTTGTGGCGAGTCAGGATATTAGCAGCTGGTGTAGCTGGTATCAGCATAAACCA 186
|||
Db 21 IleThrCysArgAlaSerGlyAsnIleHisAsnTyrLeuAlaTrpTyrGlnGlnLysGln 40
|||
QY 187 GGGAAAGCCCTTAAGCTCTGATCTATGTCATCCAGTTTGCNAAGTGGGTCCCATCA 246
|||
Db 41 GlyLysSerProGlnLeuValTyrAsnAlaLysThrLeuAlaAspGlyValProSer 60
|||
QY 247 AGGTTTCAGCGGAGTGGATCTGGACAGATTTTCATCTCCATCAGCAGCTGCAGCCT 306
|||
Db 61 ArgPheSerGlySerGlyThrGlnTyrSerLeuLysIleAsnSerLeuGlnPro 80
|||
QY 307 GAAGATTTTGCACCTTACTTATGTCACAGGCTAAATAGTTTCCCGTACACTTTTGCCACG 366
|||
Db 81 GluAspPheGlySerTyrTyrCysGlnHisPheTyrSerThrProTyrPheGlyGly 100
|||
QY 367 GGGACCAAGCTGGAGATCAAA 387
|||
Db 101 GlyThrLysLeuGluIleLys 107
|||
RESULT 15
Q9QYF0 PRELIMINARY; PRT; 298 AA.
AC Q9QYF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CN 8 scFv.
CN 8.
OS Mus musculus (Mouse).

```


GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 08:56:21 ; Search time 25.0964 Seconds
(without alignments)
4120.219 Million cell updates/sec

Title: US-08-728-463B-206

Perfect score: 698

Sequence: 1 ATGGACATGATGTCCTCCGCC.....GACCAAGCTGGAGATCAAC 388

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 1816940

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=A_Geneseq_101002 -QFMT=faetan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLING=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptt -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-NO MAP -LARGEQUERY -NEG SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
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15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
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18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	624	89.4	236	23	AAU74297	Anti-human AILIM m
2	589.5	84.5	241	22	AA82912	Human immune respo
3	588	84.2	130	16	AA875394	Anti-interleukin-1
4	584	83.7	230	21	AA556737	Amino acid sequenc
5	578.5	82.9	237	21	AA596298	Human IGFAM-10 imm
6	575	82.4	129	19	AA570379	Anti-human CD23 SE
7	574.5	82.3	237	21	AA596289	Human IGFAM-1 immu
8	574.5	82.3	237	21	AA596301	Human IGFAM-13 imm
9	573	82.1	128	17	AAW01527	Monoclonal antibody
10	573	82.1	128	18	AAW24990	Monoclonal antibody
11	573	82.1	129	21	AA556722	Amino acid sequenc
12	571	81.8	129	23	ABG35326	Thrombopoietin ago
13	571	81.8	132	18	AAW22842	Human anti-tumour
14	571	81.8	134	23	AAW47645	Human protein sequ
15	569	81.5	260	23	ABP41164	Human ovarian anti
16	568	81.4	124	21	AA556723	Amino acid sequenc
17	568	81.4	129	16	AAAR65018	93KA9 anti-Varicel
18	567.5	81.3	234	14	AAAR38162	Sequence of the ka
19	567	81.2	234	13	AAAR20058	Light chain of 3p6
20	565	80.9	146	22	AA893115	Human protein SEQ
21	558	79.9	139	23	ABP43157	Human ovarian anti
22	557	79.8	129	15	AAAR57482	Humanized 1308F VL
23	557	79.8	129	17	AAAR92085	Humanized antibody
24	556	79.7	236	21	AA596297	Human IGFAM-9 immu
25	554.5	79.4	128	21	AA556717	Amino acid sequenc
26	553.5	79.3	237	21	AAAB15546	Human immune syste
27	553	79.2	129	21	AA556724	Amino acid sequenc
28	553	79.2	236	14	AAAR42065	Human anti-HBs lig
29	548	78.5	234	18	AAW11638	Human anti-RSV mon
30	545	78.1	236	21	AA596293	Human IGFAM-5 immu
31	543	77.8	133	17	AAAR7057	CDR grafted anti-1
32	541.5	77.6	212	22	ABG18767	Novel human diagno
33	540	77.4	129	21	AA556721	Amino acid sequenc
34	539	77.2	117	14	AAAR38651	Human V-kappa frag
35	539	77.2	117	15	AAAR62931	Human V-kappa vk65
36	539	77.2	117	17	AAW03949	DNA fragment vk65.
37	539	77.2	117	18	AAW41147	Human vkappa65.15
38	539	77.2	117	19	AAW62185	Human DNA vkappa65
39	539	77.2	117	20	AAW40432	Amino acid sequenc
40	539	77.2	171	17	AAW03725	Humanised MAB 39-1
41	535	76.6	236	16	AAAR77614	Humanised 5G1.1 VL
42	535	76.6	236	23	ABP51696	5G1.1 light chain
43	534	76.5	128	15	AAAR54053	Sequence of the VL
44	532	76.2	264	19	AAAR73049	Humanised A33 scAb
45	532	76.2	532	19	AAW73051	Z33dCH2.z chimeric

ALIGNMENTS

RESULT 1
AAU74297
ID AAU74297 standard; Protein; 236 AA.
XX
AC AAU74297;
XX
DT 12-MAR-2002 (first entry)
XX
DE Anti-human AILIM monoclonal antibody clone Jmab-136, light chain.
XX
KW Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiallergic; antiulcer; neuroprotective; antithyroid; vasotropic;
KW immunosuppressive; dermatologic; antiinflammatory; hepatotropic;
KW activation inducible lymphocyte immunomodulatory molecule; AILIM;
KW monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;
KW multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;
KW allergic contact-type dermatitis; chronic inflammatory dermatosis;
KW systemic lupus erythematosus; autoimmune disorder; inflammation;
KW graft versus host reaction; immune rejection; intestinal immunity;

CC The sequence represents the variable light chain segment of a human
 CC monoclonal antibody (HuMab) against interleukin-1-alpha. The MAb is
 CC of subclass IgG4 and binds to lymphokines/monokines with an affinity
 CC of 10(9)/M. The Mab or fragment (Fv, single-chain Fv, Fab or F(ab'))
 CC 2) is used in the treatment of inflammation e.g. rheumatoid
 CC arthritis, osteoarthritis and inflammatory bowel diseases, and in
 CC the treatment of psoriasis, allergy, septic shock, graft vs host
 CC disease and tumours. The Mab or fragment can also be used for
 CC diagnosis.
 XX
 SQ Sequence 130 AA;

Alignment Scores:

Pred. No.: 1.56e-52 Length: 130
 Score: 588.00 Matches: 113
 Percent Similarity: 93.02% Conservative: 7
 Best Local Similarity: 87.60% Mismatches: 9
 Query Match: 84.24% Indels: 0
 DB: 16 Gaps: 0

US-08-728-463B-206 (1-388) x AAR75394 (1-130)

QY 1 ATGGACATGATGTCCTCCCGCTCAGCTCTGGGGCTCTGCTGCTGTTCCAGGTTC 60
 DB 1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpPheProGlySer 20
 QY 61 AGATGGACATCCAGATGACCCAGTCTCCATCTTCGCTGCTGTCATCTGTAGGAGACAGA 120
 DB 21 ArgCysAspIleGlnMetThrGlnSerProSerValSerAlaSerValGlyAspArg 40
 QY 121 GTCACCATCACTTGTGCGGGAGTCAGGATATTAGCAGCTGGTTCAGCTGGTATCAGCAT 180
 DB 41 ValThrIleThrCysArgAlaSerGlnGlyIleSerSerTrpLeuAlaTrpTyrGlnGln 60
 QY 181 AAACCCAGGAAAGCCCTTAAGCTCTGATCTATGCTGATCCAGTTTGCAAGTGGGTC 240
 DB 61 LysProGlyLysAlaProLysLeuLeuIleTyrGluAlaSerAsnLeuGluThrGlyVal 80
 QY 241 CCATCAAGGTTTCAGCGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCTG 300
 DB 81 ProSerArgPheSerGlySerGlySerGlySerAspPheThrLeuThrIleSerSerLeu 100
 QY 301 CAGCCTGAAGATTTGCAACTTACTATTGTCACAGGCTAATAGTTTCCCGTACACTTTT 360
 DB 101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnThrSerSerPheLeuLeuSerPhe 120
 QY 361 GGCACGGGACCAAGCTGGAGATCAAA 387
 DB 121 GlyGlyGlyThrLysValGluHisLys 129

RESULT 4

AAV56737
 ID AAV56737 standard; protein; 130 AA.

AC AAV56737;

XX 15-FEB-2000 (first entry)

XX Amino acid sequence of Cynomolgus V kappa cDNA clone 4-10.

XX Complementarity determining region; antibody; primate; immunogenicity;
 KW Old World ape; Old World monkey; antigen-binding affinity.

XX Macaca cynomolgus.

XX WO9955369-A1.

XX 04-NOV-1999.

XX 28-APR-1999; 99WO-US09131.

XX 28-APR-1998; 98US-0083367.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX Taylor AH;

XX WPI: 2000-023265/02.

XX N-PSDB; AA239340.

XX Antibodies containing donor complementarity determining regions and
 PT non-human primate acceptor frameworks, having reduced immunogenicity in
 PT humans -

XX Example 4; Page 96-97; 123pp; English.

XX The invention provides an antibody (Ab) comprising donor CDRs
 CC (complementarity determining regions) derived from a non-human antigen-
 CC specific donor antibody, and an acceptor framework from a non-human
 CC primate. The Abs are prepared by grafting CDRs from a non-human antigen-
 CC specific donor antibody onto homologous Old World ape or monkey acceptor
 CC frameworks. The Abs have reduced immunogenicity and are better tolerated
 CC in humans (because of the close similarity between the human and primate
 CC proteins), but retain the full antigen-binding affinity of the donor
 CC antibody.

XX Sequence 130 AA;

Alignment Scores:

Pred. No.: 4.04e-52 Length: 130
 Score: 584.00 Matches: 111
 Percent Similarity: 93.02% Conservative: 9
 Best Local Similarity: 86.05% Mismatches: 9
 Query Match: 83.67% Indels: 0
 DB: 21 Gaps: 0

US-08-728-463B-206 (1-388) x AAV56737 (1-130)

QY 1 ATGGACATGATGTCCTCCCGCTCAGCTCTGGGGCTCTGCTGCTGTTCCAGGTTC 60
 DB 1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpPheProGlyAla 20
 QY 61 AGATGGACATCCAGATGACCCAGTCTCCATCTTCGCTGCTGTCATCTGTAGGAGACAGA 120
 DB 21 ArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArg 40
 QY 121 GTCACCATCACTTGTGCGGGAGTCAGGATATTAGCAGCTGGTTCAGCTGGTATCAGCAT 180
 DB 41 ValThrIleThrCysGlnAlaSerGlnGlyIleSerAsnTrpLeuAlaTrpTyrGlnGln 60
 QY 181 AAACCCAGGAAAGCCCTTAAGCTCTGATCTATGCTGATCCAGTTTGCAAGTGGGTC 240
 DB 61 LysProGlyLysAlaProLysLeuLeuIleTyrAlaAlaSerThrPheGlnSerGlyVal 80
 QY 241 CCATCAAGGTTTCAGCGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCTG 300
 DB 81 ProSerArgPheSerGlySerGlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeu 100
 QY 301 CAGCCTGAAGATTTGCAACTTACTATTGTCACAGGCTAATAGTTTCCCGTACACTTTT 360
 DB 101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnThrSerSerPheLeuLeuSerPhe 120
 QY 361 GGCACGGGACCAAGCTGGAGATCAAA 387
 DB 121 GlyGlyGlyThrLysValGluHisLys 129

RESULT 5

AAV96298
 ID AAV96298 standard; protein; 237 AA.

XX AAV96298;

XX 16-AUG-2000 (first entry)

XX Human IGFAM-10 immunoglobulin.

XX

FT Region /note= "immunoglobulin and MHC protein motif"
 FT 158..180
 FT /note= "immunoglobulin and MHC protein motif"
 FT 219..236
 FT /note= "immunoglobulin and MHC protein motif"
 FT
 PN WO200168696-A1.
 XX
 XX
 XX
 PD 20-SEP-2001.
 XX
 PF 15-MAR-2001; 2001WO-US08518.
 XX
 PR 15-MAR-2000; 2000US-189417P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 FI Tang YT, Hillman JL, Baughn MR;
 XX WPI; 2001-590044/66.
 DR N-PSDB; AAH26799.
 XX
 XX Novel human immune response proteins, for treating immunological
 PT disorders and cell proliferative disorders, and for assessing the
 FT effects of exogenous compounds on the expression of HIRP molecules
 FT
 PS Claim 1; Page 85; 95pp; English.
 XX
 CC The invention is based on the discovery of new human immune
 CC response proteins (HIRP), the polynucleotides encoding them, and
 CC the use of these compositions for the diagnosis, treatment or
 CC prevention of immunological and cell proliferative disorders.
 CC The present sequence is that of human immune response protein 1
 CC (HIRP1, Incyte ID No. 6100311CD1), as determined from a
 CC polynucleotide assembled e.g. from a lung adenocarcinoma CDNA
 CC library clone. The amino acid sequence shows homology, from
 CC residue W123 to C241, to an HIV-1 antigen binding protein, and
 CC further homologues suggest that it may be an immunoglobulin.
 CC polynucleotides and polypeptides are useful for the diagnosis,
 CC treatment and prevention of cell proliferative disorders (e.g.
 CC cancers, arteriosclerosis, actinic keratosis, bursitis, mixed
 CC connective tissue disease (MCTD), myelofibrosis, psoriasis, and
 CC leukaemia, hepatitis, cirrhosis and atherosclerosis), and
 CC immunological disorders e.g. AIDS, Addison's disease, adult
 CC respiratory distress syndrome (ARDS), anaemia, asthma, autoimmune
 CC diseases, contact dermatitis, diabetes mellitus, cholecystitis,
 CC Crohn's disease, atrophic gastritis, Goodpasture's syndrome,
 CC multiple sclerosis, irritable bowel syndrome, osteoporosis,
 CC rheumatoid arthritis, ulcerative colitis, trauma, and viral,
 CC bacterial, fungal, parasitic, protozoal and helminthic infections.
 CC The polypeptides are also used to screen for agonist and
 CC antagonist compounds of therapeutic use.
 XX
 SQ Sequence 241 AA;
 Alignment Scores:
 Pred. No.: 1.23e-52 Length: 241
 Score: 589.50 Matches: 112
 Percent Similarity: 91.79% Conservative: 11
 Best Local Similarity: 83.58% Mismatches: 6
 Query Match: 84.46% Indels: 5
 DB: 22 Gaps: 1
 US-08-728-463B-206 (1-388) x AAB82912 (1-241)
 QY 1 ATGGACATGATGTCCTCCGCTCAGCTCTGGGGCTCTGCTCTGTTCCAGTTCC 60
 Db 1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuProGlyAla 20
 QY 61 AGATCGCATCCAGATGACCCAGTCTCCATCTCCGCTGTCGATCTAGGAGACAGA 120
 Db 21 LysCysAspIleGlnMetThrGlnSerProSerThrLeuSerAlaSerValGlyAspArg 40
 QY 121 GTCACCATCACTTGTGGCGGAGTCAGGATATTAGC-----AGCTGGTTA 165

Db 41 ValThrIleThrCysArgAlaSerGlnSerIleSerSerGlnSerIleGlySerTrpLeu 60
 QY 166 GCCTGGTATCAGCATAAACCCAGGAAAGCCCTAAGCTCTGATCTATGCTGATCCAGT 225
 Db 61 AlaTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeuIleTyrLysAlaSerSer 80
 QY 226 TTGCAAGTGGGTCCCATCAGGTTTCAGGGCAGTGGATCTGGGACAGATTTCACTCTC 285
 Db 81 LeuGluSerGlyValProSerArgPheSerGlySerGlyThrGluPheThrLeu 100
 QY 286 ACCATCAGCAGCTGAGGCTGAAGATTTTGAACCTTACTATTGTCAACAGGCTAATAGT 345
 Db 101 ThrIleSerSerLeuGlnProAspPheAlaThrTyrTyrCysGlnGlnTyrAenAen 120
 QY 346 TTCCCGTACACTTTGGCCAGGGACCAAGCTGGAGATCAAA 387
 Db 121 TyrProTrpThrPheGlyGlnGlyThrLysValGluIleLys 134
 RESULT 3
 AAR75394
 ID AAR75394 standard; Protein; 130 AA.
 XX
 AC AAR75394;
 XX
 DT 04-NOV-1995 (first entry)
 XX
 DE Anti-interleukin-1-alpha human monoclonal antibody VL segment.
 XX
 KW Monoclonal antibody; interleukin-1-alpha; cytokine;
 KW antiinflammatory; prophylactic; therapeutic.
 XX
 OS Homo sapiens.
 XX
 Key Location/Qualifiers
 Peptide 1..22
 FT /note= "signal peptide"
 FT Region 23..45
 FT /note= "Framework (FR) 1 (+1 to +23)"
 FT Region 46..56
 FT /note= "CDR 1 (+24 to +34)"
 FT Region 57..71
 FT /note= "FR 2 (+35 to +49)"
 FT Region 72..78
 FT /note= "CDR 2 (+50 to +56)"
 FT Region 79..110
 FT /note= "FR 3 (+57 to +88)"
 FT Region 111..117
 FT /note= "CDR 3 (+89 to +95)"
 FT Region 118..130
 FT /note= "JK 4 (+96 to +108)"
 XX
 PN W09514780-A.
 XX
 PD 01-JUN-1995.
 XX
 PF 21-NOV-1994; 94WO-US13188.
 XX
 PR 23-NOV-1993; 93EP-0402846.
 XX
 PA (SCHE) SCHERING-PLOUGH.
 PA (SCHE) SCHERING CORP.
 XX
 PI Banchemareau J, Djossou O, Fossiez F, Garonne P;
 XX WPI; 1995-206937/27.
 DR N-PSDB; AAQ87237.
 DR
 XX Human monoclonal antibody against a human cytokine - used to mfr. a
 FT medicament to treat inflammation.
 FT
 PS Claim 7; Page 45-46; 70pp; English.
 XX

KW Human; immunoglobulin; IGFAM-10; IGFAM; immune disorder; cancer;
 KW infection; inflammation; haematopoiesis; AIDS; allergy.
 XX Homo sapiens.

XX Key Location/Qualifiers
 XX Peptide 1..22
 FT /label= signal_peptide
 FT Protein 23..237
 FT /label= IGFAM-10
 FT Domain 38..112
 FT /label= Ig_domain
 FT Domain 150..219
 FT /label= Ig_domain
 FT Domain 193..236
 FT /label= Ig_domain

XX WO200029583-A2.

XX 25-MAY-2000..

XX 19-NOV-1999; 99WO-US27566.

XX 19-NOV-1998; 99US-0113635.

XX 22-DEC-1998; 98US-0113635.

XX 07-APR-1999; 99US-0128194.

XX (INCY-) INCYTE PHARM INC.

XX Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;
 PI Lu DM, Lal P, Hillman JL, Yang J;
 XX

XX WPI; 2000-387796/33.

XX N-PSDB; AAA27390.

XX Immunoglobulin superfamily proteins, the agonist and antagonist of the
 PT protein is useful for preventing and treating disorders associated with
 PT altered levels of the protein such as cancer, immune system disorders
 PT

XX Claim 1; Page 85-86; 105pp; English.

XX The present sequence is the human immunoglobulin superfamily protein
 CC IGFAM-10. Its gene was isolated from a cDNA library of colon
 CC tissue. It is expressed in reproductive, gastrointestinal and
 CC cardiovascular tissue, where cancer and inflammation are common. The
 CC gene, protein, its antibodies, agonists and antagonists are suitable for
 CC diagnosing and treating many diseases, including cancer, immune system
 CC disorders (such as inflammation, AIDS, allergies, anaemia,
 CC arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
 CC disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,
 CC multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
 CC systemic lupus erythematosus and ulcerative colitis), complications of
 CC cancer, haemodialysis and extracorporeal circulation, trauma and
 CC haematopoietic cancer (such as leukaemia) and infections caused by
 CC bacteria, viruses, fungi or parasites.
 XX

XX Sequence 237 AA;

Alignment Scores:
 Pred. No.: 1.69e-51 Length: 237
 Score: 578.50 Matches: 115
 Percent Similarity: 92.31% Conservative: 5
 Best Local Similarity: 88.46% Mismatches: 9
 Query Match: 82.88% Indels: 1
 DB: 21 Gaps: 1

US-08-728-463B-206 (1-388) x AAY96298 (1-237)

QY 1 ATGCAGCATGATGCTCCCGCTCAGCTCCTGGGCTCTGCTGCTGCTCCAGGTTC 60
 Db 1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpLeuArgGlyAla 20

QY 61 AGATCGGACATCCAGATGACCCAGCTCTCCATCTTCGCTGCTCTGATAGGAGACAGA 120
 Db 21 ArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArg 40
 QY 121 GTCACCATCAGTTGTCGGCGAGTCAGGATATTAGCAGCTGGTTAGCCCTGGTATCAGCAT 180
 Db 41 ValThrIleThrCysArgAlaSerGlnSerIleSerSerTyrlleuAsnTrpTyrlleuGln 60
 QY 181 AAACACGAGGAAAGCCCTAAGCTCTGATCTATGCTGTCATCCAGTTTGCAAGTGGGTC 240
 Db 61 LysProGlyLysAlaProLysLeuLeuIleTyrlleuAlaAlaSerSerLeuGlnSerGlyVal 80
 QY 241 CCATCAAGTTTCAGCGGAGTCGATCGGACAGATTTTCACTCTCACCATCAGCACCTG 300
 Db 81 ProSerArgPheSerGlySerGlyThrAspPheThrleuThrIleSerSerLeu 100
 QY 301 CAGCCTGAAGATTTTGCACTTACTATTCTCAACAGGCTAAAGTTTC---CGGTACACT 357
 Db 101 GlnProGluAspPheAlaThrTyrlleuGlnSerTyrlleuThrProProlleThr 120
 QY 358 TTTGGCCAGGGACCAAGCTGGAGATCAAA 387
 Db 121 PheGlyGlnGlyThrArgLeuGluIleLys 130

RESULT 6

AAW70379
 ID AAW70379 standard; Protein; 129 AA.

XX AAW70379;

XX 18-NOV-1998 (first entry)

XX Anti-human CD23 5B8 monoclonal antibody light chain variable region.
 KW human CD23 5B8 monoclonal antibody; light chain variable region;
 KW gamma-3 constant region; IgE; FcεRII/CD23; gamma-1 constant region;
 KW allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia.

XX Macaca fascicularis

XX Key Location/Qualifiers

FT Protein 1..22
 FT /note= "signal peptide"

FT Protein 23..129

FT /note= "anti-human CD23 5B8 light chain variable region"

FT Binding-site 46..56
 FT /note= "CDR 1"

FT Binding-site 72..77
 FT /note= "CDR 2"

FT Binding-site 111..119
 FT /note= "CDR 3"

XX WO9837099-A1.

XX 27-AUG-1998.

XX 17-FEB-1998; 98WO-US02253.

XX 05-FEB-1998; 98US-0803085.

XX 20-FEB-1997; 97US-0803085.

XX (IDEC-) IDEC PHARM CORP.

XX (SEKK) SEIKAGAKU CORP.

XX Kloetzer WS, Nakamura T, Reff ME;

XX WPI; 1998-467495/40.

XX N-PSDB; AAV33309.

XX New anti-human CD23 monoclonal antibody - used for inhibiting IgE
 PT expression to treat or prevent allergic, inflammatory and

PT auto:immune conditions

XX Example 1; Pages 106-108; 146pp; English.

XX The present sequence represents the light chain variable region of
 CC primate monoclonal antibody anti-human CD23 5E8. The invention
 CC provides prime monoclonal antibodies which specifically bind human
 CC CD23, the low affinity receptor for IgE (FcεRI/CD23), and comprise
 CC either of a human gamma-1 or human gamma-3 constant region that binds
 CC to human Fc gamma receptors and inhibits IgE expression. The monoclonal
 CC antibodies of the invention are claimed to be useful for inhibiting
 CC induced IgE production for treating or preventing allergic, inflammatory
 CC and autoimmune conditions e.g. allergic rhinitis conjunctivitis,
 CC autoimmune haemolytic anaemia, etc.

XX Sequence 129 AA;

Alignment Scores:

Pred. No.:	3 45e-51	Length:	129
Score:	575.00	Matches:	111
Percent Similarity:	90.70%	Conservative:	6
Best Local Similarity:	86.05%	Mismatches:	12
Query Match:	82.38%	Indels:	0
DB:	19	Gaps:	0

US-08-728-463B-206 (1-388) x AAW70379 (1-129)

QY	1	ATGGACATGATGGTCCCGCTCAGCTCTGGGGCTCTGCTGCTCTGCTGCTCCAGGTTCC	60
Db	1	MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTyrLeuProGlyAla	20
QY	61	AGATGCGACATCCAGATGACCCAGCTCCATCTCCGTCGTGCTGATCTGTAGGAGACAGA	120
Db	21	ArgCysAspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArg	40
QY	121	CTCACCATCACTTGTGGGGCGAGTCAGGATATTAGCAGCTGGTTAGCTGTATCAGCAT	180
Db	41	ValThrIleThrCysArgAlaSerGlnAspIleArgTyrTyrLeuAsnIlePyrGlnGln	60
QY	181	AAACAGGGAAGCCCTAGCTCTGATCTATGCTGCATCTCCATGCTTGCAGAGTGGGTC	240
Db	61	LysProGlyLysAlaProLysLeuLeuIleTyrValAlaSerSerLeuGlnSerGlyVal	80
QY	241	CCATCAAGTTTCAGCGCAGTGGATCTGGACAGATTTCTACTCTCCATCAGCAGCTG	300
Db	81	ProSerArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrValSerSerLeu	100
QY	301	CAGCTGAAGATTTGCAACTTACTATTGTCACAGGCTTAATAGTTTCCGTCACACTTTT	360
Db	101	GlnProGluAspPheAlaThrTyrTyrCysLeuGlnValTyrSerThrProArgThrPhe	120
QY	361	GGCCAGGGGACCAAGCTGGAGATCAA	387
Db	121	GlyGlnGlyThrLysValGluIleLys	129

RESULT 7

AAAY96289

ID AAY96289 standard; protein; 237 AA.

XX AC AAY96289;

XX DT 16-AUG-2000 (first entry)

XX XX Human IGFAM-1 immunoglobulin.

DE Human; immunoglobulin; IGFAM-1; IGFAM; immune disorder; cancer;

XX infection; inflammation; haematopoiesis; AIDS; allergy.

XX OS Homo sapiens.

XX FH . Key Location/Qualifiers

FT Peptide 1..22

FT /label= signal_peptide

FT Protein	23..237	/label= IGFAM-1
FT Domain	38..112	/label= Ig_domain
FT Domain	150..219	/label= Ig_domain
FT Region	154..176	/label= Ig_signature
FT Domain	193..236	/label= Ig_domain
FT Region	215..232	/label= Ig_signature

W0200029583-A2.

25-MAY-2000.

19-NOV-1999; 99WO-US27566.

19-NOV-1998; 99US-0113635.

22-DEC-1998; 98US-0113635.

07-APR-1999; 99US-0128194.

(INCY-) INCYTE PHARM INC.

Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;

Lu DAM, Lal P, Hillman JL, Yang J;

WPI; 2000-387796/33.

N-PSDB; AAA27381.

Immunoglobulin superfamily proteins, the agonist and antagonist of the

protein is useful for preventing and treating disorders associated with

altered levels of the protein such as cancer, immune system disorders

Claim 1; Page 77-78; 105pp; English.

The present sequence is the human immunoglobulin superfamily protein

IGFAM-1. Its gene is isolated from a cDNA library of synovial membrane

tissue. It is expressed in reproductive, gastrointestinal and

cardiovascular tissue, where cancer and inflammation are common. The

gene, protein, its antibodies, agonists and antagonists are suitable for

diagnosing and treating many diseases, including cancer, immune system

disorders (such as inflammation, AIDS, allergies, anaemia, Crohn's

arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's

disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,

multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,

systemic lupus erythematosus and ulcerative colitis), complications of

cancer, haemodialysis and extracorporeal circulation, trauma and

haematopoietic cancer (such as leukaemia) and infections caused by

bacteria, viruses, fungi or parasites.

XX Sequence 237 AA;

Alignment Scores:

Pred. No.:	4 38e-51	Length:	237
Score:	574.50	Matches:	114
Percent Similarity:	91.54%	Conservative:	5
Best Local Similarity:	87.69%	Mismatches:	10
Query Match:	82.31%	Indels:	1
DB:	21	Gaps:	1

US-08-728-463B-206 (1-388) x AAY96289 (1-237)

QY 1 ATGGACATGATGGTCCCGCTCAGCTCTGGGGCTCTGCTGCTCTGCTGCTCCAGGTTCC

60

Db 1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTyrLeuProGlyAla

20

QY 61 AGATGCGACATCCAGATGACCCAGCTCCATCTCCGTCGTGCTGATCTGTAGGAGACAGA

120

Db 21 ArgCysAspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArg

40

QY 121 GTCACATCACTGTCTGGCGAGTCAGGATATTAGCAGCTGTAGCTGGTATCAGCAT 180
 Db 41 ValThrIleThrCysArgAlaGlyGlnSerIleSerSerTyLeuAsnTrpTyGlnGln 60
 QY 181 AAACACAGGAAAGCCCTAAGCTCTCTGATCTATGCTGTCATCCAGTTTGCAAAAGTGGGTC 240
 Db 61 LysProGlyLysAlaProLysLeuLeuIleTyAlaAlaSerSerLeuGlnSerGlyVal 80
 QY 241 CCATCAGGTTACGGCGAGTCGATCTGGACAGATTTCACTCTCAGCATCAGCAGCCTG 300
 Db 81 ProSerArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100
 QY 301 CAGCCTGAAGATTTCACACTTACTATTCTCAACAGGCTAATAGTTTC---CCGTACACT 357
 Db 101 GlnProGluAspPheAlaThrTyTyCysGlnGlnSerPheAsnThrHisMetTyThr 120
 QY 358 TTGGCCAGGGACCAAGCTGGAGATCAAA 387
 Db 121 PheGlyGlnGlyThrArgLeuGluIleLys 130
 RESULT 8
 AAY96301
 ID AAY96301 standard; protein; 237 AA.
 AC AAY96301;
 XX
 DT 16-AUG-2000 (first entry)
 DE Human IGFAM-13 immunoglobulin.
 KW Human; immunoglobulin; IGFAM-13; IGFAM; immune disorder; cancer;
 KW infection; inflammation; haematopoiesis; AIDS; allergy.
 OS Homo sapiens.
 FH Key
 FT Peptide
 FT 1..22 Location/Qualifiers
 FT /label= signal_peptide
 FT Protein 23..237
 FT /label= IGFAM-13
 FT Domain 38..112
 FT /label= Ig_domain
 FT Domain 150..219
 FT /label= Ig_domain
 FT Domain 193..236
 FT /label= Ig_domain
 XX WO200029583-A2.
 XX
 PD 25-MAY-2000.
 PF 19-NOV-1999; 99WO-US27566.
 XX
 PR 19-NOV-1998; 99US-0113635.
 PR 22-DEC-1998; 98US-0113635.
 PR 07-APR-1999; 99US-0128194.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;
 PI Lu DAN, Lal P, Hillman JL, Yang J;
 XX
 DR WPI; 2000-387796/33.
 DR N-PSDB; AAA27393.
 XX
 PT Immunoglobulin superfamily proteins, the agonist and antagonist of the
 PT protein is useful for preventing and treating disorders associated with
 PT altered levels of the protein such as cancer, immune system disorders
 PT
 XX
 PS Claim 1; Page 87-88; 105pp; English.
 XX
 XX The present sequence is the human immunoglobulin superfamily protein

CC IGFAM-13. Its gene was isolated from a cDNA library of lung tumour
 CC tissue. It is expressed in reproductive, gastrointestinal and
 CC cardiovascular tissue, where cancer and inflammation are common. The
 CC gene, protein, its antibodies, agonists and antagonists are suitable for
 CC diagnosing and treating many diseases, including cancer, immune system
 CC disorders (such as inflammation, AIDS, allergies, anaemia,
 CC arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
 CC disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,
 CC multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
 CC systemic lupus erythematosus and ulcerative colitis), complications of
 CC cancer, haemodialysis and extracorporeal circulation, trauma and
 CC haematopoietic cancer (such as leukaemia) and infections caused by
 CC bacteria, viruses, fungi or parasites.
 XX Sequence 237 AA;
 SQ
 Alignment Scores:
 Pred. No.: 4,38e-51 Length: 237
 Score: 574.50 Matches: 112
 Percent Similarity: 93.08% Conservative: 9
 Best Local Similarity: 86.15% Mismatches: 8
 Query Match: 82.31% Indels: 1
 DB: 21 Gaps: 1
 US-08-728-463B-206 (1-388) x AAY96301 (1-237)
 QY 1 ATGGACATGATGGTCCCGCTCAGCTCTGGGGCTCTGCTCTCTGTTCCAGGTTCC 60
 Db 1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuArgGlyAla 20
 QY 61 AGATCGGACATCCAGATGACCCAGTCTCCATCTTCGGTGTCTGCATCTCTAGGAGACAGA 120
 Db 21 ArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArg 40
 QY 121 GTCACATCACTTGTCTGGCGAGTCAGGATATTAGCAGCTGTAGCTGGTATCAGCAT 180
 Db 41 ValThrMetThrCysArgAlaSerGlnSerIleSerThrTyLeuAsnTrpTyGlnGln 60
 QY 181 AAACACAGGAAAGCCCTAAGCTCTCTGATCTATGCTGTCATCCAGTTTGCAAAAGTGGGTC 240
 Db 61 LysProGlyLysAlaProLysLeuLeuIleTyAlaAlaSerSerLeuGlnSerGlyVal 80
 QY 241 CCATCAGGTTACGGCGAGTCGATCTGGACAGATTTCACTCTCAGCATCAGCAGCCTG 300
 Db 81 ProSerArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100
 QY 301 CAGCCTGAAGATTTCACACTTACTATTCTCAACAGGCT---AATAGTTTCCCGTACACT 357
 Db 101 GlnProGluAspPheAlaThrTyTyCysGlnGlnSerPheAsnThrHisMetTyThr 120
 QY 358 TTGGCCAGGGACCAAGCTGGAGATCAAA 387
 Db 121 PheGlyGlnGlyThrArgLeuGluMetLys 130
 RESULT 9
 AAW01527
 ID AAW01527 standard; Protein; 128 AA.
 XX
 AC AAW01527;
 XX
 DT 04-MAR-1997 (first entry)
 DE Monoclonal antibody ZM1-2 light chain variable region.
 XX
 KW Monoclonal antibody; diagnosis; treatment; infection; hepatitis B;
 KW xenogeneic hybridoma; SP24 4; PEI-1; ZM1-1; ZM1-2; MD3-4; L03-3;
 KW IgG1 class; heavy chain; light chain; variable region.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Peptide
 FT 1..20 Location/Qualifiers
 FT /label= leader_sequence

1 ATGGACATGATGGTCCCGCTCAGCTCTGGGGCTCTGTGCTCTGTTCTCCAGGTCC 60
|||
1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuProGlyAla 20
|||
61 AGATGCGACATCCAGATGACCCAGTCTCCATCTTCCGTCTGTCATCTGTAGGACAGAGA 120
|||

CC human MAB CLN"-Igm identified by western blotting.

XX Sequence 132 AA;

Alignment Scores:

Pred. No.: 9e-51 Length: 132
Score: 571.00 Matches: 112
Percent Similarity: 90.70% Conservative: 5
Best Local Similarity: 86.82% Mismatches: 12
Query Match: 81.81% Indels: 0
DB: 18 Gaps: 0

US-08-728-463B-206 (1-388) x AAW22842 (1-132)

```
QY 1 ATGGACATGATGTCCTCCGCTCAGCTCTCGTGGGCTCTCTGCTGTGGTTCCAGGTTCC 60
DB 1 MetAspMetGluAlaHisValGlnLeuLeuGlyLeuLeuLeuTrpLeuArgGlyAla 20
QY 61 AGATCGGACATCCAGATGACCCAGTCTCCATCTCCGTCGTCATCTCTAGGAGACAGA 120
DB 21 ArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArg 40
QY 121 GTCACCATCATCTGTCCGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGTATCAGCAT 180
DB 41 ValThrIleThrCysArgAlaSerGlnSerIleSerSerThrLeuAsnTrpTyrGlnGln 60
QY 181 AAACAGGAGAAAGCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGTC 240
DB 61 LysProGlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyVal 80
QY 241 CCATCAAGCTTCAGCGGCGAGTCGATCTGGGACAGATTTCACTCTCACCATCAGCCTG 300
DB 81 ProSerArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100
QY 301 CAGCCTGAAGATTTGCAACTTACTATTGTCAACAGGCTAAATAGTTTCCCGTACACTTT 360
DB 101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerThrProGlnThrPhe 120
QY 361 GGCCAGGAGACCAAGCTGGAGATCAAA 387
DB 121 GlyGlnGlyThrLysValGluIleLys 129
```

RESULT 14

AAW47645

ID AAW47645 standard; Protein; 134 AA.

XX AC AAW47645;

DT 15-FEB-2002 (first entry)

DE Human protein sequence #3.

XX KW Human; cytostatic; antiinflammatory; antianaemic; vasotropic;
KW antibody; signal transmission; cancer; inflammation; hormonal disorder;
KW leukaemia; lymphoma; aplastic anaemia; skeletal malformation.

OS Homo sapiens.

XX PN WO200179494-A1.

PD 25-OCT-2001.

XX PF 17-APR-2001; 2001WO-JP03288.

XX PR 17-APR-2000; 2000JP-0115246.

XX PR 20-OCT-2000; 2000JP-0321821.

XX PR 20-OCT-2000; 2000JP-0321822.

XX PR 12-MAR-2001; 2001WO-JP01912.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PI Fukushima N, Tsuchiya M, Oheda M, Uno S, Kikuchi Y, Ohtomo T;

XX

DR

XX N-PSDB; ABA04572.

PT Antibodies for treatment of diseases associated with cell
PT proliferation, hormonal disorders and cytokines comprise agonist
PT activity to signal transmission across cell membranes -

PS Disclosure; Page 164; 173pp; Japanese.

XX The present invention relates to modified antibodies. The antibodies
CC contain two or more H chain V domains and two or more L chain V domains
CC of a monoclonal antibody (Mab) which is capable of transmitting a signal
CC across the cell membrane by cross-linking a cell surface molecule, where
CC the antibodies can serve as signal transmission agonists. The antibodies
CC are useful for treatment and prevention of a broad range of disorders in
CC which signal transmission is implicated, such as cancer, inflammation,
CC hormonal disorders, leukaemia, malignant lymphoma, aplastic anaemia, and
CC skeletal malformations. The present sequence was used to illustrate the
CC present invention.

XX Sequence 134 AA;

Alignment Scores:

Pred. No.: 9.03e-51 Length: 134
Score: 571.00 Matches: 107
Percent Similarity: 90.70% Conservative: 10
Best Local Similarity: 82.95% Mismatches: 12
Query Match: 81.81% Indels: 0
DB: 23 Gaps: 0

US-08-728-463B-206 (1-388) x AAW47645 (1-134)

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QY 1 ATGGACATGATGTCCTCCGCTCAGCTCTCGTGGGCTCTCTGCTGTGGTTCCAGGTTCC 60
DB 1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpLeuProGlyAla 20
QY 61 AGATCGGACATCCAGATGACCCAGTCTCCATCTCCGTCGTCATCTCTAGGAGACAGA 120
DB 21 LysCysAspIleGlnMetThrGlnSerProSerThrLeuSerAlaSerIleGlyAspArg 40
QY 121 GTCACCATCATCTGTCCGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGTATCAGCAT 180
DB 41 ValThrIleThrCysArgAlaSerGluGlyIleTyrHisTrpLeuAlaTrpTyrGlnGln 60
QY 181 AAACAGGAGAAAGCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGTC 240
DB 61 LysProGlyLysAlaProLysLeuLeuIleTyrLysAlaSerSerLeuAlaSerGlyAla 80
QY 241 CCATCAAGCTTCAGCGGCGAGTCGATCTGGGACAGATTTCACTCTCACCATCAGCCTG 300
DB 81 ProSerArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100
QY 301 CAGCCTGAAGATTTGCAACTTACTATTGTCAACAGGCTAAATAGTTTCCCGTACACTTT 360
DB 101 GlnProAspAspPheAlaThrTyrTyrCysGlnGlnTyrSerAsnTyrProLeuThrPhe 120
QY 361 GGCCAGGAGACCAAGCTGGAGATCAAA 387
DB 121 GlyGlyGlyThrLysLeuGluIleLys 129
```

RESULT 15

ABP41164

ID ABP41164 standard; Protein; 260 AA.

XX AC ABP41164;

XX DT 23-AUG-2002 (first entry)

XX DE Human ovarian antigen HRACW30, SEQ ID NO:2296.

XX KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;

XX KW ovarian cancer; breast cancer; reproductive system disorder;

XX KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;

KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive; chromosome 2p12.
 XX Homo sapiens.
 OS
 XX
 XX WO200200677-A1.
 PN
 XX
 XX 03-JAN-2002.
 PD
 XX
 XX 07-JUN-2001; 2001WO-US18569.
 PF
 XX
 XX 07-JUN-2000; 2000US-209467P.
 PR
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX
 XX Birse CE, Rosen CA;
 PI
 XX
 DR WPI; 2002-147878/19.
 DR N-PSDB; ABQ54241.
 XX
 XX
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g.
 PT ovarian cancer), immune disorders, cardiovascular disorders and
 PT neurological diseases -
 XX

Claim 11; SEQ ID No 2296; 2922pp; English.

XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 CC disorders, infectious (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC blood-related disorders, autoimmune oophoritis, systemic lupus erythematosus),
 CC respiratory disorders, neurological disorders, cardiovascular disorders,
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX

SQ Sequence 260 AA;

Alignment Scores:

Pred. No.:	1.65e-50	Length:	260
Score:	569.00	Matches:	110
Percent Similarity:	90.70%	Conservative:	7
Best Local Similarity:	85.27%	Mismatches:	12
Query Match:	81.52%	Indels:	0
DB's:	23	Gaps:	0

US-08-728-463B-206 (1-388) x ABP41164 (1-260)

Qy	1	ATGGACATGATGTCCTCCCGCTCAGCTCTCTGGGCTCTCTGCTCTGTTCCAGGTTCC	60
Db	25	MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpLeuArgGlyAla	44
Qy	61	AGATGGACATCCAGATGACCCAGTCTCCATCTTCGCTGCTGTCATCTCTAGGACAG	120
Db	45	ArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArg	64
Qy	121	GTCAACATCACTTGTCTGGCGAGTCAAGATATTAGCAGCTGCTTAGCCTGGTATCAGCAT	180
Db	65	ValThrIleThrCysArgAlaSerGlnSerIleSerAsnTyrLeuAsnTrpTyrGlnGln	84
Qy	181	AAACAGGGAAGCCCTTAAGCTCTGATCTATGTCATCCAGTTTGCAAAAGTGGGTC	240
Db	85	LysProGlyLysAlaProLysLeuLeuIleTyrAlaAlaSer***LeuGlnSerGlyVal	104
Qy	241	CCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGATTTTCACTCTCACCATCAGCAGCTG	300
Db	105	ProSerArgPheSerGlySerGlyThrAspPheThr***ThrIleSerSerLeu	124
Qy	301	CAGCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTT	360
Db	125	GlnProGluAspPheAlaThrTyrTyrCysGlnGlnTyrAspAsn***ProLeuThrPhe	144
Qy	361	GGCAGGGGACCAAGCTGGAGATCAA 387	
Db	145	Gly***GlyThrLysValGluIleLys 153	

Search completed: June 3, 2003, 09:02:18

Job time : 28.263 secs

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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 09:04:15 ; Search time 16.4856 Seconds
(without alignments)
4764.744 Million cell updates/sec

Title: US-08-728-463B-206

Perfect score: 698

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Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 767038

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:
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7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pcp.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pcp.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pcp.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pcp.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	624	89.4	236	10	US-09-859-053-30 Sequence 30, Appl
2	548	78.5	234	10	US-09-740-002-24 Sequence 24, Appl
3	543	77.8	128	10	US-09-855-271-26 Sequence 26, Appl
4	535	76.6	236	9	US-10-006-593-69 Sequence 69, Appl

5	526.5	75.4	234	10	US-09-740-002-26
6	524	75.1	127	9	US-10-283-349-71
7	521.5	74.7	109	10	US-09-798-058-4
8	513	73.5	244	9	US-09-880-748-1881
9	509	72.9	127	9	US-10-283-349-88
10	505	72.3	267	10	US-09-766-543-10
11	504	72.2	107	9	US-10-268-501-5
12	504	72.2	108	10	US-09-056-160B-12
13	504	72.2	109	10	US-09-811-123-6
14	498	71.3	127	9	US-10-283-349-92
15	497	71.2	240	9	US-09-968-561A-2
16	497	71.2	240	10	US-09-192-854-2
17	494	70.8	106	9	US-10-027-725A-12
18	494	70.8	107	9	US-10-035-637-2
19	493.5	70.7	106	9	US-10-040-244-17
20	493	70.6	128	10	US-09-992-524-6
21	492	70.5	107	9	US-09-848-798-40
22	491	70.3	108	9	US-10-125-687-8
23	491	70.3	108	12	US-10-025-687-8
24	491	70.3	234	10	US-09-800-729-150
25	490.5	70.3	235	10	US-09-800-729-152
26	490	70.2	111	10	US-09-920-171-7
27	490	70.2	237	9	US-09-880-748-1906
28	490	70.2	237	9	US-09-880-748-2003
29	490	70.2	237	9	US-09-880-748-2005
30	490	70.2	237	9	US-09-880-748-2017
31	490	70.2	237	9	US-09-880-748-2019
32	490	70.2	237	9	US-09-880-748-2020
33	490	70.2	237	9	US-09-880-748-2027
34	490	70.2	237	9	US-09-880-748-2028
35	490	70.2	237	9	US-09-880-748-2040
36	490	70.2	237	9	US-09-880-748-2043
37	490	70.2	237	9	US-09-880-748-2104
38	490	70.2	237	9	US-09-880-748-2114
39	490	70.2	242	9	US-09-880-748-1580
40	490	70.2	245	9	US-09-880-748-1291
41	490	70.2	248	9	US-09-880-748-1004
42	490	70.2	248	9	US-09-880-748-1385
43	490	70.2	248	9	US-09-880-748-1717
44	490	70.2	248	9	US-09-880-748-1719
45	490	70.2	248	9	US-09-880-748-1733

ALIGNMENTS

RESULT 1
US-09-859-053-30
; Sequence 30, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-30

Alignment Scores:

Pred. No.: 3.2e-46 Length: 236

Db 61 GlyLysAlaProLysLeuLeuIleTyrGlyAlaAsnSerLeuGlnThrGlyValProSer 80
QY 247 AGTTTCAGCGGAGTGGATCTGGGACAGATTTTCACTCTCACCATCAGCAGCCTGCAGCCT 306
Db 81 ArgPheSerGlySerGlySerAlaThrAspTyrThrLeuThrIleSerSerLeuGlnPro 100
QY 307 GAAGATTTTGCACCTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAG 366
Db 101 GluAspPheAlaThrTyrTyrCysGlnGlnSerTyrLysPheProAsnThrPheGlyGln 120
QY 367 GGGACCAAGCTGGAGATCAAA 387
Db 121 GlyThrLysValGluValLys 127

RESULT 4

US-10-006-593-69
; Sequence 69, Application US/10006593
; Publication No. US20030049683A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2
; CURRENT APPLICATION NUMBER: US/10/006,593
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 236
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized antibody light chain
US-10-006-593-69

Alignment Scores:
Pred. No.: 1,58e-38 Length: 236
Score: 535.00 Matches: 104
Percent Similarity: 86.82% Conservative: 8
Best Local Similarity: 80.62% Mismatches: 17
Query Match: 76.65% Indels: 0
DB: 9 Gaps: 0

US-08-728-463B-206 (1-388) x US-10-006-593-69 (1-236)

QY 1 ATGGACATGATGCTCCCGCTCAGCTCTGGGGCTCCTGCTGCTGTTCCAGGTTCC 60
Db 1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpLeuArgGlyAla 20
QY 61 AGATGGACATCCAGATGACCCAGTCTCCATCTTCGGTGTCTGCTATCTGTAGGAGACAGA 120
Db 21 ArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArg 40
QY 121 GTCCACCATCACTTGTTCGGGCGAGTCAGGATATTAGCAGCTGGTTCAGCTATCAGCAT 180
Db 41 ValThrIleThrCysArgAlaSerGlnSerIleAlaSerTyrValAsnTrpTyrGlnGln 60
QY 181 AAACAGGGAAGCCCTTAAGCTCTGATCTATGTGTGATCCAGTTTGCAGTGGGTC 240
Db 61 LysProGlyLysAlaProLysLeuLeuIleTyrGlyAlaThrAsnLeuAlaAspGlyVal 80
QY 241 CCATCAAGTTTCAGCGCAGTGGATCTGGGACAGATTTTCACTCTCACCATCAGCAGCTG 300
Db 81 ProSerArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100

QY 301 CAGCTGAAGATTTTGCACCTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTT 360
Db 101 GlnProGluAspPheAlaThrTyrTyrCysGlnAsnValLeuAsnThrProLeuThrPhe 120
QY 361 GCCCAGGGGACCAAGCTGGAGATCAAA 387
Db 121 GlyGlnGlyThrLysValGluLys 129

RESULT 5

US-09-740-002-26
; Sequence 26, Application US/09740002
; Patent No. US20020001798A1
; GENERAL INFORMATION:
; APPLICANT: MORROW, PHILLIP
; APPLICANT: BRAMS, PETER
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
; TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
; FILE REFERENCE: 037003-0275759
; CURRENT APPLICATION NUMBER: US/09/740,002
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/335,697
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/488,376
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-740-002-26

Alignment Scores:

Pred. No.: 8,6e-38 Length: 234
Score: 526.50 Matches: 102
Percent Similarity: 91.47% Conservative: 16
Best Local Similarity: 79.07% Mismatches: 10
Query Match: 75.43% Indels: 1
DB: 10 Gaps: 1

US-08-728-463B-206 (1-388) x US-09-740-002-26 (1-234)

QY 1 ATGGACATGATGCTCCCGCTCAGCTCTGGGGCTCCTGCTGCTGTTCCAGGTTCC 60
Db 1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpLeuArgGlyAla 20
QY 61 AGATGGACATCCAGATGACCCAGTCTCCATCTTCGGTGTCTGCTATCTGTAGGAGACAGA 120
Db 21 ArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArg 40
QY 121 GTCCACCATCACTTGTTCGGGCGAGTCAGGATATTAGCAGCTGGTTCAGCTATCAGCAT 180
Db 41 ValThrIleThrCysArgAlaSerGlnSerIleAlaSerTyrValAsnTrpTyrGlnGln 60
QY 181 AAACAGGGAAGCCCTTAAGCTCTGATCTATGTGTGATCCAGTTTGCAGTGGGTC 240
Db 61 LysProGlyLysAlaProLysLeuLeuIlePheAlaSerAlaAsnLeuValSerGlyVal 80
QY 241 CCATCAAGTTTCAGCGGCGAGTGGATCTGGGACAGATTTTCACTCTCACCATCAGCAGCTG 300
Db 81 ProSerArgPheSerGlySerGlyThrValPheThrLeuThrIleSerAsnLeu 100
QY 301 CAGCTGAAGATTTTGCACCTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTT 360
Db 101 GlnProGluAspPheAlaThrTyrPheCysGlnGlnSerTyrThr---AsnPheSerPhe 119
QY 361 GCCCAGGGGACCAAGCTGGAGATCAAA 387
Db 120 GlyGlnGlyThrLysLeuGluLys 128

RESULT 6

US-10-283-349-71

```

: Sequence 71, Application US/10283349
: Publication No. US20030096977A1
: GENERAL INFORMATION:
: APPLICANT: KOIKE, Masamichi
: FURUYA, Akiko
: NAKAMURA, Kazuyasu
: IIDA, Akihiro
: ANAZAWA, Hideharu
: HANAI, NO. US20030096977A1uo
: TAKATSU, Kiyoshi
: TITLE OF INVENTION: Antibody Against Human Interleukin-5
: NUMBER OF SEQUENCES: 106
: CORRESPONDENCE ADDRESS:
:

```

ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,349
FILING DATE: 29-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115
TELECOMMUNICATION INFORMATION:
TELEPHONE 212-790-9090

TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
STRAINEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 71:
JUS-10-283-349-71

Alignment Scores:

Pred. No.:	1.47e-37	Length:	127
Score:	524.00	Matches:	103
Percent Similarity:	85.93%	Conservative:	6
Local Similarity:	81.10%	Mismatches:	18
Query Match:	75.07%	Indels:	0
DB:	9	Gaps:	0

US-08-728-463B-206 (1-388) x US-10-283-349-71 (1-127)

	7	ATGATGTGCCCGCTCAGCTCTGGGGCTCTGCTGCTTCCAGGTTCCAGATGC	66
b	1	MecMetSerSerAlaGlnPheLeuGlyLeuLeuLeuLeuCysPheGlnAspIleArgCys	20
	67	GACATCCAGATGACCAGTCTTCATCTTCGGTGCTGCATCTCTTAGGAGACAGAGTCACC	126
	21	AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr	40
	127	ATCACTTGTCGGCGAGTCAGGATTATAGCAGCTGGTTAGCCCTGGTATCAGCATAAACA	186
	41	IleThrCysGlyThrSerGluAspIleIleAsnTyxLeuAsnTrpTyrGlnGlnLysPro	60

187	QY	GGGAAGCCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAGATGGGGTCCCATCA	246
	Db		
61	QY	GlyLeuAlaProLysLeuLeuIleTyrHisThrSerArgLeuGlnSerGlyValProSer	80
	Db		
247	QY	AGGTCACAGCGGAGTGGATCTGGGACAGATTCTACTCTCACCATCAGCAGCCTGACGCT	306
	Db		
81	QY	ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro	100
	Db		
307	QY	GAAGATTTTGCACCTACTATTGTCAACAGAGCTAATAGTTTCCGTACACTTTTGGCCAG	366
	Db		
101	QY	GluaspPheAlaThrTyrTyrCysGlnGlnGlyTyrThrLeuProTyrThrPheGlyGln	120
	Db		
367	QY	GGGACCAAGCTGGAGATCAAA	387
	Db		
121	QY	GlyThrLysValGluIleLys	127
	Db		

RESULT 7

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US-09-798-058-4
; Sequence 4, Application US/09798058
; Patent No. US20020098523A1
; GENERAL INFORMATION:
; APPLICANT: Vaughan, Tristan John
; APPLICANT: Vaughan, Alison Jane
; APPLICANT: Wilton, Stephen
; APPLICANT: Smith, Stephen
; APPLICANT: Main, Sarah Helen
; TITLE OF INVENTION: Human antibodies against eotaxin and their use
; FILE REFERENCE: 84632-000100
; CURRENT APPLICATION NUMBER: US/09/798,058
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 60/187,246
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-798-058-4

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Alignment Scores:

Pred. No.:	2,438-37	Length:	109
Score:	521.50	Matches:	103
Percent Similarity:	97.22%	Conservative:	2
Best Local Similarity:	95.37%	Mismatches:	2
Query Match:	74.71%	Indels:	1
DB:	10	Gaps:	1

US-08-728-463B-206 (1-388) x US-09-798-058-4 (1-109)

QY	67	GACATCCAGATGACCCAGTCTCCACTTCCGTGCTGCATCTCTAGGAGACAGAGTCACC	126
Db	1	AspIleGlnMetThrGlnSerProSerValSerAlaSerValGlyAepArgValThr	20
QY	127	ATCACTTCTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCCTGGTATCAGCATAAACCA	186
Db	21	IleThrCysArgAlaSerGlnAspIleSerSerTrpLeuAlaTrpTyGlnGlnLysPro	40
QY	187	GGGAAGCCCCCTAAGCTCCTGTATCTATCTGCATCCAGTTTGCAAGTGGGGTCCCATCA	246
Db	41	GlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSer	60
QY	247	AGGTTACAGCGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCTCGACGCT	306
Db	61	ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro	80
QY	307	GAACATTTGCACCTTACTATTCTCACAGGCTAATAGTTTCCCG---TACACTTTTGGC	363
Db	81	GlusPheAlaThrTyTyCysGlnGlnAlaSerPheProSerIleThrPheGly	100
QY	364	CAGGGGACCAAGCTGGAGATCAAA	387
Db	101	GlnGlyThrArgLeuGluIleLys	108


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Db      81 GluAspPheAlaThrTyrTyrCysGlnGlnTyrAsnSerLeuProtrpThrPheGlyGln 100
      |||||||
QY      367 GGGACCAAGCTGGAGATCAA 387
      |||||||
Db      101 GlyThrLysValGluLeuLys 107
      |||||||

RESULT 12
US-09-056-160B-12
; Sequence 12, Application US/09056160B
; Patent No. US20020032315A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-Apr-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1093R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-056-160B-12

Alignment Scores:
Pred. No.: 7,938-36 Length: 108
Score: 504.00 Matches: 97
Percent Similarity: 96.26% Conservative: 6
Best Local Similarity: 90.65% Mismatches: 4
Query Match: 72.21% Indels: 0
DB: 10 Gaps: 0

US-08-728-463B-206 (1-388) x US-09-056-160B-12 (1-108)

QY      67 GACATCCAGATGACCCAGTCTCCATCTTCGGTGTCTGTCATCTGTAGGACAGAGTCACC 126
      |||||||
Db      1 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
      |||||||

QY      127 ATCACTTGTGGGGAGTCAAGATATTAGCAGCTGGTGTAGCTGGTATCAGCATAAACCA 186
      |||||||
Db      21 IleThrCysArgAlaSerGlnSerIleSerAsnTyrLeuAlaTrpTyrGlnGlnLysPro 40
      |||||||

QY      187 GGGAAAGCCCTAAGCTCCTGATCTATGCTGCATCCAGTTGCAGAGTGGGTCCCATCA 246
      |||||||
Db      41 GlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSer 60
      |||||||

QY      67 GACATCCAGATGACCCAGTCTCCATCTTCGGTGTCTGTCATCTGTAGGACAGAGTCACC 126
      |||||||
Db      1 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
      |||||||

QY      127 ATCACTTGTGGGGAGTCAAGATATTAGCAGCTGGTGTAGCTGGTATCAGCATAAACCA 186
      |||||||
Db      21 IleThrCysArgAlaSerGlnSerIleSerAsnTyrLeuAlaTrpTyrGlnGlnLysPro 40
      |||||||

QY      187 GGGAAAGCCCTAAGCTCCTGATCTATGCTGCATCCAGTTGCAGAGTGGGTCCCATCA 246
      |||||||
Db      41 GlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSer 60
      |||||||

QY      67 GACATCCAGATGACCCAGTCTCCATCTTCGGTGTCTGTCATCTGTAGGACAGAGTCACC 126
      |||||||
Db      1 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
      |||||||

QY      127 ATCACTTGTGGGGAGTCAAGATATTAGCAGCTGGTGTAGCTGGTATCAGCATAAACCA 186
      |||||||
Db      21 IleThrCysArgAlaSerGlnSerIleSerAsnTyrLeuAlaTrpTyrGlnGlnLysPro 40
      |||||||

QY      187 GGGAAAGCCCTAAGCTCCTGATCTATGCTGCATCCAGTTGCAGAGTGGGTCCCATCA 246
      |||||||
Db      41 GlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSer 60
      |||||||

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QY      247 AGGTTACGGCGAGTGGATCTGGGACAGATTTTCACTTCACCATCAGCAGCCTGCAGCCT 306
      |||||||
Db      61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80
      |||||||

QY      307 GAAGATTTTGCACCTACTATTGTCAACAGGCTAATAGTTTCCCGTACACACTTTTGGCCAG 366
      |||||||
Db      81 GluAspPheAlaThrTyrTyrCysGlnGlnTyrAsnSerLeuProtrpThrPheGlyGln 100
      |||||||

QY      367 GGGACCAAGCTGGAGATCAA 387
      |||||||
Db      101 GlyThrLysValGluLeuLys 107
      |||||||

RESULT 13
US-09-811-123-6
; Sequence 6, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
; APPLICANT: Sharon Erickson
; APPLICANT: Ralph Schwall
; APPLICANT: Mark Sliwowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ErbB
; FILE REFERENCE: ANTIBODY-MAVTANSINOID CONJUGATES
; CURRENT APPLICATION NUMBER: US/09/811,123
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/238,327
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 09/602,530
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized Antibody Sequence
; US-09-811-123-6

Alignment Scores:
Pred. No.: 7,928-36 Length: 109
Score: 504.00 Matches: 97
Percent Similarity: 96.26% Conservative: 6
Best Local Similarity: 90.65% Mismatches: 4
Query Match: 72.21% Indels: 0
DB: 10 Gaps: 0

US-08-728-463B-206 (1-388) x US-09-811-123-6 (1-109)

QY      67 GACATCCAGATGACCCAGTCTCCATCTTCGGTGTCTGTCATCTGTAGGACAGAGTCACC 126
      |||||||
Db      1 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
      |||||||

QY      127 ATCACTTGTGGGGAGTCAAGATATTAGCAGCTGGTGTAGCTGGTATCAGCATAAACCA 186
      |||||||
Db      21 IleThrCysArgAlaSerGlnSerIleSerAsnTyrLeuAlaTrpTyrGlnGlnLysPro 40
      |||||||

QY      187 GGGAAAGCCCTAAGCTCCTGATCTATGCTGCATCCAGTTGCAGAGTGGGTCCCATCA 246
      |||||||
Db      41 GlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSer 60
      |||||||

QY      247 AGGTTACGGCGAGTGGATCTGGGACAGATTTTCACTTCACCATCAGCAGCCTGCAGCCT 306
      |||||||
Db      61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80
      |||||||

QY      307 GAAGATTTTGCACCTACTATTGTCAACAGGCTAATAGTTTCCCGTACACACTTTTGGCCAG 366
      |||||||
Db      81 GluAspPheAlaThrTyrTyrCysGlnGlnTyrAsnSerLeuProtrpThrPheGlyGln 100
      |||||||

QY      367 GGGACCAAGCTGGAGATCAA 387
      |||||||
Db      101 GlyThrLysValGluLeuLys 107
      |||||||

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Db 189 GlyValProSerArgPheSerGlySerGlyThrAspPheThrLeuThrIleSer 208
QY 295 AGCTGCAGCCTGAAGATTTTCCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTAC 354
Db 209 SerLeuGlnProGluAspPheAlaThrTyTyCysGlnGlnSerTySerThrProAsn 228
QY 355 ACTTTTGGCCAGGGACCAAGCTGGAGATCAAA 387
Db 229 ThrPheGlyGlnGlyThrLysValGluIleLys 239

Search completed: June 3, 2003, 09:51:15
Job time : 18.4856 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 09:02:35 ; Search time 8.83156 Seconds
(without alignments)
2585.294 Million cell updates/sec

Title: US-08-728-463B-206
Perfect score: 698
Sequence: 1 ATGGACATGATGTCCTCCGC.....GACCAAGCTGGAGATCAAC 388

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 525148

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/cgn2_1/USPTO.spool/US08728463/runat_03062003_085615_16867/app.query.fasta_1.3690
-DB=Issued Patents AA -QFMT=fastan -SUFFIX=ra1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human0.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-USER=US08728463 @CIGN 1 1 97 @runat_03062003_085615_16867 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
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5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	573	82.1	128	1	US-08-259-372A-14
2	573	82.1	128	1	US-08-468-671-14
3	573	82.1	129	1	US-08-217-918-2
4	553	79.2	236	1	US-08-157-101A-5
5	543	77.8	128	2	US-08-470-139-26
6	543	77.8	128	4	US-09-347-061-26
7	539	77.2	117	4	US-09-042-353-48
8	539	77.2	117	4	US-08-758-417A-313
9	532	76.2	116	1	US-08-053-131-185
10	532	76.2	116	2	US-08-096-762-185
11	529	75.8	128	4	US-08-569-147-80
12	526	75.4	127	2	US-08-621-751A-6

13	524	75.1	127	3	US-08-836-561-71	Sequence 71, Appl
14	517	74.1	109	2	US-07-934-373C-3	Sequence 3, Appl1
15	517	74.1	109	3	US-08-437-642B-3	Sequence 3, Appl1
16	517	74.1	109	4	US-08-146-206C-3	Sequence 3, Appl1
17	517	74.1	109	5	PCT-US93-07832-3	Sequence 3, Appl1
18	517	74.1	127	4	US-09-136-315-8	Sequence 8, Appl1
19	513	73.5	131	4	US-08-579-378A-18	Sequence 18, Appl
20	512	73.4	128	4	US-08-569-147-78	Sequence 18, Appl
21	509	72.9	127	3	US-08-836-561-88	Sequence 88, Appl
22	509	72.9	235	3	US-08-812-586-16	Sequence 16, Appl
23	507	72.6	233	3	US-08-812-586-45	Sequence 45, Appl
24	506	72.5	127	2	US-08-621-751A-2	Sequence 2, Appl1
25	504	72.2	107	2	US-07-934-373C-18	Sequence 18, Appl
26	504	72.2	107	3	US-08-437-642B-18	Sequence 18, Appl
27	504	72.2	107	4	US-08-146-206C-18	Sequence 18, Appl
28	504	72.2	107	5	PCT-US93-07832-18	Sequence 18, Appl
29	504	72.2	108	3	US-08-974-899-3	Sequence 3, Appl1
30	504	72.2	127	3	US-08-649-100-33	Sequence 33, Appl
31	503	72.1	133	1	US-08-461-284-2	Sequence 2, Appl1
32	503	72.1	133	1	US-08-462-939-2	Sequence 2, Appl1
33	503	72.1	133	1	US-08-253-877C-2	Sequence 2, Appl1
34	503	72.1	133	2	US-08-452-164A-2	Sequence 2, Appl1
35	498	71.3	127	3	US-08-836-561-92	Sequence 92, Appl
36	495	70.9	109	4	US-09-157-370-3	Sequence 3, Appl1
37	495	70.9	127	2	US-08-646-981-8	Sequence 8, Appl1
38	495	70.9	134	4	US-08-718-323A-10	Sequence 10, Appl
39	495	70.9	134	4	US-09-587-526-10	Sequence 10, Appl
40	494.5	70.8	133	1	US-08-253-877C-28	Sequence 28, Appl
41	494.5	70.8	133	2	US-08-452-164A-28	Sequence 28, Appl
42	494.5	70.8	133	3	US-08-603-024-27	Sequence 27, Appl
43	493	70.6	128	4	US-09-450-520A-6	Sequence 6, Appl1
44	492	70.5	107	4	US-09-240-274-40	Sequence 40, Appl
45	492	70.5	138	4	US-08-976-183A-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1

US-08-259-372A-14
; Sequence 14, Application US/08259372A
; Patent No. 5565354
; GENERAL INFORMATION:
; APPLICANT: Ostberg, Lars G.
; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,372A
; FILING DATE: 14-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/871,426
; FILING DATE: 21-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,036
; FILING DATE: 27-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/538,796
; FILING DATE: 15-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/192,754

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STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,671
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/259,372
FILING DATE: 14-JUN-1994
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-MAR-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 118223-50-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-671-14

Alignment Scores:
Pred No.: 4,05e-55 Length: 128
Score: 573.00 Matches: 10
Percent Similarity: 94.31% Conservative: 7
Best Local Similarity: 88.62% Mismatches: 7
Query Match: 82.09% Indels: 0
DB: 1 Gaps: 0

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Db 5 AlaGlnLeuLeugLyLeuLeuLeuLrpPheProGlySer
QY 79 ACCCAGTCTCCATCTTCGGTGCTCGCATCTGTAGACACAGA
Db 25 ThrGlnSerProSerValSerAlaSerValGlyAspArg
QY 139 GCAGTCAAGATATTAGCAGCTGGTTAGCCCTGGTATCAGCAT
Db 45 AlaSerGlnGlyLeuSerSerTripleuAlaTrpIyrGlnGln
QY 199 AAGCTCTCTGATCTATGCTGCATCCAGTTTGAAGTGGGTC
Db 65 LysLeuLeuIleHisAlaLeuSerLeuGlnSerGlyVal

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; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-096-762-185

Alignment Scores:
Pred. No.:      Length:    116
Score:          532.00     Matches:   105
Percent Similarity: 93.10% Conservative: 3
Best Local Similarity: 90.52% Mismatches:   8
Query Match:    76.22% Indels:         0
DB:              2        Gaps:           0

US-08-728-463B-206 (1-388) x US-08-096-762-185 (1-116)

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Db      1  MetAspMetArgValLeuAlaGlnLeuLeuglyLeuLeuLeuCysPheProGlyAla 20
Qy      61  AGATGGCATCTCCAGATCACCCAGTCTCCATCTCCGTGTCTGCATCTGTAGGAGACAGA 120
Db      21  ArgCysAspIleGlnMethrGlnSerProSerSerLeuSerAlaSerValGlyAspArg 40

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US-08-728-463B-206 (1-388) x US-08-096-762-185 (1-116)

Qy 1 ATGGACATGATGTCCCGCTCAGCTCCTGGGGTCTCTGGTTCCAGGTTCC 60
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RESULT 11
US-08-569-147-80
; Sequence 80, Application US/08569147
; Patent No. 6180377
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANISED ANTIBODIES
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESS: No. 6180377ris, LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,147
; FILING DATE: 25-March-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yatto
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0047
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 80:

Db 101 GlyThrLysValGluIleLys 107
RESULT 15
US-08-437-642B-3
; Sequence 3, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-3

Alignment Scores:
Pred. No.: 5.56e-49 Length: 109
Score: 517.00 Matches: 99
Percent Similarity: 97.20% Conservative: 5
Best Local Similarity: 92.52% Mismatches: 3
Query Match: 74.07% Indels: 0
DB: 3 Gaps: 0

US-08-728-463B-206 (1-388) x US-08-437-642B-3 (1-109)

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Db |||||||
1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
QY 127 ATCACTTTCGGCGAGTCCAGATATTACAGCTGGTGTAGCTGGTATCAGCATAAACCA 186
Db |||||||
21 IleThrCysArgAlaSerGlnAspValSerTyrLeuAlaTyrTyrGlnGlnLysPro 40
QY 187 GGGAAAGCCCTTAAGTCTCTGATCTATGCTGATCCAGTTTCAGGTTCCCATCA 246
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Search completed: June 3, 2003, 09:47:25
Job time : 10.8316 secs

Db 41 GlyLysAlaProLysLeuLeuIleTyrAlaAlaSer-SerLeuGluSerGlyValProSer 60
QY 247 AGGTTTCAGCGCAGTGTGATCTGGGACAGATTTTCACCTCTCACCATCAGCAGCTGCAGCCT 306
Db |||||||
61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80
QY 307 GAAGATTTTGCACCTTACTATTCTCAACAGGCTTAATAGTTTCCGTACACATTTTGGCCAG 366
Db |||||||
81 GluAspPheAlaThrTyrTyrCysGlnGlnTyrAsnSerLeuProTyrThrPheGlyGln 100
QY 367 GGGACCAAGCTGGAGATCAA 387
Db |||||||
101 GlyThrLysValGluIleLys 107

GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 19.5421 Seconds

(without alignments)
4545.477 Million cell updates/sec

Title: US-08-728-463B-207

Perfect score: 846

Sequence: 1 ATGGGGTCAACGCCCATCTCT.....CACCTCTCTCCAGAGGCTT 462

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 566448

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-O=/cgn2.1/USPTO spool/US08728463/runat_03062003_085615_16827/app query.fasta_1.3690
-DB=pir_73 -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=BITS -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US08728463 @CEN 1 1 177 @runat_03062003_085615_16827 -NCPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	649.5	76.8	139	2	PH1558 Ig heavy chain V r
2	630	74.5	136	2	PH1559 Ig heavy chain V r
3	618.5	73.1	137	2	PH1562 Ig heavy chain V r
4	602	71.2	144	2	E41287 Ig heavy chain pre
5	601	71.0	128	2	S16685 Ig heavy chain V r
6	598	70.7	138	2	PH1565 Ig heavy chain V r
7	595	70.3	117	2	A28846 Ig heavy chain pre
8	593	70.1	138	2	PH1564 Ig heavy chain V r
9	590	69.7	115	2	PH1557 Ig heavy chain V r
10	586.5	69.3	147	2	PH1557 Ig heavy chain V r
11	584.5	69.1	136	2	A49047 Ig heavy chain V r
12	584.5	69.1	141	2	S31685 Ig heavy chain V r
13	582	68.8	144	2	PH1563 Ig heavy chain V r
14	575	68.0	127	2	PH1414 Ig heavy chain V r

15	567	67.0	113	2	PH1428 Ig heavy chain V r
16	565	66.8	123	2	C36006 Ig heavy chain V r
17	563	66.5	127	2	PH1415 Ig heavy chain V r
18	560	66.2	127	2	PH1420 Ig heavy chain V r
19	559	66.1	123	2	S38492 Ig heavy chain - h
20	558	66.0	123	2	PH1413 Ig heavy chain V r
21	558	66.0	123	2	PH1423 Ig heavy chain V r
22	545.5	64.5	134	2	PH1422 Ig heavy chain V r
23	542.5	64.1	126	2	PH1424 Ig heavy chain V r
24	542	64.1	127	2	PH1411 Ig heavy chain V r
25	541	63.9	115	2	PH1560 Ig heavy chain V r
26	539	63.7	117	2	S19670 Ig heavy chain V r
27	537.5	63.5	126	2	PH1419 Ig heavy chain V r
28	536	63.4	102	2	PH1279 Ig heavy chain V r
29	533	63.0	102	2	PH1252 Ig heavy chain V r
30	533	63.0	102	2	PH1266 Ig heavy chain V r
31	531.5	62.8	126	2	PH1417 Ig heavy chain V r
32	531.5	62.8	126	2	PH1418 Ig heavy chain V r
33	531	62.8	125	2	PH1410 Ig heavy chain V r
34	530	62.6	101	2	S12424 Ig heavy chain V r
35	530	62.6	102	2	PH1258 Ig heavy chain V r
36	530	62.6	102	2	PH1278 Ig heavy chain V r
37	530	62.6	102	2	PH1281 Ig heavy chain V r
38	530	62.6	102	2	PH1271 Ig heavy chain V r
39	529.5	62.6	122	2	PH1426 Ig heavy chain V r
40	528	62.4	102	2	PH1254 Ig heavy chain V r
41	527.5	62.4	126	2	PH1412 Ig heavy chain V r
42	526.5	62.2	126	2	PH1416 Ig heavy chain V r
43	526	62.2	109	2	PH1672 Ig heavy chain V r
44	525	62.1	101	2	S12428 Ig heavy chain V r
45	524	61.9	102	2	PH1247 Ig heavy chain V r

ALIGNMENTS

RESULT 1

PH1558
Ig heavy chain V region (clone DOB) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 16-Aug-1996
C:Accession: PH1558
R:Rassenti, L. Z.; Kipps, T. J.
J. Exp. Med. 177, 1039-1046, 1993
A:Title: Lack of extensive mutations in the VHS genes used in common B cell chronic lymphocytic leukemia
A:Reference number: PH1557; MUID:93210459; PMID:7681468
A:Accession: PH1558
A:Molecule type: DNA
A:Residues: 1-139 <RAS>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:32-115/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 3,18e-43 Length: 139
Score: 649.50 Matches: 127
Percent Similarity: 91.37% Conservative: 0
Best Local Similarity: 91.37% Mismatches: 7
Query Match: 76.77% Indels: 5
DB: 2 Gaps: 1

US-08-728-463B-207 (1-462) x PH1558 (1-139)

QY	7	TCAACGCCCATCTCTCGCCCTCTCTCGCTGTCTTCCAGGAGTCTGTCCGAGGTGCAG	66
Db	1	SerThrAlaIleLeuAlaLeuLeuAlaValLeuGlnGlyValCysAlaGluValGln	20
QY	67	CTGTGTCAGTCTGGAGCAGAGTGTAAGCCCGGGAGTCTCTGAAGTCTCTCTTAAG	126
Db	21	LeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIleSerCysLys	40
QY	127	GGTTCCTGGATACAGTTTACCGGCTACTCGATCGGCTGGTGGCCAGATGCCCGGAAA	186
Db	41	GlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValArgGlnMetProGlyLys	60

QY 187 GGCCTGGAGTGGGATCATCTATCTCTGGTGAATCTGATACCATACATACAGCCCGTCC 246
 Db 61 GlyLeuGluTrpMetGlyLeileTyrProGlyAspSerAspThrArgTyrSerProSer 80
 QY 247 TTCGAAGCCAGGTCACCATCTCAGCCGACAGTCCATCAGCAGCCGCTACCTCAGTGG 306
 Db 81 PheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 100
 QY 307 AGCAGCCTGAAGCCCTCGGACACCGCCATGTATTACTGTGGAGAGAC----- 354
 Db 101 SerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgSerIleSerSerSer 120
 QY 355 ---CAACTGGCCCTTTGACTACTGGGCGCAGGAACCCCTGGTCAACCGTCTCCTCA 408
 Db 121 GlyTyrTyrSerAsnPheAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 139

RESULT 2

PH1559

Ig heavy chain V region (clone HAN) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 21-Jan-2000

C:Accession: PH1559

R:Assessenti, L.Z.; Kippes, T.J.

J. Exp. Med. 177, 1039-1046, 1993

A:Title: Lack of extensive mutations in the VHS genes used in common B cell chronic lymph

A:Reference number: PH1557; MUID:93210459; PMID:7681468

A:Accession: PH1559

A:Molecule type: DNA

A:Residues: 1-136 <RAS>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;32-115/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	1,07e-41	Length:	136
Score:	630.00	Matches:	123
Percent Similarity:	90.44%	Conservative:	0
Best Local Similarity:	90.44%	Mismatches:	11
Query Match:	74.47%	Indels:	2
DB:	2	Gaps:	1

US-08-728-463B-207 (1-462) x PH1559 (1-136)

QY 7 TCACCGCCATCTCGCCCTCTCTGGTGTCTTCCAGGAGTCTGTGCCGAGTGCAG 66
 Db 1 SerThrAlaIleLeuAlaLeuLeuAlaValLeuGlnGlyValCysAlaGluValGln 20
 QY 67 CTGGTGCAGTCTCGAGCAGAGGTGAAAGCCCGGGAGTCTCTGAAGATCTCTGTAAG 126
 Db 21 LeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuLysIleSerCysLys 40
 QY 127 GGTCTGGATACAGCTTTACCGGCTACTGGATCGGTCGGCGCAGATGCCCGGAAA 186
 Db 41 GlySerArgTyrSerPheThrSerTyrTrpIleGlyTyrValArgGlnMetProGlyLys 60
 QY 187 GGCCTGGATGGGATCATCTATCTCTGGTGAATCTGATACCATACAGCCCGTCC 246
 Db 61 GlyLeuGluTrpMetGlyArgIleAspProSerAspSerTyrThrAsnTyrSerProSer 80
 QY 247 TTCGAAGCCAGTCAACCATCTCAGCCGACAGTCCATCAGCAGCCGCTACCTGCAGTGG 306
 Db 81 PheGlnGlyGlnValThrPheSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 100
 QY 307 AGCAGCCTGAAGCCCTCGGACACCGCCATGTATTACTGTGGAGAGAC----- 354
 Db 101 SerArgLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgLeuTyrGlyAspPhe 120
 QY 361 GGCCTCTTGTACTACTGGGCGCAGGAACCCCTGGTCAACCGTCTCCTCA 408
 Db 121 SerThrValAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 136

RESULT 3

PH1562

Ig heavy chain V region: (clone HOW) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 21-Jan-2000

C:Accession: PH1562

R:Assessenti, L.Z.; Kippes, T.J.

J. Exp. Med. 177, 1039-1046, 1993

A:Title: Lack of extensive mutations in the VHS genes used in common B cell chronic lymph

A:Reference number: PH1557; MUID:93210459; PMID:7681468

A:Accession: PH1562

A:Molecule type: DNA

A:Residues: 1-137 <RAS>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;32-115/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	8,52e-41	Length:	137
Score:	618.50	Matches:	122
Percent Similarity:	90.51%	Conservative:	2
Best Local Similarity:	89.05%	Mismatches:	10
Query Match:	73.11%	Indels:	3
DB:	2	Gaps:	1

US-08-728-463B-207 (1-462) x PH1562 (1-137)

QY 7 TCACCGCCATCTCGCCCTCTCTGGTGTCTTCCAGGAGTCTGTGCCGAGTGCAG 66
 Db 1 SerThrAlaIleLeuAlaLeuLeuAlaValLeuGlnGlyValCysAlaGluValGln 20
 QY 67 CTGGTGCAGTCTCGAGCAGAGGTGAAAGCCCGGGAGTCTCTGAAGATCTCTGTAAG 126
 Db 21 LeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuLysIleSerCysLys 40
 QY 127 GGTCTGGATACAGCTTTACCGGCTACTGGATCGGTCGGCGCAGATGCCCGGAAA 186
 Db 41 GlySerGlyTyrSerPheThrSerTyrTrpIleSerTyrValArgGlnMetProGlyLys 60
 QY 187 GGCCTGGAGTGGATGGGATCATCTATCTCTGGTGAATCTGATACCATACAGCCCGTCC 246
 Db 61 GlyLeuGluTrpMetGlyArgIleAspProSerAspSerTyrThrAsnTyrSerProSer 80
 QY 247 TTCGAAGCCAGTCAACCATCTCAGCCGACAGTCCATCAGCAGCCGCTACCTGCAGTGG 306
 Db 81 PheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 100
 QY 307 AGCAGCCTGAAGCCCTCGGACACCGCCATGTATTACTGTGGAGAGAC----- 357
 Db 101 SerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgGluGlnTrpLeuVal 120
 QY 358 CTGGGCGCTCTTTGACTACTGGGCGCAGGAACCCCTGGTCAACCGTCTCCTCA 408
 Db 121 LeuSerAsnPheAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 137

RESULT 4

E41287

Ig heavy chain precursor V-V region (257-D) (anti-HIV-1) - human

C:Species: Homo sapiens (man)

C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 21-Jan-2000

C:Accession: E41287

R:Andrieu, J.S.; Johnson, S.; Zolla-Pazner, S.; Capra, J.D.

Proc. Natl. Acad. Sci. U.S.A. 88, 7783-7787, 1991

A:Title: Molecular characterization of five human anti-human immunodeficiency virus type

A:Reference number: A41287; MUID:91352074; PMID:1909030

A:Accession: E41287

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-144 <AND>

A:Cross-references: GB:M67504; NID:g185413; PIDN:AA52946.1; PID:g185414

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>


```

Db      21  LeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuArgIleSerCysLys 40
Qy      127 GGTCTGGATACAGCTTTACCGCTACTTGGATCGGTGGTGGCCAGATGCCCGGAAA 186
Db      41  GlySerGlyTyrSerPheThrSerTyrTrpIleSerTrpValArgGlnMetProGlyLys 60
Qy      187 GGCCTGGAGTGGATGGGATCATCTATCTGTGTGATCTGTATACCATACACATACAGCCGTC 246
Db      61  GlyLeuGluTrpMetGlyArgIleAepProSerAspSerTyrThrAsnTyrSerProSer 80
Qy      247 TTCCAAGGCGGCTGACCATCTCAGCCGACAGTCCATCAGCAGCCGCTACTCTGAGTGG 306
Db      81  PheGlnGlyHisValThrIleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 100
Qy      307 AGCAGCTGAAGCCTCGACACCGCCATGTATTACTGTGGCAGAGACCAACTGGGCTC 366
Db      101 SerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgHisThrProThrLeu 120
Qy      367 -----TTTGACTACTGGGGCCAGGAGAACCTGGTCACTGGTCTCTCTCA 408
Db      121 TyrTyrTyrGlyPheAspSerTrpGlyGlnGlyThrLeuValThrValSerSer 138
RESULT 7
A28846
Ig heavy chain precursor V region (VH251) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
R:Humphries, C.G.; Shen, A.; Kuziel, W.A.; Capra, J.D.; Blattner, F.R.; Tucker, P.W.
Nature 331, 446-449, 1988
A:Title: A new human immunoglobulin V-H family preferentially rearranged in immature B-cells
A:Reference number: A28846; MUID:88122615; PMID:3123998
A:Accession: A28846
A:Molecule type: DNA
A:Residues: 1-117 <HUM>
A:Note: the authors translated the codon ATC for residue 89 as His
R:Shen, A.; Humphries, C.; Tucker, P.; Blattner, F.
Proc. Natl. Acad. Sci. U.S.A. 84, 8563-8567, 1987
A:Title: Human heavy-chain variable region gene family nonrandomly rearranged in families
A:Reference number: A39982; MUID:98068629; PMID:3120193
A:Accession: A39982
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <SHE>
A:Cross-references: GB:M18806; NID:g185574; PIDN:AAA53013.1; PID:g567178
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>
Alignment Scores:
Pred. No.: 5.97e-39 Length: 117
Score: 595.00 Matches: 113
Percent Similarity: 97.44% Conservative: 1
Best Local Similarity: 96.58% Mismatches: 3
Query Match: 70.33% Indels: 0
DB: 2 Gaps: 0
US-08-728-463b-207 (1-462) x A28846 (1-117)
Qy      1  ATGGGTCAACGCCATCTCGCCCTCTCTGGCTGTCTCCAGGAGTCTGTGCCGAG 60
Db      1  MetGlySerThrAlaIleLeuAlaLeuLeuLeuAlaIleLeuGlnGlyValCysAlaGlu 20
Qy      61  GTGCAGCTGTGCTGAGTGGAGCAGAGTGTAACCGCTACTGATCGGCTGGTGGCCAGATGCC 120
Db      21  ValGlnLeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuLysIleSer 40
Qy      121 TGTAAAGGTTCTGGATACAGCTTTTACCGCTACTGATCGGCTGGTGGCCAGATGCC 180
Db      41  CysLysGlySerGlyTyrSerPheThrSerTyrTrpIleSerTrpValArgGlnMetPro 60
Qy      181 GGAAGAGCCTGGAGTGGATGGGATCATCTATCTGCTGGTCACTGTGATACACATACAGC 240

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Db      61  GlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAepSerAspThrArgTyrSer 80
Qy      241 CCCTCTCTTCAAGCCAGGTCCACCATCTCAGCCGACAGTCCATCAGACCCGCTACCTG 300
Db      81  ProSerPheGlnGlyGlnValThrIleSerAlaAepLysSerIleSerThrAlaTyrLeu 100
Qy      301 CAGTGGAGCAGCTGAAGCCCTCGGACACCGCCATGTATTACTGTGCGAGA 351
Db      101 GlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArg 117
RESULT 8
PH1564
Ig heavy chain V region (clone ANG) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 21-Jan-2000
R:Rassenti, L.Z.; Kippes, T.J.
J. Exp. Med. 177, 1039-1046, 1993
A:Title: Lack of extensive mutations in the VH5 genes used in common B cell chronic lymphocytic leukemia
A:Reference number: PH1557; MUID:93210459; PMID:7681468
A:Accession: PH1564
A:Molecule type: DNA
A:Residues: 1-138 <RAS>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:32-115/Domain: immunoglobulin homology <IMM>
Alignment Scores:
Pred. No.: 8.45e-39 Length: 138
Score: 593.00 Matches: 118
Percent Similarity: 87.68% Conservative: 3
Best Local Similarity: 85.51% Mismatches: 13
Query Match: 70.09% Indels: 4
DB: 2 Gaps: 1
US-08-728-463b-207 (1-462) x PH1564 (1-138)
Qy      7  TCACCCGCCATCTCTCGCCCTCTCTGGCTGTCTCCAGGAGTCTGTGCCGAGTGCAG 66
Db      1  SerThrAlaIleLeuAlaLeuLeuLeuAlaValLeuGlnGlyValCysAlaGluValGln 20
Qy      67  CTGCTGAGTCTGGAGCAGAGGTGAAAGCCCGGGAGTCTCTGAAGATCTCTCTGAAG 126
Db      21  LeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuArgIleSerCysLys 40
Qy      127 GGTCTTGGATACAGCTTTTACCGCTACTCGATCGGTGGTGGCCAGATGCCCGGAAA 186
Db      41  GlySerGlyTyrSerPheThrSerTyrTrpIleSerTrpValArgGlnMetProGlyLys 60
Qy      187 GGCCTGGAGTGGATGGGATCATCTATCTGTGTGATCTGTATACCATACACATACAGCCGTC 246
Db      61  GlyLeuGluTrpMetGlyArgIleAepProSerAspSerTyrThrAsnTyrSerProSer 80
Qy      247 TTCCAAGGCGGCTGACCATCTCAGCCGACAGTCCATCAGCAGCCGCTACTCTGAGTGG 306
Db      81  PheGlnGlyHisValThrIleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 100
Qy      307 AGCAGCTGAAGCCTCGGACACCGCCATGTATTACTGTGCGAGAGACCAACTGGGCTC 366
Db      101 SerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgHisThrValGly 120
Qy      367 TTT-----GACTACTGGGCGGAGAACCTGGTCACTGGTCTCTCTCA 408
Db      121 TyrSerGlyCysSerGlnSerTrpGlyGlnGlyThrLeuValThrValSerSer 138
RESULT 9
PH1557
Ig heavy chain V region (clone 5-2R1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 16-Aug-1996
C:Accession: PH1557
R:Rassenti, L.Z.; Kippes, T.J.

```

J. Exp. Med. 177, 1039-1046, 1993
A:Title: Lack of extensive mutations in the VHS genes used in common B cell chronic lymph
A:Reference number: PH1557; MUID:93210459; PMID:7681468
A:Accession: PH1557
A:Molecule type: DNA
A:Residues: 1-115 <RAS>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:32-115/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 1,47e-38 Length: 115
Score: 590.00 Matches: 113
Percent Similarity: 98.26% Conservative: 0
Best Local Similarity: 98.26% Mismatches: 2
Query Match: 69.74% Indels: 0
DB: 2 Gaps: 0

US-08-728-463B-207 (1-462) x PH1557 (1-115)

```
QY 7 TCACCGCCATCTCGCCCTCTCTCGGCTGTTCTCCAAAGGAGTCTGTCCCGAGGTGCG 66
Db 1 SerThrAlaIleLeuAlaLeuLeuAlaValLeuGlnGlyValCysAlaGluValGln 20
QY 67 CTGGTGCACTCTGGACGACAGGTGAAGCCCGGGAGTCTCTGAAGATCTCTCTTAAG 126
Db 21 LeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIleSerCysLys 40
QY 127 GGTTCCTGGATACAGCTTTTACCGCTACTCGGCTGCGGTGGCGCAGATGCCCGGAAA 186
Db 41 GlySerGlyTyrSerPheThrSerTyrTrpLleGlyTrpValArgGlnMetProGlyLys 60
QY 187 GGCCTGGAGTGGATGGGATCATCTATCTCTGTGACTCTGTATACCATACACCGCGTCC 246
Db 61 GlyLeuGlnTrpMetGlyIleLeuTyrProGlyAepSerAspThrArgTyrSerProSer 80
QY 247 TTCCAAGCCAGTCACTATCTCAGCCGACAGTCCATCAGCACCGCTCTACCTGCGAGTGG 306
Db 81 PheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 100
QY 307 AGCAGCTGAAGCCCTCGGACACCGCCATGATTACTGTGCGAGA 351
Db 101 SerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArg 115
```

RESULT 10

PH1561
Ig heavy chain V region (clone CAV) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 21-Jan-2000
C:Accession: PH1561
R:Rassenti, L.Z.; Kipps, T.J.
J. Exp. Med. 177, 1039-1046, 1993
A:Title: Lack of extensive mutations in the VHS genes used in common B cell chronic lymph
A:Reference number: PH1557; MUID:93210459; PMID:7681468
A:Accession: PH1561
A:Molecule type: DNA
A:Residues: 1-147 <RAS>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:32-115/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 2,71e-38 Length: 147
Score: 586.50 Matches: 117
Percent Similarity: 81.63% Conservative: 3
Best Local Similarity: 79.59% Mismatches: 14
Query Match: 69.33% Indels: 13
DB: 2 Gaps: 1

US-08-728-463B-207 (1-462) x PH1561 (1-147)

```
QY 7 TCACCGCCATCTCGCCCTCTCTCGGCTGTTCTCCAAAGGAGTCTGTCCCGAGGTGCG 66
Db 1 SerThrAlaIleLeuAlaLeuLeuAlaValLeuGlnGlyValCysAlaGluValGln 20
```

```
Db 1 SerThrAlaIleLeuAlaLeuLeuAlaValLeuGlnGlyValCysAlaGluValGln 20
QY 67 CTGGTGCACTCTGGACGACAGGTGAAGCCCGGGAGTCTCTGAAGATCTCTCTTAAG 126
Db 21 LeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIleSerCysLys 40
QY 127 GGTTCCTGGATACAGCTTTTACCGCTACTCGGCTGCGGTGGCGCAGATGCCCGGAAA 186
Db 41 GlySerGlyTyrSerPheThrSerTyrTrpLleGlyTrpValArgGlnMetProGlyLys 60
QY 187 GGCCTGGAGTGGATGGGATCATCTATCTCTGTGACTCTGTATACCATACACCGCGTCC 246
Db 61 GlyLeuGlnTrpMetGlyArgIleAspProSerAspSerTyrThrAsnTyrSerProSer 80
QY 247 TTCCAAGCCAGTCACTATCTCAGCCGACAGTCCATCAGCACCGCTCTACCTGCGAGTGG 306
Db 81 PheGlnGlyHisValThrIleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 100
QY 307 AGCAGCTGAAGCCCTCGGACACCGCCATGATTACTGTGCGAGAGACCAACTGGGCGTC 366
Db 101 SerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgGlnIleAlaGlyIle 120
QY 367 -----TTTGACTACTTGGGGCCAGGCA 387
Db 121 AlaAlaAlaGlyMetTrpGlyProTyrTyrTyrTyrMetAspValTrpGlyLysGly 140
QY 388 ACCCTGGTCACGTCCTCTCA 408
Db 141 ThrThrValThrValSerSer 147
```

RESULT 11

A49047
Ig heavy chain V region (monoclonal striational autoantibody StrAB SA-1A VH) - human (f.
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998
C:Accession: A49047
R:Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A:Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A:Reference number: A49047; MUID:92387224; PMID:1516616
A:Accession: A49047
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-136 <VIC>
A:Experimental source: thymic B lymphocytes
A:Note: sequence extracted from NCBI backbone (NCBI:113206, NCBI:113207)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 3,92e-38 Length: 136
Score: 584.50 Matches: 111
Percent Similarity: 83.82% Conservative: 3
Best Local Similarity: 81.62% Mismatches: 7
Query Match: 69.03% Indels: 15
DB: 2 Gaps: 1

US-08-728-463B-207 (1-462) x A49047 (1-136)

```
QY 46 GGAGTCTGTCCGAGGTGCGAGTCTGTGAGTCTGGAGCAGAGGTGAAGAGCCCGGGAG 105
Db 1 GlyValCysAlaGluValGlnLeuValGlnSerGlyAlaGluValLysProGlyGlu 20
QY 106 TCTCTGAAGATCTCTCTGAAGGTTCTTGATACAGCTTTTACCGGCTTACGAGTCTCG 165
Db 21 SerLeuLysIleSerCysLysGlySerGlyTyrSerPheThrSerTyrTrpLleGlyTrp 40
QY 166 GTGCCCCAGATGCCCGGAAAGCCCTGGAGTGGATCATCTATCTCTGCTACTCT 225
Db 41 ValArgGlnMetProGlyLysGlyLeuGluTyrMetGlyIleIleTyrProGlyAspSer 60
QY 226 GATACCATACAGCCCGCTCTTCCAGGCCAGGTCCACCATCTCAGCCGACAGTCCATC 285
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Db 61 AspThrArgTyrSerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIle 80
 QY 286 AGCACCGCCTTACCTGAGTGGAGCAGCTGAGAGGCTCGGACACCGCATGTATTACTGT 345
 Db 81 SerThrAlaTyrLeuGlnTrpSerLeuLysAlaSerAspThrAlaMetTyrTyrCys 100
 QY 346 GCGAGAGACAACTGGGCTCTTTGACTAC----- 375
 Db 101 AlaArgGlnSerTyrGlyTyrTyrAspPheAspSerGlyTyrTyrProAlaTyrTyrTyr 120
 QY 376 -----TGGGCGCAGAGAACCTCGTTCACCGCTCTCTCA 408
 Db 121 TyrGlyMetAspValTrpGlyGlnGlyThrThrValThrValSerSer 136
 RESULT 12
 S11685
 Ig heavy chain V region - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C:Accession: S31685
 R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
 submitted to the EMBL Data Library, June 1992
 A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
 A:Reference number: S31585
 A:Accession: S31685
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-141 <CUI>
 A:Cross-references: EMBL:Z14183; NID:G31033; PIDN:CAA78552.1; PID:G31034
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:34-117/Domain: immunoglobulin homology <IMM>
 Alignment Scores:
 Pred. No.: 3.9e-38 Length: 141
 Score: 584.50 Matches: 117
 Percent Similarity: 85.82% Conservative: 4
 Best Local Similarity: 82.98% Mismatches: 15
 Query Match: 69.09% Indels: 5
 DB: 2 Gaps: 2
 US-08-728-463B-207 (1-462) x S31685 (1-141)
 QY 1 ATGGGGTCAACCGCATCTCGCCCTCTCTCGCTGTTCTTCCAAAGAGTCTGTGCGGAG 60
 Db 1 MetGlySerThrAlaIleLeuAlaLeuLeuLeuAlaValLeuGlnGlyValCysAlaGlu 20
 QY 61 GTCAGCTGTGAGTCTGAGCAGAGGTGAAAGCCCGGGAGTCTCTGAAGATCTCC 120
 Db 21 ValGlnLeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuArgIleSer 40
 QY 121 TGTAAGGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGTGGCGCCAGATGCC 180
 Db 41 CysLysGlySerGlyTyrSerPheThrSerTyrTrpIleSerTrpAlaArgGlnMetPro 60
 QY 181 GGAAGAGGCTGGAGTGGATGGGATCATCTATCTCTGTGACTCTGTATACCATACATACAGC 240
 Db 61 GlyLysGlyLeuGlnTrpMetGlyArgIleAspProSerAspProTyrThrAsnTyrSer 80
 QY 241 CCCTCTCTCCAGGCCAGTCCACCATCTCAGCGGCAAGTCCATCAGCACCGCTTACCTG 300
 Db 81 ProSerPheGlnGlyHisValThrIleSerAlaAspLysSerIleSerThrAlaTyrLeu 100
 QY 301 CAGTGGAGCAGCTGAAGCCCTCGGACACCGCATGTATTACTGTGCGGAGACCACTG 360
 Db 101 GlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgHisGlyVal 120
 QY 361 ---GGCTCTTT-----GACTACTGGGCGCAGGAAACCTGTGTCACCGTCTCC 405
 Db 121 ArgGlyTyrTyrTyrTyrTyrMetAspValTrpGlyLysGlyThrThrValThrValSer 140
 QY 406 TCA 408
 |||

Db 141 Ser 141

RESULT 13

PH1563
 Ig heavy chain V region (clone PET) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 21-Jan-2000
 C:Accession: PH1563
 R:Rassenti, L.Z.; Kippes, T.J.
 J. Exp. Med. 177, 1039-1046, 1993
 A:Title: Lack of extensive mutations in the VHS genes used in common B cell chronic lymphoma
 A:Reference number: PH1557; MUID:9310459; PMID:7681466
 A:Accession: PH1563
 A:Molecule type: DNA
 A:Residues: 1-144 <RAS>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:32-115/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.: 6.11e-38 Length: 144
 Score: 582.00 Matches: 117
 Percent Similarity: 82.64% Conservative: 2
 Best Local Similarity: 81.25% Mismatches: 15
 Query Match: 68.73% Indels: 10
 DB: 2 Gaps: 1

US-08-728-463B-207 (1-462) x PH1563 (1-144)

QY 7 TCAACCGCATCTCGCCCTCTCTCGCTGTTCTTCCAAAGAGTCTGTGCGGAGTGCAG 66

Db 1 SerThrAlaIleLeuAlaLeuLeuLeuAlaValLeuGlnGlyValCysAlaGluValGln 20

QY 67 CTGTGTCAGTCTGGAGCAGAGGTGAAAGCCCGGGAGTCTCTGAAGATCTCTCTGTAAG 126

Db 21 LeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuArgIleSerCysLys 40

QY 127 GGTCTGTGATACAGCTTTACCGGCTACTGGATCGGCTGGTGGCGCCAGATGCCCGGAAA 186

Db 41 GlySerGlyTyrSerPheThrSerTyrTrpIleSerTrpValArgGlnMetProGlyLys 60

QY 187 GCCTGGAGTGGATGGGATCATCTATCTGTGACTCTGTATACCATACATACAGCCGCTCC 246

Db 61 GlyLeuGlnTrpMetGlyArgIleAspProSerAspSerTyrThrAsnTyrSerProSer 80

QY 247 TTCAAGGCCAGGTCAACCATCTCAGCGCAGCAAGTCCATCAGCACCGCTTACCTGCGAGTGG 306

Db 81 PheGlnGlyHisValThrIleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 100

QY 307 AGCAGCTGAAGCCTCGGACACCGCATGTATTACTGTGCGGAGACCAACTGGGC--- 363

Db 101 SerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgLeuLeuTyrGlyAla 120

QY 364 -----CTCTTGACTACTGGGCGCAGGAAACCTGTGTC 396

Db 121 AlaAlaAlaTrpGlyTyrTyrTyrTyrTyrMetAspValTrpGlyLysGlyThrThrVal 140

QY 397 ACCGCTCTCTCTCA 408

Db 141 ThrValSerSer 144

RESULT 14

PH1414

Ig heavy chain V region (clone PI-54) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
 C:Accession: PH1414
 R:van der Stoep, N.; van der Linden, J.; Logtenberg, T.
 J. Exp. Med. 177, 99-107, 1993
 A:Title: Molecular evolution of the human immunoglobulin E response: High incidence of dermatitis.
 A:Reference number: PH1409; MUID:93115676; PMID:8418213
 A:Accession: PH1414

THIS PAGE BLANK (USPTO)

A:Molecule type: mRNA
A:Residues: 1-127 <VAN>

A:Experimental source: PBM

A:Note: the authors translated the codon TTG for residue 119 as Met

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	2,18e-37	Length:	127
Score:	575.00	Matches:	111
Percent Similarity:	89.76%	Conservative:	3
Best Local Similarity:	87.40%	Mismatches:	7
Query Match:	67.97%	Indels:	6
DB:	2	Gaps:	1

US-08-728-463B-207 (1-462) x PH1428 (1-113)

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QY 58 GAGGTGAGCTGGTGCAGTCTGGAGCAGAGGTGAAAGCCCGGGAGTCTCTGAAGATC 117
Db 1 GluValGlnLeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuLysIle 20
QY 118 TCCTGTAAGGGTTCTGGATACAGCTTTACCGGCTACTTGGATCGGCTGGGTGCCAGATG 177
Db 21 SerCysLysGlySerGlyTyrSerPheThrAsnTyrTrpIleGlyTrpValArgGlnMet 40
QY 178 CCCGGGAAGGCTGGAGTGGATGGGATCATCTATCTCTGGTGAATCTGTATACCATAC 237
Db 41 ProGlyLysGlyLeuGluTrpMetGlyIleTyrProGlyAspSerAspThrArgTyr 60
QY 238 AGCCCGTCTCTTCCAAAGGCCAGGTCCACCATCTCAGCCGACAAAGTCCATCAGCCGCTAC 297
Db 61 SerProSerPheGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80
QY 298 CTGCAGTGGAGCAGCTTGAAGGCTTCGGACACCGCCATGTATTACTGTCCGAGACCA 357
Db 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgAsp 100
QY 352 -----GACCAACTGGGCTCTTTGACTACTGGGGCAGGAAACCTGTCTCTCA 408
Db 101 TyrGlyAspTyrGlnSerThrGlyGlyPheAspProTrpGlyGlnGlyThrLeuValThr 120
QY 400 GTCTCTCAGCTCCACCAAG 420
Db 121 ValSerSerAlaSerThrGln 127
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RESULT 15

PH1428

Ig heavy chain V region (clone VH5-1R1) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 28-May-1999

C:Accession: PH1428

R:van der Stoep, N.; van der Linden, J.; Logtenberg, T.

J. Exp. Med. 177, 99-107, 1993

A:Title: Molecular evolution of the human immunoglobulin E response: High incidence of dermatitis.

A:Reference number: PH1409; MUID:93115676; PMID:8418213

A:Accession: PH1428

A:Molecule type: mRNA

A:Residues: 1-113 <VAN>

A:Cross-references: GB:S51905; NID:g262690; PIDN:AAC80261.1; PID:g262691

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	9,33e-37	Length:	113
Score:	567.00	Matches:	108
Percent Similarity:	93.16%	Conservative:	1
Best Local Similarity:	92.31%	Mismatches:	4
Query Match:	67.02%	Indels:	4
DB:	2	Gaps:	1

US-08-728-463B-207 (1-462) x PH1428 (1-113)

```
QY 58 GAGGTGAGCTGGTGCAGTCTGGAGCAGAGGTGAAAGCCCGGGAGTCTCTGAAGATC 117
Db 1 GluValGlnLeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuLysIle 20
QY 118 TCCTGTAAGGGTTCTGGATACAGCTTTACCGGCTACTTGGATCGGCTGGGTGCCAGATG 177
Db 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValArgGlnMet 40
QY 178 CCCGGGAAGGCTGGAGTGGATGGGATCATCTATCTCTGGTGAATCTGTATACCATAC 237
Db 41 ProGlyLysGlyLeuGluTrpMetGlyIleTyrProGlyAspSerAspThrArgTyr 60
QY 238 AGCCCGTCTCTTCCAAAGGCCAGGTCCACCATCTCAGCCGACAAAGTCCATCAGCCGCTAC 297
Db 61 SerProSerPheGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80
QY 298 CTGCAGTGGAGCAGCTTGAAGGCTTCGGACACCGCCATGTATTACTGTCCGAGACCA 357
Db 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArg----- 98
QY 358 CTGGGCTCTTGTACTACTGGGGCAGGAAACCTGTCTCTCTCA 408
Db 99 -----AlaPheAspValTrpGlyGlnGlyThrMetValThrValSerSer 113
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Search completed: June 3, 2003, 09:07:55

Job time : 21.5421 secs


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FT CHAIN 20 139 IG HEAVY CHAIN V REGION BI-8/186-2.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC9F465 CRC64;

Alignment Scores:
Pred. No.: 1.4e-22 Length: 139
Score: 396.50 Matches: 76
Percent Similarity: 70.50% Conservative: 22
Best Local Similarity: 54.68% Mismatches: 38
Query Match: 46.87% Indels: 3
DB: 1 Gaps: 2

US-08-728-463B-207 (1-462) x HV07_MOUSE (1-139)
QY 1 ATGGGGTCAACGCCCATCTCGCCCTCTCGCTGCTTCTCCAGGAGTCTGTGCCGAG 60
Db 1 MetGlyTrpSerCysIleMetLeuPheLeuAlaAlaThrAlaThrGlyValHisSerGln 20
QY 61 GTGACGCTGGTCTGAGTCTGGAGCAGAGTGAAAGCCCGGGAGTCTCTGAAGATCTCC 120
Db 21 ValGlnLeuGlnProGlyAlaGluLeuValLysProGlyAlaSerValLysLeuSer 40
QY 121 TGTAGGGTCTGGATACAGCTTACCGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 41 CysLysAlaSerGlyTyrThrPheThrSerTyrTrpMetHisTrpValLysGlnArgPro 60
QY 181 GGGAAAGGCTGGAGTGGAGTGGAGTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 61 GlyArgGlyLeuGluTrpIleGlyArgIleAspProAsnSerGlyThrLysTyrAsn 80
QY 241 CGCTCTTCAAGCCAGGCTGACCATCTCAGCCGACAGTCCATGATCTGCTGCTGCTGCTG 300
Db 81 GluLysPheLysSerLysAlaThrLeuThrValLysProSerSerThrAlaTyrMet 100
QY 301 CAGTGGAGCAGCTGAGGCTCGGACCGCCATGATCTATCTGCTGCTGCTGCTGCTGCTG 360
Db 101 GlnLeuSerSerLeuThrSerGluAspSerAlaValTyrTyrCysAlaArgTyrAspTyr 120
QY 358 CTGGGC-----CTCTTTGACTCTGGGCGGGAACCTGTGCTACCGCTCTCTCTCA 408
Db 121 TyrGlySerSerTyrPheAspTyrTrpGlyGlnGlyThrLeuThrValSerSer 139

RESULT 2
HV11_MOUSE
ID HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region S43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell'24:625-637(1981).
CC -I- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).

```

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CC -----
DR EMBL; J00539; AAA38172.1; -.
DR PIR; A02038; G2MS43.
DR HSSP; P01810; 2PB1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Alignment Scores:
Pred. No.: 2.79e-22 Length: 137
Score: 392.50 Matches: 76
Percent Similarity: 70.80% Conservative: 21
Best Local Similarity: 55.47% Mismatches: 39
Query Match: 46.33% Indels: 1
DB: 1 Gaps: 1

US-08-728-463B-207 (1-462) x HV11_MOUSE (1-137)
QY 1 ATGGGGTCAACGCCCATCTCGCCCTCTCTGCTGCTTCTCCAGGAGTCTGTGCCGAG 60
Db 1 MetGlyTrpSerCysIleMetLeuPheLeuAlaAlaThrAlaThrGlyValHisSerGln 20
QY 61 GTGACGCTGGTCTGAGTCTGGAGCAGAGTGAAAGCCCGGGAGTCTCTGAAGATCTCC 120
Db 21 ValGlnLeuGlnProGlyAlaGluPheValLysProGlyAlaSerValLysLeuSer 40
QY 121 TGTAGGGTCTGGATACAGCTTACCGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 41 CysLysAlaSerGlyTyrThrPheThrSerTyrLeuMetHisTrpValAsnGlnArgPro 60
QY 181 GGGAAAGGCTGGAGTGGAGTGGAGTCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 61 GlyArgGlyLeuGluTrpIleGlyArgIleAspProAsnSerGlyThrLysTyrAsn 80
QY 241 CGCTCTTCAAGCCAGGCTGACCATCTCAGCCGACAGTCCATGATCTGCTGCTGCTGCTG 300
Db 81 GluHisPheArgSerLysAlaThrLeuThrValLysProSerSerThrAlaTyrMet 100
QY 301 CAGTGGAGCAGCTGAGGCTCGGACCGCCATGATCTATCTGCTGCTGCTGCTGCTGCTG 360
Db 101 GlnLeuSerSerLeuThrSerGluAspSerAlaValTyrTyrCysAlaArgTyrArgLeu 120
QY 361 GGC---CTCTTTGACTCTGGGCGGGAACCTGTGCTACCGCTCTCTCTCA 408
Db 121 GlyArgTyrPheAspTyrTrpGlyGlnGlyThrLeuThrValSerSer 137

RESULT 3
HV02_MOUSE
ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)

```


DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 93G7 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A/J;
 RX MEDLINE=82152818; PubMed=6801765;
 RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
 RA "Somatic mutation in genes for the variable portion of the
 RT immunoglobulin heavy chain.";
 RL Science 216:309-311(1982).
 CC -----
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 CC -----
 DR EMBL; J00493; AAA38128.1; -.
 DR PIR; A02028; HVM5G7.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 KW Immunoglobulin V region; Antiarsenate antibody; Hybridoma; Signal.
 FT CHAIN 1 19
 FT NON_TER 140 140 IG HEAVY CHAIN V REGION 93G7.
 FT SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Alignment Scores:

Pred. No.: 1.44e-21 Length: 140
 Score: 383.00 Matches: 76
 Percent Similarity: 70.71% Conservative: 23
 Best Local Similarity: 54.29% Mismatches: 37
 Query Match: 45.2% Indels: 4
 DB: 1 Gaps: 2

US-08-728-463B-207 (1-462) x HV01_MOUSE (1-140)

QY 1 ATGGGGTCAACCGCATCTCCGCTCTCTCTGCTGTCTTCAAGAGTCTGTCCGAG 60
 Db 1 MetGlyTrpSerPheilePheLeuPheLeuSerValThrAlaGlyValHisSerGlu 20
 QY 61 GTGCAGCTGGTCTGGAGCAGAGGTGAAAGCCGCGGAGTCTCTGAAGATCTCC 120
 Db 21 ValGlnLeuGlnGlnSerGlyAlaGluLeuValArgAlaGlySerSerValHisMetSer 40
 QY 121 TCTAAGGGTCTGGATACAGCTTTACCGCTACTGATCGGTGGTGGCCAGATGCC 180
 Db 41 CysLysAlaSerGlyTyrThrPheThrSerTyrGlyIleAsnTrpValLysGlnArgPro 60
 QY 181 GGGAAAGGCTGGATGGATGGGATCATCTATCTGTTGATCTGTATCACCACATACAGC 240
 Db 61 GlyGlnGlyLeuGluTrpIleGlyTyrIleAsnProGlyAsnGlyTyrIleAsnTyrAsn 80
 QY 241 CGGTCTCTCAAGCCAGGTCAACATCTCAGCCGCAAGTCCATCAGACCCGCTACCTG 300
 Db 81 GluLysPheGlyLysThrThrLeuThrValAspLysSerSerThrAlaTyrMet 100
 QY 301 CAGTGGAGCAGCTGAAGGCTCGGACACCGCATGTATTACTGTGCGAGACCAACTG 360
 Db 101 GlnLeuArgSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgSerHisTyr 120
 QY 361 -----GGCCTC-----TTTGACTACTGGGGCCAGGAAACCCCTGTCTACCTCTCA 408

Db 121 TyrGlyGlySerTyrAspPheAspTyrTrpGlyGlnGlyThrProLeuThrValSerSer 140
 RESULT 4
 HV01_MOUSE
 ID HV01_MOUSE STANDARD; PRT; 121 AA.
 AC P01745;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region MPC 11.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81053741; PubMed=6253904;
 RA Zakut R., Cohen J., Givol D.;
 RT "Cloning and sequence of the cDNA corresponding to the variable
 RT region of immunoglobulin heavy chain MPC11.";
 RL Nucleic Acids Res. 8:3591-3601(1980).
 RN [2]
 RP REVISIONS.
 RA Zakut R., Cohen J., Givol D.;
 RL Nucleic Acids Res. 8:4839-4840(1980).
 CC -!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
 CC FROM A MYELOMA THAT SECRETES IGG2B.
 DR PIR; A02027; GVMS11.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 KW Immunoglobulin V region.
 FT NON_TER 121 121
 FT SEQUENCE 121 AA; 13135 MW; 227AEF3EC5ED0BF CRC64;
 Alignment Scores:
 Pred. No.: 5.72e-21 Length: 121
 Score: 375.00 Matches: 69
 Percent Similarity: 74.38% Conservative: 21
 Best Local Similarity: 57.02% Mismatches: 27
 Query Match: 44.33% Indels: 4
 DB: 1 Gaps: 1
 US-08-728-463B-207 (1-462) x HV01_MOUSE (1-121)
 QY 58 GAGGTGACGTGGTGTGCTGAGTCTGGAGCAGGTGAAAGCCGCGGAGTCTCTGAAGATC 117
 Db 1 GluAlaGlnLeuGlnGlnSerGlyAlaGluLeuValArgProGlyThrSerValLysile 20
 QY 118 TCCTTAAGGGTCTGGATACAGCTTTACCGCTACTGATCGGTGGTGGCCAGATG 177
 Db 21 SerCysLysAlaAlaGlyTyrThrPheThrAsnTyrTrpIleGlyTrpValLysGluArg 40
 QY 178 CCCGGAAAGGCTGGAGTGGATGGGATCATCTATCTGTTGATCTGTATCACCACATAC 237
 Db 41 ProGlyHisGlyLeuGluTrpIleGlyAspIleTyrProGlyGlyGlyPheThrAsnTyr 60
 QY 238 AGCCCGTCTTCCAAAGCCAGGTCAACATCTCAGCCGCAAGTCCATCAGACCCGCTAC 297
 Db 61 AsnAspAsnLeuLysGlyLysAlaThrLeuThrAlaAspThrSerSerThrAlaTyr 80
 QY 298 CTGCAGTGGAGCAGCTGAAGCCCTCGGACACCGCCATGTATTACTGTGCGAGA----- 351
 Db 81 IleGlnLeuSerSerLeuThrSerGluAspSerAlaIleTyrHisCysAlaArgGlyIle 100
 QY 352 -----GACCAACTGGGCTCTTTGACTACTGGGCGCCAGGAAACCCCTGTCTACCGCTCTCC 405
 Db 101 TyrTyrAsnSerSerProTyrPheAspSerTrpGlyGlnGlyThrThrLeuThrValSer 120
 QY 406 TCA 408

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Db      121 Ser 121
RESULT 5
HV48 MOUSE
AC P0390; STANDARD; PRT; 138 AA.
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region TPC 1017 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
delta in an IgD-secreting plasmacytoma."
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR HSSP; P01810; HVMS7.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TPC 1017.
FT DOMAIN 21 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 59 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 128 138 FRAMEWORK-4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Alignment Scores:
Pred. No.: 6,79e-21 Length: 138
Score: 374.00 Matches: 72
Percent Similarity: 69.78% Conservative: 25
Best Local Similarity: 51.80% Mismatches: 38
Query Match: 44.21% Indels: 4
DB: 1 Gaps: 2

US-08-728-463b-207 (1-462) x HV48_MOUSE (1-138)
QY 1 ATGGGTCACCGCCATCTCGCCCTCTCTGCTGTTCTCAAGAGTCTGTGCCGAG 60
Db 1 MetGlyTrpSerTyrIleLeuPheLeuValAlaThrAlaThrAspValHisSerGln 20
QY 61 GTCCAGCTGGTGCAGTCTGGAGCAGAGTGAAAGCCCGGGAGTCTCTGAAGATCTCC 120
Db 21 ValGlnLeuGlnProGlyAlaGluLeuValLysProGlyAlaSerValGlnLeuSer 40
QY 121 TGTAAAGGTTCTGGATACAGCTTTACCGCTACTCGATCGGCTGGTGGCCAGATGCC 180
Db 41 CysLysAlaSerGlyHisThrPheThrAsnTyrTrpIleHisTrpValLysGlnArgPro 60
QY 181 GGAAGAGCCCTGGAGTGGATGGGATCATCTATCTGCTGCTGATCATACACATACAGC 240
Db 61 GlyGlnGlyLeuGluTrpIleGlyGluLeuAsnProAsnAspGlyArgSerAsnTyrAsn 80
QY 241 CCGTCTTCCAAAGGCCAGGTACCATCTCAGCCGACAGTCCATCAGCCGCTACTACTG 300
Db 81 GluLysPheLysAsnLysAlaThrLeuThrValAlaPheLysSerSerThrAlaTyrMet 100

301 CAGTGGAGCAGCTGAAGCCCTGGACACCGCCATGTATTACTGTGCGAGACCAACTG 360
Db 101 GlnLeuSerSerLeuThrProGluGluPheAlaValTyrTyrCysAlaArgSerAsp 119
QY 361 GGCCTCTTTGAC-----TACTGGGCGCAGGGAACCTCGTCCACCGTCTCTCTCA 408
Db 120 GlyTyrTyrAspTrpPheValTyrTrpGlyGlnGlyThrLeuValThrPheSerAla 138

RESULT 6
HV06_MOUSE
ID HV06_MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 102 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
antibodies: somatic mutation evident in a gamma 2a variable region."
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
CC PIR; A02032; HVMS02.
DR HSSP; P01810; 2PBJ.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;

Alignment Scores:
Pred. No.: 1.61e-20 Length: 117
Score: 369.00 Matches: 66
Percent Similarity: 75.86% Conservative: 22
Best Local Similarity: 56.90% Mismatches: 28
Query Match: 43.62% Indels: 0
DB: 1 Gaps: 0

US-08-728-463b-207 (1-462) x HV06_MOUSE (1-117)
QY 1 ATGGGTCACCGCCATCTCGCCCTCTCTGCTGTTCTCAAGAGTCTGTGCCGAG 60
Db 1 MetGlyTrpSerCysAlaIleLeuPheLeuValAlaThrAlaThrGlyValHisSerHis 20
QY 61 GTCCAGCTGGTGCAGTCTGGAGCAGAGTGAAAGCCCGGGAGTCTCTGAAGATCTCC 120
Db 21 ValGlnLeuGlnProGlyAlaGluLeuValLysProGlyAlaSerValLysValSer 40
QY 121 TGTAAAGGTTCTGGATACAGCTTTACCGCTACTCGATCGGCTGGTGGCCAGATGCC 180
Db 41 CysLysAlaSerGlyTyrThrPheThrSerTyrTrpMetHisTrpValLysGlnArgPro 60
QY 181 GGAAGAGCCCTGGAGTGGATGGGATCATCTATCTGCTGCTGATCATACACATACAGC 240

```

```
Db      61 GlyGlnGlyLeuGluTrpIleGlyArgIleHisProSerAspSerAspThrAsnTyrAsn 80
QY      241 CGGTCTTCCAGGCGAGTACCATCTCAGCGGACAGAGTCCATCATGACGACGCGCTACCTG 300
Db      81 GlnLysPheLeuGlyLeuAlaThrLeuThrValAspLysSerSerSerThrAlaTyrMet 100
QY      301 CAGTGGAGCAGCCTCAGAGCCTCGACACCGCCGTCATGTTACTTACTGTCGCG 348
Db      101 GlnLeuSerSerLeuThrSerGluAspSerAlaValTyrTyrCysAla 116

RESULT 7
HV1B HUMAN
ID HV1B HUMAN STANDARD; PRT; 117 AA.
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-I region HG3 precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83144028; PubMed=6298778;
RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region
  (VH) gene subgroups";
RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; J00240; AAA52988.1; -
DR PIR; A02024; HVHUNG.
DR HSSP; P01772; 2F84.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION HG3.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

Alignment Scores:
Pred. No.: 2,27e-20 Length: 117
Score: 367.00 Matches: 67
Percent Similarity: 78.70% Conservative: 18
Best Local Similarity: 62.04% Mismatches: 23
Query Match: 43.38% Indels: 0
DB: 1 Gaps: 0

US-08-728-463B-207 (1-462) x HV1B_HUMAN (1-117)

QY 28 CTCCTGGCTGTTCTCAAGAGTCTGTGCCAGGTGCAGTCTGTCAGTCTGAGCAGAG 87
Db 10 LeuLeuAlaValAlaProGlyAlaHisSerGlnValGlnLeuValGlnSerGlyAlaGlu 29
QY 88 GTGAAAAGCCGGGAGTCTCTGAGATCTCTGTAGGTTCTGGATACAGCTTTACC 147
Db 30 ValLysLysProGlyAlaSerValLysValSerCysLysAlaSerGlyTyrThrPheAsn 49
QY 148 GCCTACTGATCGGTGGTGGTCGCAGATGCCCGGAAAGCCCTGGAGTGGATGGGATC 207
Db 50 SerTyrTyrMetHisTrpValArgGlnAlaProGlyGlnGlyLeuGluTrpMetGlyIle 69
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QY      208 ATCTATCTCTGCTGACTCTGTATACCATACACGCGCTCTTCCAGGCGCAGTCCACCATC 267
Db      70 IleAsnProSerGlyGlySerThrSerTyrAlaGlnLysPheGlnGlyArgValThrMet 89
QY      268 TCAGCCGACAAAGTCCATCAGACCGCCCTACCTGAGTGGAGCAGCAGCTGAAGGCTCGGAC 327
Db      90 ThrArgAspThrSerThrValTyrMetGluLeuSerSerLeuArgSerGluAsp 109
QY      328 ACCGCCATGTATTACTGTGCGAGA 351
Db      110 ThrAlaValTyrTyrCysAlaArg 117

RESULT 8
HV05_MOUSE
ID HV05_MOUSE STANDARD; PRT; 117 AA.
AC P01749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 3 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
  antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GENE LINE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00536; AAA38605.1; -
DR PIR; A02031; HVMS3.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13016 MW; 427C861C53975EDC CRC64;

Alignment Scores:
Pred. No.: 2,7e-20 Length: 117
Score: 366.00 Matches: 65
Percent Similarity: 76.07% Conservative: 24
Best Local Similarity: 55.56% Mismatches: 28
Query Match: 43.26% Indels: 0
DB: 1 Gaps: 0

US-08-728-463B-207 (1-462) x HV05_MOUSE (1-117)
```

S-08-728-463B-207 (1-462) x HV13_MOUSE (1-117)

58 GAGTGCAGCTGTGCAGTCTCGGAGCAGAGTAAAAAGCCCGGGCAGTCTCTGAAGATC 117
1 GluValGlnLeuGlnGlnSerGlyProGluLeuVallysProGlyAlaSerVallysMet 20
118 TCCTGTAAGGGTTCTGGATACAGCTTTTACCCGGTACTGATCGGCTGGCGTGGCCAGATG 177

Alignment Scores:	
Pred. No.:	4.93e-20
Score:	362.50
Percent Similarity:	63.27%
Best Local Similarity:	48.30%
Query Match:	42.85%
DB:	1
Length:	147
Matches:	71
Conservative:	22
Mismatches:	43
Indels:	11
Gaps:	1

US-08-728-463B-207 (1-462) x HV1C_HUMAN (1-147)

QY	1	ATGGGGTCAACCGCCATCCTCGCCCTCTCTCTGGCTGTCTCTCAAGGAGTCTGTGCGCGAG	60
Db			
Db	1	MetAspTrpThr*****PheLeuValAlaAlaAlaThrArgValHisSerGln	20
QY	61	GTGCGAGCTGGTGCACTCTGGAGCAGAGGTGAAAGCCGGGAGTCTCTGAAGATCTCC	120
Db			
Db	21	ThrGlnLeuValGlnSerGlyAlaGluValArgLysProGlyAlaSerValArgValSer	40
QY	121	TGTAAGGGTTCTGGATACAGCTTTACCGGCTACTCGGCTCGCTGGGTGGCCAGATGCC	180
Db			
Db	41	CysLysAlaSerGlyTyrThrPheIleAspSerTyrIleHisTrpIleArgGlnAlaPro	60
QY	181	GGGAAGGCGCTGGAGTGGATGGGATCATCTATCCTCGTGACTCTGTATACCATCACAC	240
Db			
Db	61	GlyHisGlyLeuGluTrpValGlyTrpIleAsnProAsnSerGlyGlyThrAsnTyrAla	80
QY	241	CGGTCTCTCCAGGCCAGCTCACCATCTCAGCCGACAGTCCATCAGCACCGCTCCTACTG	300
Db			
Db	81	ProArgPheGlnGlyArgValThrMetThrArgAspAlaSerPheSerThrAlaTyrMet	100
QY	301	CAGTGGAGCAGCGCTCAAGCGCTCGGACACCGCCATGTATTACTGTGCGAGA-----	351
Db			
Db	101	AspLeuArgSerLeuArgSerAspSerAlaValPheTyrCysAlaLysSerAspPro	120
QY	352	-----GACCAACTGGGCGCTCTTTGACTACTGGGCGCCAGGGA	387
Db			
Db	121	PheTrpSerAspTyrTyrAsnPheAspTyrSerTyrThrLeuaspValTrpGlyGlnGly	140
QY	388	ACGCTGGTCACCGTCTCTCTCA	408
Db			
Db	141	ThrThrValThrValSerSer	147

RESULT 11

ID	HV12_MOUSE	STANDARD;	PRT;	117 AA.
AC	P01756;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Ig heavy chain V region MOPC 104E.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN				
RP	SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.			
RX	MEDLINE=83075344; PubMed=6816276;			
RA	Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,			
RA	Hood L.E.;			
RT	"Complete amino acid sequence of a mouse mu chain: homology among			
RT	heavy chain constant region domains.";			
RL	Biochemistry 21:5415-5424(1982).			
CC	-1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA			
CC	PROTEIN HAS ALSO BEEN DETERMINED.			
CC	-1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.			
DR	PIR; A02039; MHMS4E.			
DR	HSSP; P01789; LMCP.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF00047; Ig_1.			
DR	SMART; SM00406; IgV; 1.			
KW	Immunoglobulin v region; Glycoprotein.			
FT	DISULFID 22 96			
FT	CARBOHYD 55 55			
FT	NON_TER 117 117			
SQ	SEQUENCE 117 AA; 12983 MW; 3CP8ACE4BE447E41 CRC64;			

Alignment Scores:

Pred. No.:	6.39e-20	Length:	117
Score:	361.00	Matches:	67
Percent Similarity:	74.36%	Conservative:	20

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Score: 355.00 Matches: 68
Percent Similarity: 69.8% Conservative: 27
Best Local Similarity: 50.0% Mismatches: 41
Query Match: 41.96% Indels: 0
DB: 1 Gaps: 0

US-08-728-463B-207 (1-462) x HV15_MOUSE (1-136)

QY 1 ATGGGGTCAACCGCATCTCGCCCTCTCTGGCTGTCTCCAGGAGTCTGTGCGGAG 60
Db 1 MetGlyTrpSerCysIlePhePheLeuValAlaThrAlaThrGlyValHisSerGln 20
QY 61 GTGCAGCTGGTCCAGTCTGGAGCAGAGTGAAGAGCCGGGAGTCTCTGAAGATCTCC 120
Db 21 ValGlnLeuGlnSerGlyProGluValAlaArgProGlyValSerValIleSer 40
QY 121 TGTAAAGGCTTCGGATACAGCTTACCGGCTACTGGATCGGCTGGGTCGCCAGATGCC 180
Db 41 CysLysGlySerGlyTyrThrPheThrAspTyrAlaMetHisTrpValLysGlnSerHis 60
QY 181 GGGAAAGCCTGGAGTGGGATCATCTATCTGGTGAATCTGTGACTCTGTATACCATACAGC 240
Db 61 AlalysSerLeuGluTrpIleGlyValIleSerThrTyrAsnGlyAsnThrSerTyrAsn 80
QY 241 CCGTCCTTCAAGCCAGGTCACCATCTCAGCCGACAGTCCATCAGCAGCCGCTACCTG 300
Db 81 GlnLysPheLysGlyLysAlaThrMetThrValAspLysSerSerThrValHisMet 100
QY 301 CAGTGGAGCAGCTGAAGCCTCGGACACCGCCATGTATTACTGTGCGAGACCACTG 360
Db 101 GluLeuAlaArgLeuThrSerGluAspSerAlaAsnLeuTyrCysAlaArgTyrGly 120
QY 361 GGCTCTTCTACTACTGGGCGGAGAACCTGTGTCACCGTCTCCCTCA 408
Db 121 AsnTyrPheAspTyrTrpGlyGlnGlyThrLeuThrValSerSer 136

RESULT 15
HV04_MOUSE
ID HV04_MOUSE STANDARD; PRG: 117 AA.
AC P01748;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 23 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paskind M., Rech M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR PIR: A02030; HWS23.
DR HSP; P01810; 2FBU.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.

FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;
Alignment Scores:
Pred. No.: 2,54e-19 Length: 117
Score: 353.00 Matches: 64
Percent Similarity: 73.50% Conservative: 22
Best Local Similarity: 54.70% Mismatches: 31
Query Match: 41.73% Indels: 0
DB: 1 Gaps: 0

US-08-728-463B-207 (1-462) x HV04_MOUSE (1-117)

QY 1 ATGGGGTCAACCGCATCTCGCCCTCTCTGGCTGTCTCCAGGAGTCTGTGCGGAG 60
Db 1 MetGlyTrpSerCysIlePhePheLeuValAlaAlaAsnGlyValHisSerGln 20
QY 61 GTGCAGCTGGTCCAGTCTGGAGCAGAGTGAAGAGCCGGGAGTCTCTGAAGATCTCC 120
Db 21 ValGlnLeuGlnProGlyThrGluLeuValLysProGlyAlaSerValLysLeuSer 40
QY 121 TGTAAAGGCTTCGGATACAGCTTACCGGCTACTGGATCGGCTGGGTCGCCAGATGCC 180
Db 41 CysLysAlaSerGlyTyrThrPheThrSerTyrTrpMetHisTrpValLysGlnArgPro 60
QY 181 GGGAAAGCCTGGAGTGGGATCATCTATCTGGTGAATCTGTGACTCTGTATACCATACAGC 240
Db 61 GlyGlnGlyLeuGluTrpIleGlyAsnIleAsnProGlyAsnGlyThrAsnTyrAsn 80
QY 241 CCGTCCTTCAAGCCAGGTCACCATCTCAGCCGACAGTCCATCAGCAGCCGCTACCTG 300
Db 81 GluLysPheLysSerLysValThrLeuThrValAspLysSerSerThrAlaTyrThr 100
QY 301 CAGTGGAGCAGCTGAAGGCTCGGACACCGCCATGTATTACTGTGCGAGA 351
Db 101 GlnLeuSerSerLeuThrSerGluAspSerAlaValTyrTyrCysAlaArg 117

Search completed: June 3, 2003, 09:04:05
Job time : 10.7633 secs

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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 41.0121 Seconds

(without alignments)
4642.224 Million cell updates/sec

Title: US-08-728-463B-207

Perfect score: 846

Sequence: 1 ATGGGGTCAACGGCATCTT.....CACCTCTCTCAAGAGCTT 462

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1343160

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-O=/cgn2.1/usPTO/spool/US08728463/runat_03062003_085614_16815/app_query.fasta_1.3690
-DB=SPTRMBL 21 -OFT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cui -LIST=45
-DOCALIGN=200 -THRM SCORE=pct -THRM MAX=100 -THRM MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08728463 @CGN 1 1 380 @runat_03062003_085614_16815 -NCPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

SPTRMBL 21:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archaeap:

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	No.	Score	Match	Length	ID	Description
1	450	53.2	473	11	Q9D8L4	Q9D8L4 mus musculus	

ID	Q9D8L4	PRELIMINARY	PRT	473 AA
AC	Q9D8L4			
DT	01-JUN-2001	(TRENBLrel. 17, Created)		
DT	01-JUN-2001	(TRENBLrel. 17, Last sequence update)		
DT	01-DEC-2001	(TRENBLrel. 19, Last annotation update)		
DE	181006009Rik protein.			
GN	IGH-1 OR 181006009Rik.			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=PANCREAS;			
RX	MEDLINE=21085560; PubMed=11217851;			
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,			
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,			
RA	Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,			
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,			

AC	Q8R3H6;				
DT	01-JUN-2002	(TREMBLrel. 21, Created)			
DT	01-JUN-2002	(TREMBLrel. 21, Last sequence update)			
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)			
DE	Hypothetical 51.7 kDa protein.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Strausberg R.				
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC025447; AAH25447.1;				
KW	Hypothetical protein.				
SQ	SEQUENCE 474 AA; 51748 MW; 860BB57C6CD2874A CRC64;				
Alignment Scores:					
Pred. No.:	1,33e-33	Length:	474		
Score:	446.00	Matches:	85		
Percent Similarity:	75.34%	Conservative:	25		
Best Local Similarity:	58.22%	Mismatches:	34		
Query Match:	52.72%	Indels:	2		
DB:	11	Gaps:	1		
US-08-728-463B-207 (1-462) x Q8R3H6 (1-474)					

QY	16	ATCTCGCCCTCTCTCTGGTGTTCTTCC	AAGGAGTCTGTGCGGAGGTGCAGTCTGGTGCAG	75
Db	6	IleuLeuPheLeuLeuSerValThr	GlulGlulValHisSerGlnValGlnLeuLeuGln	25
QY	76	TCTGGAGCAGGTGAAAAGCCCGGGAGTCTCTGA	AGATCTCTCTGTAAGGGTCTCTGGA	135
Db	26	SerGlyproGluLeuVallysproGlyAlaSerVally	IleSerCysAcdAlaSerGly	45

QY	136	TACAGCTTTACCGCTACTCGGATCGCGCTGGGTGGCCAGATGCCCGGAAAGGCCTCGAG	195
Db	46	TyAlaPheSerLysSerTrpMetAsnTrpValLysArgArgProGlyLysGlyLeuGlu	65
QY	196	TGATGGGATCATCTATCCTCGTGACCTCATACCACATACAGCCGCTCTTCCAAGGC	255
Db	66	TrpIleGlyArgIlePheProGlyAspGlyAspThrHisTyrSerGlyLysPheGlnGly	85
QY	256	CAGGTCCACCATCTCAGCCGACAGTCCATCAGCACCCGCTACTCTGAGTCGAGCAGCCGTG	315
Db	86	LySAlaLysLeuThrAlaAspLysSerSerValThrAlaPheLeuGlnLeuThrSerLeu	105
QY	316	AAGCGCTCCGACACCGCCCATGTATTACTGTGTCGAGAGACCA-----CTGGGCGCTCTTT	369
Db	106	ThrSerGluAspSerAlaValTyrPheCysAlaArgAspSerAspTyrGlyAspTyrPhe	125
QY	370	GACTACTGGGGCAGGAAACCGCTGGTCACGCTCTCTTCAGCCCTCCACCAGGGCCCCATCG	429
Db	126	AspAspTyrGlyGlnGlyAlaThrValThrValSerSerAlaLysThrThrProProSer	145
QY	430	GTCTTCCCCCTGGCACCC	447
Db	146	ValTyrProLeuAlaPro	151

RESULT 3

Q99LC4

ID	Q99LC4	PRELIMINARY;	PRT;	463 AA.
AC	Q99LC4;			
DT	01-JUN-2001	(TRENBLrel. 17, Created)		
DT	01-JUN-2001	(TRENBLrel. 17, Last sequence update)		
DT	01-JUN-2002	(TRENBLrel. 21, Last annotation update)		
DE	Similar to RIKEN CDNA 1810060009 gene.			
GN	IGH-4.			

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 ON NCBI_TaxID=10090;
 RN {1}

RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; BC003435; AA003435.1; -;
 DR HSSP; P01842; 7FAB.
 DR MGD; MGI:96446; Igh-4.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003600; Ig_Like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00407; IGc1; 2.
 DR SMART; SM00406; IGV; 1.
 DR SMART; SM00410; IG_Like; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Alignment Scores:
 Pred. No.: 2,838-33 Length: 463
 Score: 442.50 Matches: 83
 Percent Similarity: 73.1% Conservative: 26
 Best Local Similarity: 55.7% Mismatches: 37
 Query Match: 52.3% Indels: 3
 DB: 11 Gaps: 1

US-08-728-463B-207 (1-462) x Q99LC4 (1-463)

QY 16 ATCTCGCCCTCTCTGCTGCTTCTCAAGAGTCTGTGCGAGGTGCGAGTGTGCGAG 75
 Db 6 lIePheLeuPheileuSerGlyThrAlaGlyValHisSerGlnValGlnLeuGln 25
 QY 76 TCTGAGCAGAGGTGAAAGCCCGGGAGTCTCTGAAGATCTCTGTAAGGGTCTGGA 135
 Db 26 SerGlyAlaGluLeuAlaArgProGlyAlaSerValArgLeuSerCysLysAlaSerGly 45
 QY 136 TACAGCTTACCGGTACTGGATCGGCTGGTGGCCAGATCCCGGGAAGCCCTGGAG 195
 Db 46 TyrThrPheThrGlyTyrGlyValSerTrpValLysGlnArgThrGlyGlnGlyLeuGlu 65
 QY 196 TGGATGGGATCATCTATCTCTGCTGCTGTATGATACACATACAGCCCGCTCTCAAGGC 255
 Db 66 TrpValGlyGluLeuTyrProGlySerGlySerGlySerGlySerGlySerGlySerGly 85
 QY 256 CAGGTCACCATCTCAGCCGACAGTCCATCAGCAGCCGCTACTGAGTGGAGCAGCCTG 315
 Db 86 LysAlaThrLeuThrThrAspLysSerSerSerSerSerSerSerSerSerSerSer 105
 QY 316 AAGGCTCGGACCGCCATGATTACTGTGGAGAGAC-----CAACTGGGCTC 366
 Db 106 ThrSerGluAspSerAlaValTyrPheCysAlaArgSerSerTyrTyrSerTyrAspLeu 125
 QY 367 TTTGACTACTGGGCGAGGACCTGTGTCACCGTCTCTCAGCTCCAGCTCCAGGCGCCA 426
 Db 126 PheAlaTyrTrpGlyGlnGlyThrLeuValThrValSerAlaAlaLysThrThrPro 145
 QY 427 TCGGCTCTCCCTCGGACCCCTCTCC 453
 Db 146 SerValTyrProLeuAlaProGlySer 154

RESULT 4

Q8VDC9 PRELIMINARY; PRT; 168 AA.
 AC Q8VDC9;
 DT 01-MAR-2002 (TRENBLrel. 20, Created)
 DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Anti-MOG 212 variable gamma 2a (Fragment).
 GN IGG2A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RA Cherna'jovsky Y.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBSJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RA Sembi P.;
 RT "Targeting T cells to the CNS";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; AJ416332; CAC94867.1; -;
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR InterPro; IPR001230; Prenyl_site.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00409; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00294; PRENYLATION; UNKNOWN 1.
 FT NON TER 168 168
 SQ SEQUENCE 168 AA; 18293 MW; 1E3719FCC0E72723 CRC64;

Alignment Scores:
 Pred. No.: 1,58-32 Length: 168
 Score: 434.00 Matches: 82
 Percent Similarity: 70.27% Conservative: 22
 Best Local Similarity: 55.41% Mismatches: 42
 Query Match: 51.30% Indels: 2
 DB: 11 Gaps: 1

US-08-728-463B-207 (1-462) x Q8VDC9 (1-168)

QY 10 ACCGCGATCTCTGCTGCTTCTCAAGAGTCTGTGCGAGTGTGCGAGTGTGCGAGTGTG 69
 Db 4 ThrTrpValPheLeuPheLeuLeuSerValThrAlaGlyValHisSerGlnValGlnLeu 23
 QY 70 GTGAGTCTGGAGCAGAGGTGAAAAGCCCGGGAGTCTCTGAAGATCTCTCTGTAAGGT 129
 Db 24 GlnGlnSerGlyAlaGluLeuMetLysProGlyAlaSerValLysLysSerCysLysAla 43
 QY 130 TCTGATACAGCTTACCGGCTACTGGATCGGCTGGTGGTGGCCAGATCCCGGGAAGGC 189
 Db 44 ThrGlyTyrThrPheSerSerTyrTrpIleAspTrpValLysGlnArgProGlyHisGly 63
 QY 190 CTGAGTGGAGTGGATCATCTATCTCTGCTGCTGTATGATACACATACAGCCCGCTCTC 249
 Db 64 LeuGlnTrpIleGlyGluLeuProGlySerGlyArgThrAsnTyrAsnGlnLysPhe 83
 QY 250 CAAGCCAGGTCAACCATCTCAGCCGACAAAGTCCATCAGCAGCCGCTACTCTGAGTGAGC 309
 Db 84 LysGlyLysThrThrPheThrAlaAspThrSerSerAsnThrAlaTyrIleGlnPheSer 103
 QY 310 AGCTGAAGGCTCGGACACCGCATGATTACTGTGGAGA-----GACCACTGGGC 363
 Db 104 SerLeuThrSerGluAspSerAlaValTyrTyrCysAlaAsnTyrGlySerSerArgTrp 123
 QY 364 CTCTTTGACTACTGGGCGAGGACCTGTGTCACCGTCTCTCAGCTCCAGCTCCACCAAGGC 423
 Db 124 TyrPheAspValTrpGlyAlaGlyThrValThrValSerSerThrLysThrThrAla 143
 QY 424 CCATCGGTCTTCCCGCTGGCACCC 447
 Db 144 ProSerValTyrProLeuAlaPro 151

RESULT 5

Q8TC77 PRELIMINARY; PRT; 471 AA.
 ID Q8TC77;
 AC Q8TC77;
 DT 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC018315; AAH18315.1; -.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 5.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00407; Igc1; 4.
 DR SMART; SM00406; Igv; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 KW Hypothetical protein.
 SQ SEQUENCE 613 AA; 67855 MW; 41A9384DDA22862 CRC64;

Alignment Scores:

Pred. No.: 7,71e-32 Length: 613
 Score: 427.50 Matches: 86
 Percent Similarity: 69.87% Conservative: 23
 Best Local Similarity: 55.13% Mismatches: 40
 Query Match: 50.53% Indels: 7
 DB: 11 Gaps: 3

US-08-728-463B-207 (1-462) x Q8VCX7 (1-613)

QY 10 ACCGCCATCTCGCCCTCTCTCGGTGTTCTCCAGGAGTCTGTGCCAGGTGCGAGTG 69
 DB 4 ThrTrpValPheLeuPheLeuLeuSerValThrAlaGlyValHisSerGlnValGlnLeu 23
 QY 70 GTGCAGTCTGGAGCAGAGGTGAAAGCCGGGGAGTCTCTCAAGATCTCTGTAAGGT 129
 DB 24 GlnGlnSerGlyValGlnLeuMetLysProGlyAlaSerValLysIleSerCysLysAla 43
 QY 130 TCTGATACAGCTTTACCGGCTACTGATCGGTGCGCCAGATGCCCGGAAAGGC 189
 DB 44 ThrGlyTyrThrPheSerSerTyrTrpIleGluTrpValLysGlnArgProGlyHisGly 63
 QY 190 CTGGAGTGTGATGGGATCATCTCTGCTGACTCTGATACACATACAGCCCGCTCTTC 249
 DB 64 LeuGluTrpIleGlyValLeuProGlySerGlySerThrAsnTyrAsnGlnLysPhe 83
 QY 250 CAAGCCAGGTCAACATCTCAGCCAGCAAGTCCATCAGCAGCCGCTACTCTGAGTGGAGC 309
 DB 84 LysGlyLysAlaThrPheThrAlaAspThrSerSerAsnThrAlaTyrMetGlnLeuSer 103
 QY 310 AGCTGAAGCCTCGGACACCCCATGTATTACTGTGCGAGAGCAACTGGCC----- 363
 DB 104 SerLeuThrSerGluAspSerAlaValTyrCysAlaArg---ArgLeuGlyArgTrp 122
 QY 364 CTCTTGACTACTGGGCGGAGGACCTGGTCCAGCTCTCTCAGCTCCAGCCAGGCGC 423
 DB 123 TyrPheAspValTrpGlyAlaGlyThrThrValThrValSerSerGlnSerPhe 142
 QY 424 CCATCGTCTCTCCCTCG-----GCACCTCTCTCCAAAGAG 459
 DB 143 ProAsnValPheProLeuValSerCysGluSerProLeuSerAspLys 158

RESULT 8

Q91WT1 PRELIMINARY; PRT; 481 AA.
 AC Q91WT1;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
 DE Hypothetical 52.1 kDa protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=COLON;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC013490; AAH13490.1; -.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Alignment Scores:

Pred. No.: 8,24e-32 Length: 481
 Score: 427.00 Matches: 80
 Percent Similarity: 72.11% Conservative: 26
 Best Local Similarity: 54.42% Mismatches: 41
 Query Match: 50.47% Indels: 0
 DB: 11 Gaps: 0

US-08-728-463B-207 (1-462) x Q91WT1 (1-481)

QY 1 ATGGGGTCAACCGCATCTCGCCCTCTCTCGGTGTTCTCCAGGAGTCTGTGCCGAG 60
 DB 1 MetGlyTrpArgTrpIlePheLeuPheLeuLeuSerGlyThrAlaGlyValGlnCysGln 20
 QY 61 GTGCAGTCTGTGTCAGTCTGGAGCAGAGGTGAAAGCCGGGGAGTCTCTGAAGATCTCC 120
 DB 21 ValGlnLeuLeuGlnSerGlyProGluLeuValLysProGlyAlaSerValLysIleSer 40
 QY 121 TGTAGGGTCTTGATACAGCTTTACCGGCTACTGATCGGTGCGGTGCGCCAGATGCC 180
 DB 41 CysLysAlaSerGlyTyrThrPheThrSerTyrTrpIleHisTrpValLysGlnArgPro 60
 QY 181 GGGAAAGCCCTGGAGTGGATCGGATCATCTCTGCTGACTCTGTATACACATACAGC 240
 DB 61 GlyGlnGlyLeuValTrpIleGlyTrpIleTyrProGlyAspGlyAsnThrLysTyrAsn 80
 QY 241 CCGTCTTCCAGGCCAGGTCAACATCTCAGCCAGCAAGTCCATCAGCAGCCGCTACTCTG 300
 DB 81 GluLysPheLysGlyLysThrThrLeuThrAlaAspLysSerSerThrAlaTyrMet 100
 QY 301 CAGTGGAGCAGCTGAAGCCTCGGACACCCCATGTATTACTGTGCGAGAGACCACTG 360
 DB 101 PheLeuSerSerLeuThrSerGluAspSerAlaValTyrPheCysThrArgGlyGly 120
 QY 361 GGCCTCTTGTACTACTGGGCGGAGGACCTGGTCCAGCTCTCTCAGCTCCAGCCAG 420
 DB 121 TrpAlaPheAspTyrTrpGlyGlnGlyThrThrLeuThrValSerSerGluProAlaArg 140
 QY 421 GGCCCATCGTCTTCCCTCGCTG 441
 DB 141 GluProThrIleTyrProLeu 147

RESULT 9

Q99L31 PRELIMINARY; PRT; 468 AA.
 AC Q99L31;
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Similar to RIKEN cDNA 1810060009 gene.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC003878; AAH03878.1; -.
 DR HSP; P01842; 7FAB.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003600; Ig_like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 3.


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DB:      *      11      Gaps:      2
US-08-728-463B-207 (1-462) x Q92400 (1-143)

QY 58 GAGGTGACGCTGGTCTGGAGCAGAGGTGAAAAAGCCCGGGAGTCTCTGAAGATC 117
   ::::::::::::::::::::
Db 1 GlnValGlnLeuGlnGlnProGlyAlaGluLeuValProGlyAlaSerValIysMet 20
   ::::::::::::::::::::
QY 118 TCCTGTAGGGTCTGATACAGCTTTACCGGCTACTGGTGGTGGCCAGATG 177
   ::::::::::::::::::::
Db 21 SerCysLysAlaSerGlyThrPheThrSerTyrTrpIleThrTrpValIysGlnArg 40
   ::::::::::::::::::::
QY 178 CCGGGAAAGGCTGGAGTGGATGGGATCATCTATCTCTGGGAGCTCTGATACCATAC 237
   ::::::::::::::::::::
Db 41 ProGlyGlnGlyLeuGluTrpIleGlyAspIleTyrProGlySerGlySerThrAsnTyr 60
   ::::::::::::::::::::
QY 238 AGCCGCTCTTCCAAAGCCGAGGTACCATCTCAGCCGAGCAAGTCCATCAGCACCGCTAC 297
   ::::::::::::::::::::
Db 61 AsnGluLysPheLysSerLysAlaThrLeuThrValAspLysProSerSerThrAlaTyr 80
   ::::::::::::::::::::
QY 298 CTGAGTGGAGGAGCTGAAGGCTCGGACACCGCATGTATTACTGTGCGAGAGACCA 357
   ::::::::::::::::::::
Db 81 MetGlnLeuSerSerLeuThrSerGluAspSerAlaValTyrCysAlaProAspSer 100
   ::::::::::::::::::::
QY 358 CTGGGCTC---TTTGACTACTGGGGCCAGGAACTGGTCACTCTCTCAGCTCC 414
   ::::::::::::::::::::
Db 101 AsnHisLeuTyrPheAspTyrTrpGlyGlnGlyThrLeuThrValSerSerGluSer 120
   ::::::::::::::::::::
QY 415 ACCAAGGGCCCATCGTCTTCCCTCCCTG-----GCACCTCTCTCCCAAGAG 459
   ::::::::::::::::::::
Db 121 GlnSerPheProAsnValPheProLeuValSerCysGluSerProLeuSerAspLys 139
   ::::::::::::::::::::

RESULT 12
Q99L25 PRELIMINARY; PRT; 473 AA.
ID Q99L25;
AC Q99L25;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to RIKEN CDNA 181006009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AH03888.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 52449 MW; BE9898B7986DA155 CRC64;

Alignment Scores:
Pred. No.: 6,46e-31 Length: 473
Score: 417.50 Matches: 81
Percent Similarity: 70.20% Conservative: 25
Best Local Similarity: 53.64% Mismatches: 38
Query Match: 49.35% Indels: 7
DB: 11 Gaps: 1
US-08-728-463B-207 (1-462) x Q99L25 (1-473)

DB:      *      11      Gaps:      2
US-08-728-463B-207 (1-462) x Q92400 (1-143)

QY 58 GAGGTGACGCTGGTCTGGAGCAGAGGTGAAAAAGCCCGGGAGTCTCTGAAGATC 117
   ::::::::::::::::::::
Db 1 GlnValGlnLeuGlnGlnProGlyAlaGluLeuValProGlyAlaSerValIysMet 20
   ::::::::::::::::::::
QY 118 TCCTGTAGGGTCTGATACAGCTTTACCGGCTACTGGTGGTGGCCAGATG 177
   ::::::::::::::::::::
Db 21 SerCysLysAlaSerGlyThrPheThrSerTyrTrpIleThrTrpValIysGlnArg 40
   ::::::::::::::::::::
QY 178 CCGGGAAAGGCTGGAGTGGATGGGATCATCTATCTCTGGGAGCTCTGATACCATAC 237
   ::::::::::::::::::::
Db 41 ProGlyGlnGlyLeuGluTrpIleGlyAspIleTyrProGlySerGlySerThrAsnTyr 60
   ::::::::::::::::::::
QY 238 AGCCGCTCTTCCAAAGCCGAGGTACCATCTCAGCCGAGCAAGTCCATCAGCACCGCTAC 297
   ::::::::::::::::::::
Db 61 AsnGluLysPheLysSerLysAlaThrLeuThrValAspLysProSerSerThrAlaTyr 80
   ::::::::::::::::::::
QY 298 CTGAGTGGAGGAGCTGAAGGCTCGGACACCGCATGTATTACTGTGCGAGAGACCA 357
   ::::::::::::::::::::
Db 81 MetGlnLeuSerSerLeuThrSerGluAspSerAlaValTyrCysAlaProAspSer 100
   ::::::::::::::::::::
QY 358 CTGGGCTC---TTTGACTACTGGGGCCAGGAACTGGTCACTCTCTCAGCTCC 414
   ::::::::::::::::::::
Db 101 AsnHisLeuTyrPheAspTyrTrpGlyGlnGlyThrLeuThrValSerSerGluSer 120
   ::::::::::::::::::::
QY 415 ACCAAGGGCCCATCGTCTTCCCTCCCTG-----GCACCTCTCTCCCAAGAG 459
   ::::::::::::::::::::
Db 121 GlnSerPheProAsnValPheProLeuValSerCysGluSerProLeuSerAspLys 139
   ::::::::::::::::::::

RESULT 13
Q95978 PRELIMINARY; PRT; 157 AA.
ID Q95978;
AC Q95978;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE VHL protein precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jox A., Zander T., Kueppers R., Irsch J., Kanzler H., Kornacker M.,
RA Bohlen H., Diehl V., Wolf J.;
RT "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a
RT patient with mixed cellularity Hodgkin's disease is associated with
RT somatic mutations within the untranslated regions of rearranged and
RT class switch recombinated Ig genes.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ005570; CAA06599.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR SIGNAL.
FT SIGNAL 1 21 POTENTIAL.
FT NON_TER 157 157
SQ SEQUENCE 157 AA; 17304 MW; 86986EDDA84D88B5 CRC64;

Alignment Scores:
Pred. No.: 5,95e-31 Length: 157
Score: 417.00 Matches: 83
Percent Similarity: 74.15% Conservative: 26
Best Local Similarity: 56.46% Mismatches: 34
Query Match: 49.29% Indels: 4
DB: 21 Gaps: 2

```

S-08-728-463B-207 (1-462) x Q96GA6 (1-614)

Alignment Scores:				
Pred. No.:	2.34e-30	Length:	124	
Score:	410.50	Matches:	78	
Percent Similarity:	75.59%	Conservative:	18	
Best Local Similarity:	61.42%	Mismatches:	18	
Query Match:	48.52%	Indels:	13	
DB:	4	Gaps:	2	
				US-08-728-463B-207 (1-462) x Q9UL92 (1-124)

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Search completed: June 3, 2003, 09:15:53
Job time : 45.0121 secs

GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model
Run on: June 3, 2003, 08:56:21 ; Search time 29.828 Seconds
(without alignments)
4120.219 Million cell updates/sec

Title: US-08-728-463B-207
Perfect score: 846
Sequence: 1 ATGGGGTCAACGCCATCTCT.....CACCCCTCTCCAGAGCTT 462

Scoring table:
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 1816940

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+n2p.model -DEV=xlp
-O=/cpn2.1/USPTO.spool/US08728463/runat.03062003.085613.16797/app.query.fasta.1.3690
-DB=A_Geneseq_101002 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08728463 @CGN 1.1 353 @runat.03062003.085613.16797 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORE=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_101002.*
1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
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14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	681	80.5	474	22	AAU14177 Human novel protei
2	668.5	79.0	146	22	AAU91113 Human protein SFQ
3	627	74.1	225	22	AAU75056 TRO005 Humab Happa
4	623	73.6	225	22	AAU75052 TRO005 Humab Happa
5	623	73.6	225	22	AAU75053 TRO005 Humab Happa
6	601	71.0	128	22	AAU23996 Human EST encoded
7	601	71.0	140	21	AAU56712 Amino acid sequenc
8	598	70.7	117	16	AAU66339 Human immunoglobul
9	577	68.2	121	19	AAU62798 Amino acid sequenc
10	577	68.2	240	21	AAU15128 Anti-murine CTLA-4
11	577	68.2	245	22	AAU67622 Human leukocyte an
12	574	67.8	245	22	AAU67621 Human leukocyte an
13	572.5	67.7	120	18	AAU27555 Human Ab heavy cha
14	569	67.3	117	22	AAU62966 Amino acid sequenc
15	567	67.0	245	22	AAU67623 Human leukocyte an
16	567	67.0	252	23	AAU45526 Human Blys binding
17	565	66.8	117	23	AAU15186 Digi1 antibody heav
18	562.5	66.5	139	21	AAU56727 Amino acid sequenc
19	558.5	66.0	116	23	AAU48005 Human monoclonal a
20	558.5	66.0	118	22	AAU85349 Antibody AAL 160 h
21	553.5	65.4	147	15	AAU54050 Sequence of the VH
22	553.5	65.4	147	17	AAU01528 Monoclonal antibod
23	553.5	65.4	147	18	AAU24987 Monoclonal antibod
24	551.5	65.2	249	23	AAU45301 Human Blys binding
25	530	62.6	269	23	AAU20408 Chimeric SCBP C6ML
26	530	62.6	282	23	AAU20409 Chimeric SCBP C6ML
27	530	62.6	287	23	AAU20410 Chimeric SCBP C6ML
28	530	62.6	291	23	AAU20411 Chimeric SCBP C6ML
29	530	62.6	296	23	AAU20412 Chimeric SCBP C6ML
30	528.5	62.5	142	21	AAU56708 Amino acid sequenc
31	528.5	62.5	142	21	AAU56709 Amino acid sequenc
32	527	62.3	282	23	AAU75161 Anti-interleukin-1
33	526	62.2	119	23	AAU76521 Humanised 5G1.1 VH
34	525.5	62.1	249	16	AAU77610 Chimeric SCBP C6.5
35	524	61.9	255	23	AAU20407 Chimeric SCBP C6.5
36	524	61.9	470	21	AAU90936 Humanised HPA7A de
37	524	61.9	470	23	AAU74945 Humanised anti-Fas
38	523.5	61.9	515	22	AAU52162 Humanised HMPG-1 F
39	523.5	61.9	517	22	AAU52154 Humanised HMPG-1 F
40	523.5	61.9	519	22	AAU52164 Humanised HMPG-1 F
41	523.5	61.9	519	22	AAU52165 Humanised HMPG-1 F
42	523.5	61.9	521	22	AAU52163 Humanised HMPG-1 F
43	523.5	61.9	525	22	AAU52166 Humanised HMPG-1 F
44	523.5	61.9	527	22	AAU52155 Humanised HMPG-1 F
45	523.5	61.9	529	22	AAU52168 Humanised HMPG-1 F

ALIGNMENTS

RESULT 1
AAU14177
ID AAU14177 standard; Protein; 474 AA.
XX
XX
AC AAU14177;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human novel protein #48.
XX
KW Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
KW immunomodulatory; cytosolic; neuroprotective; vulnerary; nocotropic;
KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antiallergic; dermatological; haemostatic; antiaesthetic;
KW thrombolytic; immunogen; antibody; Gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.
XX
OS Homo sapiens.

XX WO200155437-A2.
 XX 02-AUG-2001.
 XX 25-JAN-2001; 2001WO-US02623.
 XX 25-JAN-2000; 2000US-0491404.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT;
 XX WPI; 2001-451939/48.
 XX N-PSDB; AAS22482.
 XX Isolated polypeptides useful for treating anti-inflammatory diseases,
 XX nervous system disorders, and for regenerating bone and cartilage -
 XX Example 4; Page 554-555; 894pp; English.

The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to raise antibodies/elicite an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, ligament and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia, Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, allergy, asthma, graft-versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence represents a protein of the invention.

SQ Sequence 474 AA;

Alignment Scores:
 Pred. No.: 7,278-54 Length: 474
 Score: 681.00 Matches: 134
 Percent Similarity: 86.25% Conservative: 4
 Best Local Similarity: 83.75% Mismatches: 14
 Query Match: 80.50% Indels: 8
 DB: 22 Gaps: 1

US-08-728-463B-207 (1-462) x AAU14177 (1-474)

QY 1 ATGGGTCAACGCCATCTCGCCCTCTCTGCTGTTCTCCAAAGGAGTCTGTCCGAG 60
 Db 1 MetGlySerThrAlaIleLeuAlaLeuLeuLeuAlaValLeuGlnGlyValCysIaGlu 20
 QY 61 GTGACGCTGGTCTGACGAGGTGAAAGCCCGGGAGTCTCTGAAGATCTCC 120
 Db 21 ValGlnLeuValGlnSerGlyAlaGluValLysProGlyGluSerValLysIleSer 40
 QY 121 TGTAAAGGTTCTGGATACAGCTTTACCGGCTACTGATCGGTGGTGGCCAGATGCC 180
 Db 41 CysLysGlySerGlyTyrSerPheSerAspTyrTrpValAlaIleValArgGlnSerPro 60
 QY 181 GGAAGGCTGGATGGATGGGATCATCTATCTCTGTGACTCTGTATACACATACAGC 240

Db 61 AspLysGlyLeuAlaTrpMetGlyIleIleTyrProGlyAspSerAspThrArgTyrSer 80
 QY 241 CGGTCTTCAAGCCAGGTCTACCATCTCAGCCGCAAGTCCATCAGCACCCGCTACCTG 300
 Db 81 ProSerPheGlnGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyrLeu 100
 QY 301 CAGTGGAGCAGCTGAAGCCCTCGGACACCGCCATGTATTACTGTGCGAGAGACCACTG 360
 Db 101 GlnTrpSerSerLeuLysAspSerAspThrAlaMetTyrTyrCysAlaArgGlyAlaArg 120
 QY 361 GGCCTC-----TTTGACTACTGGGCGCAGGGAACCTGGTCT 396
 Db 121 GlyThrAlaProSerTyrHisTyrGlyLeuAspValTrpGlyArgGlyThrSerVal 140
 QY 397 ACCGTCTCTCAGCCTCCACCAAGGCCCATCGTCTTCCCTCCCTGGCACCTCTCTCCAAG 456
 Db 141 ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLys 160

RESULT 2

AAB99113
 ID AAB99113 standard; Protein; 146 AA.

AC AAB99113;

XX 22-AUG-2001 (first entry)

XX Human protein SEQ ID 8.

XX Human; antiarthritic; cardiant; monoclonal antibody; keloid; arthritis;
 KW Tumour Growth Factor-beta II receptor; TGF-beta II receptor; atopy;
 KW signal transduction inhibition; tissue fibrosis; atherosclerosis.

XX Homo sapiens.

PN WO200136642-A1.

XX 25-MAY-2001.

XX 17-NOV-2000; 2000WO-JP08129.

PR 18-NOV-1999; 99JP-0328681.

PR 08-NOV-2000; 2000JP-0340216.

XX (NTSB) JAPAN TOBACCO INC.

XX Sakamoto S, Kamada M;

XX WPI; 2001-343825/36.

DR N-PSDB; AAH41155.

XX Human monoclonal antibodies recognizing human TGF-beta II receptor,
 PT useful for treating TGF-beta associated diseases such as tissue
 PT fibrosis

PS Claim 10; Page 100; 118pp; Japanese.

XX The present invention relates to novel human monoclonal antibodies. The
 CC antibodies can bind to human Tumour Growth Factor-beta (TGF-beta) II
 CC receptor, resulting in the inhibition of the signal transduction of human
 CC TGF-beta into cells. The antibodies can be used for the prevention and
 CC treatment of diseases associated with the production of TGF-beta, such as
 CC tissue fibrosis in the lung, liver, skin, kidney or other tissues,
 CC atherosclerosis, atopy, keloid and arthritis. The present sequence was
 CC used in the present invention.

SQ Sequence 146 AA;

Alignment Scores:
 Pred. No.: 8,398-53 Length: 146
 Score: 668.50 Matches: 133
 Percent Similarity: 91.10% Conservative: 0
 Best Local Similarity: 91.10% Mismatches: 10
 Query Match: 79.02% Indels: 3

PN WO200125492-A1.
 XX 12-APR-2001.
 XX 02-OCT-2000; 2000WO-US27237.
 XX 02-OCT-1999; 99US-0157415.
 XX 01-DEC-1999; 99US-0453234.
 XX (BIOS-) BIOSITE DIAGNOSTICS INC.
 XX (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
 XX Buechler J, Valkirs G, Gray J, Lonberg N;
 XX WPI; 2001-335567/35.
 XX Producing a human antibody phage display library comprising providing a
 PT transgenic animal whose genome comprises human immunoglobulin genes and
 PT isolating nucleic acids encoding antibody chains from lymphatic cells -
 PS Example 37; Page 122-123; 161pp; English.
 XX The present invention describes a method (M1) for producing a human
 CC antibody phage display library (I), comprising: (1) providing a nonhuman
 CC transgenic animal (II) whose genome comprises human immunoglobulin genes;
 CC (2) isolating nucleic acids encoding human antibody chains (III) from
 CC lymphatic cells; and (3) forming a library of display packages whose
 CC members comprise a nucleic acid encoding (III) which is displayed from
 CC the package. The method is used for producing a human antibody display
 CC library, e.g., a Fab phage display library. The display method may be
 CC used to screen nucleic acids encoding antibody chains obtained from
 CC immunised nonhuman transgenic animals, and from this a population of
 CC antibodies may be prepared. Production of a human monoclonal antibodies
 CC display library using this method means there is no need to immunise
 CC humans with antigens, and the difficulties faced with immortalising B
 CC cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056
 CC represent sequences used in the exemplification of the present invention.
 XX SQ Sequence 225 AA;
 Alignment Scores:
 Pred. No.: 1.27e-48 Length: 225
 Score: 623.00 Matches: 119
 Percent Similarity: 90.98% Conservative: 2
 Best Local Similarity: 89.47% Mismatches: 12
 Query Match: 73.64% Indels: 0
 DB: 22 Gaps: 0
 US-08-728-463B-207 (1-462) x AAB75052 (1-225)
 QY 58 GAGGTGACGCTGGTGCAGTCTGGAGCAGAGGTGAAAAGCCCGGGAGTCTCTGAAGATC 117
 Db 1 GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIle 20
 QY 118 TCTGTAAAGGTTCTCGATACAGCTTTACCGGCTACTGATCGGTGGTGGCCAGATG 177
 Db 21 SerCysLysGlySerGlyTyrSerPheThrAsnTyrTrpIleGlyTrpValArgGlnMet 40
 QY 178 CCGCGGAAAGCCCTGAGTGGATGGGATCATCTATCTCGGTGATCTGTATACCAATAC 237
 Db 41 ProGlyLysGlyLeuGlnTrpMetGlyPheIleTyrSerAspSerValThrArgTyr 60
 QY 238 AGCCGCTCTTCAAGGCCAGGTTCACCATCTCAGCGCAGCAAGTCCATCAGCACCGCTTAC 297
 Db 61 SerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80
 QY 298 CTGCACTGAGCAGCTGAGCGCTCGGACACCGCATGTATTACTGTGCGAGAGACCAA 357
 Db 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysThrArgAspGly 100
 QY 358 CTGGGCCTCTTTACTACTCTGGGGCAGGGAACCTGGTCACCGTCTCTCAGCTCCACC 417
 Db 101 ProGluAlaPheAspIleTrpGlyGlnGlyThrMetValThrValSerAlaSerThr 120

QY 418 AAGGCCCATCGGTCTTCCCTGGCACCCTCTCTCAAG 456
 Db 121 LysGlyProSerValPheProLeuAlaProSerSerLys 133
 RESULT 5
 AAB75053
 ID AAB75053 standard; Protein; 225 AA.
 XX AAB75053;
 XX 19-JUL-2001 (first entry)
 XX TRO005 HuMab Happa chain protein sequence 3E3H.
 XX Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;
 KW human antibody phage display library; immunisation; transgenic animal.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200125492-A1.
 XX 12-APR-2001.
 XX 02-OCT-2000; 2000WO-US27237.
 XX 02-OCT-1999; 99US-0157415.
 XX 01-DEC-1999; 99US-0453234.
 XX (BIOS-) BIOSITE DIAGNOSTICS INC.
 XX (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
 XX Buechler J, Valkirs G, Gray J, Lonberg N;
 XX WPI; 2001-335567/35.
 XX Producing a human antibody phage display library comprising providing a
 PT transgenic animal whose genome comprises human immunoglobulin genes and
 PT isolating nucleic acids encoding antibody chains from lymphatic cells -
 XX Example 37; Page 122-123; 161pp; English.
 The present invention describes a method (M1) for producing a human
 antibody phage display library (I), comprising: (1) providing a nonhuman
 transgenic animal (II) whose genome comprises human immunoglobulin genes;
 (2) isolating nucleic acids encoding human antibody chains (III) from
 lymphatic cells; and (3) forming a library of display packages whose
 members comprise a nucleic acid encoding (III) which is displayed from
 the package. The method is used for producing a human antibody display
 library, e.g., a Fab phage display library. The display method may be
 used to screen nucleic acids encoding antibody chains obtained from
 immunised nonhuman transgenic animals, and from this a population of
 antibodies may be prepared. Production of a human monoclonal antibodies
 display library using this method means there is no need to immunise
 humans with antigens, and the difficulties faced with immortalising B
 cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056
 represent sequences used in the exemplification of the present invention.
 SQ Sequence 225 AA;
 Alignment Scores:
 Pred. No.: 1.27e-48 Length: 225
 Score: 623.00 Matches: 119
 Percent Similarity: 90.98% Conservative: 2
 Best Local Similarity: 89.47% Mismatches: 12
 Query Match: 73.64% Indels: 0
 DB: 22 Gaps: 0
 US-08-728-463B-207 (1-462) x AAB75053 (1-225)
 QY 58 GAGGTGACGCTGGTGCAGTCTGGAGCAGAGGTGAAAAGCCCGGGAGTCTCTGAAGATC 117
 Db 1 GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIle 20
 QY 118 TCTGTAAAGGTTCTCGATACAGCTTTACCGGCTACTGATCGGTGGTGGCCAGATG 177
 Db 21 SerCysLysGlySerGlyTyrSerPheThrAsnTyrTrpIleGlyTrpValArgGlnMet 40
 QY 178 CCGCGGAAAGCCCTGAGTGGATGGGATCATCTATCTCGGTGATCTGTATACCAATAC 237
 Db 41 ProGlyLysGlyLeuGlnTrpMetGlyPheIleTyrSerAspSerValThrArgTyr 60
 QY 238 AGCCGCTCTTCAAGGCCAGGTTCACCATCTCAGCGCAGCAAGTCCATCAGCACCGCTTAC 297
 Db 61 SerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80
 QY 298 CTGCACTGAGCAGCTGAGCGCTCGGACACCGCATGTATTACTGTGCGAGAGACCAA 357
 Db 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysThrArgAspGly 100
 QY 358 CTGGGCCTCTTTACTACTCTGGGGCAGGGAACCTGGTCACCGTCTCTCAGCTCCACC 417
 Db 101 ProGluAlaPheAspIleTrpGlyGlnGlyThrMetValThrValSerAlaSerThr 120

Db 1 GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIle 20
 QY 118 TCTGTAGGCTTCGGATACAGCTTTACCGCTACTGATCGGCTGGTGGCCAGATG 177
 Db 21 SerCysLysGlySerGlyTyrSerPheThrAsnTyrTrpIleGlyTrpValArgGlnMet 40
 QY 178 CCGGGAAAGGCTGGAGTGGATGGGATCATCTCTGGTGACTCTGATACCATAC 237
 Db 41 ProGlyLysGlyLeuGluTrpMetGlyPheIleTyrSerAspSerValThrArgTyr 60
 QY 238 AGCCGCTCTTCCAGGCGAGGTCCACATCTCAGCCGACCAAGTCCATCAGCACCGCTAC 297
 Db 61 SerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80
 QY 298 CTGAGTGAGAGAGCTGAAGGCTCGACACCGCATATATTACTGTGGAGAGACCAA 357
 Db 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysThrArgAspGly 100
 QY 358 CTGGGCTCTTTCAGTACTTGGGGCCAGGACCTGGTCAACGCTCTCTCAGCTCCACC 417
 Db 101 ProGluAlaPheAspIleTrpGlyGlnGlyThrMetValThrValSerSerAlaSerThr 120
 QY 418 AAGGGCCCATCGTCTTCCCTCGGACCCCTCTCTCCCAAG 456
 Db 121 LysGlyProSerValPheProLeuAlaProSerSerLys 133

RESULT 6

AAM23396
 ID AAM23396 standard; Protein; 128 AA.
 AC AAM23396;
 XX

DT 12-OCT-2001 (first entry)
 XX

DE Human EST encoded protein SEQ ID NO: 1521.
 XX

KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KW diagnostics; forensic test; gene mapping; genetic disorder;
 KW biodiversity; gene therapy; nutrition.
 XX

OS Homo sapiens.
 XX

PN WO200154477-A2.
 XX

PD 02-AUG-2001.
 XX

PF 25-JAN-2001; 2001WO-US02687.
 XX

PR 25-JAN-2000; 2000US-0491404.
 PR 17-JUL-2000; 2000US-0617746.
 PR 03-AUG-2000; 2000US-0631451.
 PR 15-SEP-2000; 2000US-0663870.
 XX

PA (HYSE-) HYSEQ INC.
 XX

PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;
 XX

DR WPI: 2001-476164/51.
 DR N-PSDB; AAM98655.
 XX

PT Isolated polypeptide for treatment of diseases, diagnostics, raising
 PT antibodies and research use -
 XX

PS Claim 20; Page 1050; 1275pp; English.
 XX

CC The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess

CC biodiversity and for nutritional purposes. The present sequence is a
 CC protein of the invention.
 XX

SQ Sequence 128 AA;
 XX

Alignment Scores:

Pred. No.: 1-19e-46 Length: 128
 Score: 601.00 Matches: 115
 Percent Similarity: 98.2% Conservatives: 2
 Best Local Similarity: 98.2% Mismatches: 2
 Query Match: 71.04% Indels: 0
 DB: 22 Gaps: 0

US-08-728-463B-207 (1-462) x AAM23396 (1-128)

QY 1 ATGGGTCAACCGCCATCTCGCCCTCTCTGGCTGTCTTCCAAGGAGTCTGTGCCGAG 60
 Db 1 MetGlySerThrAlaIleLeuAlaLeuLeuAlaValLeuGlnGlyValCysAlaGlu 20
 QY 61 GTGAGCTGTGTCATCTGGAGCAGAGGTGAAAAGCCGGGAGTCTCTGAAGATCTCC 120
 Db 21 ValGlnLeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuLysIleSer 40
 QY 121 TGTAAAGGTTCTGGATACAGCTTTACCGCTACTCGGCTGGTGGCCAGATGCC 180
 Db 41 CysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValArgGlnMetPro 60
 QY 181 GGGAAAGCCTGGAGTGGATGGGATCATCTATCTGTGTGACTCTGATACCATACAGC 240
 Db 61 GlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSerAspThrArgTyrSer 80
 QY 241 CCGTCTCTCCAGGCCAGGTCAACATCTCAGCCGACCAAGTCCATCAGCACCGCTACCTG 300
 Db 81 ProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyrLeu 100
 QY 301 CAGTCGAGCAGCTCAAGCCCTCGACACCGCATGTATTACTGTGCCGAGA 351
 Db 101 GlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArg 117

RESULT 7

AAY56712
 ID AAY56712 standard; protein; 140 AA.
 XX

AC AAY56712;
 XX

DT 15-FEB-2000 (first entry)
 XX

DE Amino acid sequence of chimpanzee VH cDNA clone 41-9.
 XX

KW Complementarity determining region; antibody; primate; immunogenicity;
 KW Old World ape; Old World monkey; antigen-binding affinity.
 XX

OS Pan troglodytes.
 XX

PN WO955369-A1.
 XX

PD 04-NOV-1999.
 XX

PF 28-APR-1999; 99WO-US09131.
 XX

PR 28-APR-1998; 98US-0083367.
 XX

PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX

PI Taylor AH;
 XX

DR WPI; 2000-023265/02.
 DR N-PSDB; AAZ39315.
 XX

PT Antibodies containing donor complementarity determining regions and
 PT non-human primate acceptor frameworks, having reduced immunogenicity in
 PT humans -
 XX

Example 1; Page 46; 123pp; English.

PS The invention provides an antibody (Ab) comprising donor CDRs
 CC (complementarity determining regions) derived from a non-human antigen-
 CC specific donor antibody, and an acceptor framework from a non-human antigen-
 CC prime. The Abs are prepared by grafting CDRs from a non-human antigen-
 CC specific donor antibody onto homologous Old World ape or monkey acceptor
 CC frameworks. The Abs have reduced immunogenicity and are better tolerated
 CC in humans (because of the close similarity between the human and primate
 CC proteins), but retain the full antigen-binding affinity of the donor
 CC antibody.

SQ Sequence 140 AA;

Alignment Scores:

Pred. No.: 1.2e-46 Length: 140
 Score: 601.00 Matches: 119
 Percent Similarity: 88.49% Conserv: 4
 Best Local Similarity: 85.61% Mismatches: 12
 Query Match: 71.04% Indels: 4
 DB: 21 Gaps: 1

US-08-728-463B-207 (1-462) x AAY56712 (1-140)

QY 1 ATGGGCTCAACCGCATCTCGCCCTCTCTCGCTCTCTCTCAAGAGTCTGCGCCGAG 60
 Db 2 MetGlySerThrAlaIleLeuAlaLeuLeuLeuValLeuGlnGlyValCysAlaGlu 21
 QY 61 GTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAGCCCGGGAGTCTCTGAAGATCTCC 120
 Db 22 ValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIleSer 41
 QY 121 TGTAAGGCTTCGATACAGCTTACCGCTACTGATCGGTGGTGGCCAGATGCC 180
 Db 42 CysLysGlySerGlyTyrSerPheThrAsnTyrTrpMetGlyTrpValCysGlnMetPro 61
 QY 181 GGGAAAGCCCTGAGTGGATCATCTATCTGCTGCTGATCTGATACCATACAGC 240
 Db 62 GlyLysGlyProGluCysMetGlyIleTyrProAspSerAspThrArgTyrSer 81
 QY 241 CCCTCTCTCAAGCCAGGTACCATCTCAGCCGACAGTCCATCAGCCGCTACCTG 300
 Db 82 ProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyrLeu 101
 QY 301 CAGTGGAGCAGCTTGAAGGCTCGGACACCGCCATGATTACTGTCGAGA----- 351
 Db 102 GlnTrpSerAsnLeuLysAlaSerAspThrAlaIleTyrTyrCysAlaArgCysTyrGly 121
 QY 352 ---GACCACTGGCCCTTTGACTACTGGGCGCAGGGAACCTGTCTACCGTCTCC 405
 Db 122 TrpThrThrCysGluAlaPheAspIleTyrGlyGlnGlyThrMetValThrValSer 140

RESULT 8

AAW62798

ID AAR66339 standard; Protein; 117 AA.

XX

AC AAR66339;

XX

DT 04-AUG-1995 (first entry)

XX

DE Human immunoglobulin variable heavy chain #45.

KW Primer; PCR; amplif; human; immunoglobulin; variable; heavy chain;
 KW cosmid; placenta; vector; pJB81; E.coli; mammalian.

OS Homo sapiens.

XX

PN WO9426895-A.

XX

PD 24-NOV-1994.

XX

PF 10-MAY-1993; 93WO-JP00603.

XX

PR 10-MAY-1993; 93WO-JP00603.

XX (NIBS) JAPAN TOBACCO INC.
 XX Honjo T, Matsuda F;

XX WPI; 1995-006791/01.
 DR N-PSDB; AAQ78989.

XX DNA fragment comprising human immunoglobulin Vh genes - for the
 PT production of human immunoglobulin in mammalian hosts

XX Claim 58; Page 96-97; 130pp; Japanese.

XX Protein sequences (AAR6295-51) are novel human immunoglobulin heavy
 CC chain sequences encoded by novel isolated genes. The genes
 CC (AAQ78939-79002) were isolated and cloned from a series of cosmid
 CC constructs: Y202; Y103; Y21; Y6; Y24; 3-31; M84; M118 and M131, by PCR
 CC amplification using primers AAQ78917-38. The genes are subdivided into 5
 CC families of Vh genes. The fragments cover a region of 800 Kb. The DNA
 CC fragments were isolated from high molecular weight DNA from human
 CC placenta. The DNA was partially digested with TaqI restriction enzyme.
 CC The fragments were separated by gel electrophoresis and 35-45 kb fractions
 CC were collected. The fragments were ligated with ClaI-digested cosmid
 CC vector pJB81. The ligation products were in vitro packed and infected
 CC into E.coli 490A. The fragments were then subcloned and infected
 CC hybridisation. The Vh genes and the DNA fragments encoding them are
 CC useful in producing human immunoglobulin in mammalian hosts.

XX Sequence 117 AA;

SQ

Alignment Scores:

Pred. No.: 2.2e-46 Length: 117
 Score: 598.00 Matches: 114
 Percent Similarity: 98.29% Conserv: 1
 Best Local Similarity: 97.44% Mismatches: 2
 Query Match: 70.69% Indels: 0
 DB: 16 Gaps: 0

US-08-728-463B-207 (1-462) x AAR66339 (1-117)

QY 1 ATGGGTCACCGCCATCTCGCCCTCTCTCTCTCTCAAGAGTCTGTGCGGAG 60
 Db 1 MetGlySerThrAlaIleLeuAlaLeuLeuLeuValLeuGlnGlyValCysSerGlu 20
 QY 61 GTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAGCCCGGGAGTCTCTGAAGATCTCC 120
 Db 21 ValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIleSer 40
 QY 121 TGTAAGGCTTCGATACAGCTTACCGCTACTGATCGGTGGTGGCCAGATGCC 180
 Db 41 CysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValArgGlnMetPro 60
 QY 181 GGGAAAGCCCTGAGTGGATCGGATCATCTATCTGCTGCTGATCTCTGATACCATACAGC 240
 Db 61 GlyLysGlyLeuGlnTrpMetGlyIleTyrTyrProGlyAspSerAspThrArgTyrSer 80
 QY 241 CCCTCTCTCAAGCCAGGTACCATCTCAGCCGACAGTCCATCAGCAGCCGCTACCTG 300
 Db 81 ProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyrLeu 100
 QY 301 CAGTGGAGCAGCTTGAAGGCTCGGACACCGCCATGATTACTGTGCGGAGA 351
 Db 101 GlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArg 117

RESULT 9

AAW62798

ID AAW62798 standard; Peptide; 121 AA.

XX

AC AAW62798;

XX

DT 23-SEP-1998 (first entry)

XX

DE Amino acid sequence of a human antibody fragment.

XX Human; immunoglobulin; Ig; transgenic; non-human mammal;

KW inactivated endogenous Ig locus; B-cell development;

KW human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;

KW kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;

KW production; antibody.

XX Homo sapiens.

OS

PN WO9824893-A2.

XX

PD 11-JUN-1998.

XX

PF 03-DEC-1997; 97WO-US23091.

XX

PR 03-DEC-1996; 96US-0759620.

XX

PA (ABGE-) ABGENIX INC.

XX

PI Green L, Jakobovits A, Klapholz S, Kucherlapati R;

PI Mendez M;

XX

DR WPI; 1998-333314/29.

XX

PT New transgenic non-human mammals - having an inactivated

PT immunoglobulin locus and a near complete human immunoglobulin locus,

PT used for production of human antibodies

XX

PS Disclosure; Page 74; 128pp; English.

XX

CC AAW62793-822 represent fragments of human antibodies produced by

CC transgenic Xenomice, created using the method of the invention. The

CC specification describes a transgenic non-human mammal which has genome

CC modifications that comprise an inactivated endogenous immunoglobulin (Ig)

CC locus, so that the mammal does not display normal B-cell development. The

CC modified genome also has an inserted human heavy chain Ig locus in

CC germline configuration, the human heavy chain Ig locus comprising a human

CC micro constant region and regulatory and switch sequences, human J-H

CC genes, human D-H genes, and human V-H genes and an inserted human kappa

CC light chain Ig locus in germline configuration, the human kappa light

CC chain Ig locus comprising a human kappa constant region, J-kappa genes,

CC and V-kappa genes, where the number of V-H and V-kappa genes inserted

CC are selected to restore normal B-cell development in the mammal. The

CC transgenic animals have a near complete human Ig locus, including both a

CC human heavy chain locus and a human kappa light chain locus. They can

CC be used for the production of human antibodies when exposed to

CC particular antigens e.g. when exposed to human IL-8, EGFR or TNF- alpha

CC the mice will produce antibodies to IL-8, EGFR or TNF- alpha

CC respectively.

XX

SQ Sequence 121 AA;

Alignment Scores:

Pred. No.: 1,82e-44 Length: 121

Score: 577.00 Matches: 108

Percent Similarity: 93.16% Conservative: 1

Best Local Similarity: 92.31% Mismatches: 8

Query Match: 68.20% Indels: 0

DB: 19 Gaps: 0

US-08-728-463B-207 (1-462) x AAW62798 (1-121)

QY 106 TCTCTGAAGATCTCTGTAAAGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGG 165

DB 1 SerLeuLysIleSerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrp 20

QY 166 GTCCGCCAGATCCCGGGAAAGCCCTGGAGTGGATGGGATCATCTATCTGGTGACTCT 225

DB 21 ValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSer 40

QY 226 GATACCACATACAGCCCGCTCTTCAGGCCAGGTTCACATCTCAGCCGACAGTCCATC 285

DB 41 AspThrArgTyrSerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIle 60

QY 286 AGCACCGCTACCTGCTAGTGGAGCAGCTGAGGCTCGACACCGCCATGATTAATCTGT 345

DB 61 SerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCys 80

QY 346 GCGAGAGACCACTGGGCTCTTTGACTACTGGGGCCAGGACCTCGTCCACCGCTCTCC 405

DB 81 AlaArgGlnAspGlyAspSerPheAspTyrTrpGlyGlnGlyThrLeuValThrValSer 100

QY 406 TCAGCTCCACCAAGGGCCCATCGGTCTTCCCTCCCTGGCACCTCTCCCAAG 456

DB 101 SerAlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArg 117

RESULT 10

AAV15128

ID AAV15128 standard; Protein; 240 AA.

XX

AC AAV15128;

XX

DT 07-FEB-2000 (first entry)

XX

DE Anti-murine CTLA-4 M24 sFv.

XX

KW Anti-murine CTLA-4 sFv; M24 sFv; single chain antibody; murine CTLA4;

KW membrane-associated protein; chimeric construct; extracellular domain;

KW human CD8; ligand; activated T-cell; co-stimulatory signal; donor B7;

KW recipient CD28; T-cell proliferation;

KW xenograft-specific immunosuppression.

XX

OS Mus sp.

OS Synthetic.

XX

FH Key Location/Qualifiers

ET Misc-difference 153

FT /note= "Corresponds to atc codon"

XX

PN WO9957266-A2.

XX

PD 11-NOV-1999.

XX

PF 30-APR-1999; 99WO-GB01350.

XX

PR 30-APR-1998; 98GB-0009280.

XX

PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX

PI Lechler IR, Dorling A;

XX

DR WPI; 2000-038815/03.

DR N-PSDB; AAZ29000.

XX

PT Inhibiting T-cell mediated rejection of xenotransplanted organs

XX

PS Claim 9; Fig 11; 43pp; English.

XX

CC The present sequence is the anti-murine CTLA-4 sFv (M24 sFv). This is a

CC membrane-associated protein which binds to CTLA-4. Chimeric constructs

CC comprising DNA sequences encoding the extracellular domain of murine

CC CTLA4 and human CD8 were used for the study of anti-CTLA4-sFv protein.

CC The anti-hCTLA4 sFv functions as a ligand binding to CTLA-4 on activated

CC T-cells and antagonises the co-stimulatory signal provided by the

CC interaction between donor B7 and recipient CD28. Cells expressing the

CC anti-hCTLA4 sFv failed to stimulate T-cell proliferation. This is used in

CC xenograft-specific immunosuppression.

XX

SQ Sequence 240 AA;

Alignment Scores:

Pred. No.: 2,02e-44 Length: 240

Score: 577.00 Matches: 108

Percent Similarity: 94.87% Conservative: 3

Best Local Similarity: 92.31% Mismatches: 6

Query Match:	68.20%	Indels:	0
DB:	21	Gaps:	0
US-08-728-463B-207 (1-462) x AAV15128 (1-240)			
QY	58	GAGGTGCAGCTGGTTCAGTCTGGAGCAGAGGTGAAAAGCCGGGGAGTCTCTGAAGATC	117
Db	1	GlnValGlnLeuLeuGlnSerAlaAlaGluValLysLysProGlyGluSerLeuLysIle	20
QY	118	TCCTGAAGGGTTCGGATACAGCTTTACCGCTACCTGGATCGGCTGGTGGCCAGATG	177
Db	21	SerCysLysGlySerGlySerPheThrSerTyrTrpIleGlyTrpValArgGlnMet	40
QY	178	CCCGGAAAGCCCTGGAGTGGATCATCTATCTCTGGTCACTCTGATACCATAC	237
Db	41	ProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSerAspThrArgTyr	60
QY	238	AGCCCGTCTTCCAGGCCAGGTACCATCTCAGCCGACAAAGTCCATCAGCCGCTAC	297
Db	61	SerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr	80
QY	298	CTGCAGTGGAGCAGCTTAAAGCCCTCGACACCGCCATGATTCATCTGCGAGACCAA	357
Db	81	LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaValTyrCysAlaArgPheSer	100
QY	358	CTGGGCTCTTTGACTACTCTGGGCGAGGAAACCTGGTCACTCTCTCTCA	408
Db	101	LeuGlyGlyPheAspTyrTyrGlyGlnGlyThrLeuValThrValSerSer	117
RESULT 11			
ID	AAB67622	standard; Protein; 245 AA.	
AC	AAB67622;		
DT	29-MAY-2001	(first entry)	
XX	Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_6.		
XX	Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;		
XX	miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.		
XX	Homo sapiens.		
XX	WO200114558-A1.		
XX	01-MAR-2001.		
XX	28-AUG-2000; 2000WO-EP08388.		
XX	26-AUG-1999; 99EP-0116691.		
XX	(MORP-) MORPHOSYS AG.		
XX	Kretzschmar T, Tesar M, Marget M, Kroenke M;		
XX	WPI; 2001-218451/22.		
XX	Novel isolated human immunoglobulin or functional immunoglobulin		
XX	fragment specific for human leukocyte antigen Cw6, useful for treatment		
XX	of humans and for human leukocyte antigen phenotyping		
XX	Claim 3; Fig 1; 23pp; English.		
XX	AAB67617-23 represent single chain antibody (scFv) fragments which		
XX	are specific for human leukocyte antigen (HLA)-Cw6. The fragments are		
XX	derived from a synthetic human combinatorial antibody library based on		
XX	molecular consensus frameworks and CDRs randomised with trinucleotides.		
XX	The specification describes a human immunoglobulin fragments specific		
XX	for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in		
XX	studies of natural killer cell silencing as well as miscarriages.		
XX	HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions.		
XX	Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin		

XX AAB67617-23 represent single chain antibody (scFv) fragments which
 CC are specific for human leukocyte antigen (HLA)-Cw6. The fragments are
 CC derived from a synthetic human combinatorial antibody library based on
 CC molecular consensus frameworks and CDRs randomised with trinucleotides.
 CC The specification describes a human immunoglobulin fragments specific
 CC for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in
 CC studies of natural killer cell silencing as well as miscarriages.
 CC HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions.
 CC Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin
 CC fragments are useful for the preparation of a pharmaceutical for the
 CC treatment of humans. They are also useful for HLA phenotyping.
 XX
 SQ Sequence 245 AA;

Alignment Scores:
 Pred. No.: 3,81e-44 Length: 245
 Score: 574.00 Matches: 110
 Percent Similarity: 93.22% Conservative: 0
 Best Local Similarity: 93.22% Mismatches: 8
 Query Match: 67.85% Indels: 0
 DB: 22 Gaps: 0

US-08-728-463B-207 (1-462) x AAB67621 (1-245)

QY 58 GAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCGGGGAGTCTCTGAAGATC 117
 DB 1 GluValGlnLeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuLysIle 20
 QY 118 TCTGTAAAGGGTTCTGGATACAGCTTTACCGGCTACTGGTGGTGGTGGCCAGATG 177
 DB 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValArgGlnMet 40
 QY 178 CCGCGAAAGGCTGGAGTGGATCATCTATCTGGTGCATCTGATACCATAC 237
 DB 41 ProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSerAspThrArgTyr 60
 QY 238 AGCCGCTCTTCAAGCCAGGTACCATCTCAGCCGACAAAGTCCATCAGCCGCTAC 297
 DB 61 SerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80
 QY 298 CTGCGATGAGCAGCTGAAGCCCTGGACCGCCATCTATCTATCTGCGAGACCAA 357
 DB 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgSerTrp 100
 QY 358 CTGGGCTCTTTGACTACTGGGCGCAGGAACCTCGTCCAGCTCTCTCTCAGCC 411
 DB 101 AspTyrProPheAspIleTrpGlyGlnGlyThrLeuValThrValSerSerAla 118

RESULT 13

AAW27555

ID AAW27555 standard; Protein; 120 AA.

XX AAW27555;

XX 23-JAN-1998 (first entry)

XX Human Ab heavy chain variable region VH5 consensus.

XX Human; antibody; preparation; library; VH5; variable region;
 KW heavy chain; consensus.

XX Homo sapiens.

XX WO9708320-A1.

XX 06-MAR-1997.

XX 19-AUG-1996; 96WO-EP03647.

XX 18-AUG-1995; 95EP-0113021.

XX (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.

XX Ge L, Ilag V, Knappik A, Moroney S, Pack P, Plueckthun A;
 XX WPI; 1997-179277/16.
 DR N-PSDB; AAT87953.
 XX Preparation of human derived antibody gene library - using synthetic
 PT consensus sequences, and signal consensus antibody gene as universal
 PT framework for highly diverse antibody libraries
 XX Example 1; Fig 5F; 436pp; English.

XX The present sequence is the human antibody heavy chain
 CC variable region synthetic sequence VH5, used in the preparation of
 CC a human derived antibody gene library.

XX Sequence 120 AA;

Alignment Scores:
 Pred. No.: 4.69e-44 Length: 120
 Score: 572.50 Matches: 110
 Percent Similarity: 91.67% Conservative: 0
 Best Local Similarity: 91.67% Mismatches: 7
 Query Match: 67.67% Indels: 3
 DB: 18 Gaps: 1

US-08-728-463B-207 (1-462) x AAW27555 (1-120)

QY 58 GAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCGGGGAGTCTCTGAAGATC 117
 DB 1 GluValGlnLeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuLysIle 20
 QY 118 TCTGTAAAGGGTTCTGGATACAGCTTTACCGGCTACTGGTGGTGGTGGCCAGATG 177
 DB 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValArgGlnMet 40
 QY 178 CCGCGAAAGGCTGGAGTGGATCATCTATCTGGTGCATCTGCTGATACCATAC 237
 DB 41 ProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSerAspThrArgTyr 60
 QY 238 AGCCGCTCTTCAAGCCAGGTACCATCTCAGCCGACAAAGTCCATCAGCCGCTAC 297
 DB 61 SerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80
 QY 298 CTGCGATGAGCAGCTGAAGCCCTGGACCGCCATCTATCTATCTGCGGAGA----- 351
 DB 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgTrpGly 100
 QY 352 ---GACCAACTGGGCTCTTTGACTACTGGGCGCAGGAACCTCGTCCAGCTCTCTCA 408
 DB 101 GlyAspGlyPheTyrAlaMetAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 120

RESULT 14

AAW27555

ID AAW27555 standard; Protein; 117 AA.

XX AAW27555;

XX 01-OCT-2001 (first entry)

XX Amino acid sequence of variable heavy chain fragment of clone G112.

XX Antibody; heavy chain; VH; amyloid protein; blood brain barrier;
 KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
 KW transferrin receptor; neurological disease; Alzheimer's disease;
 KW prion disease; AIDS-related dementia; epilepsy; brain injury.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 82 /note= "Gln encoded by TAG"

XX

PN WO200144300-A2.
XX 21-JUN-2001.
XX 27-NOV-2000; 2000WO-GB04501.
XX 13-DEC-1999; 99US-0170599.
XX (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX Webster C, Osbourn J, Ward G, Miller K;
PI WPI: 2001-398131/42.
XX N-PSDB; AAH42410.
XX Mixture or panel of antibodies for selecting specific binding members
PT that cross the blood brain barrier, for use in delivering different
PT molecules and treating neurological diseases -
XX
PS Claim 1; Page 108; 109pp; English.
XX
CC The present sequence represents an antibody variable heavy chain (VH)
CC fragment. The fragment is used to produce a mixture or panel of 5
CC different specific binding members, each comprising an antibody VH
CC and/or VL variable domain and capable, when displayed on the surface
CC of filamentous bacteriophage particles or in the case of a specific
CC binding member comprising the DS VH and/or VL variable domain when
CC bound to human serum amyloid protein, to pass through a mammalian
CC blood brain barrier (BBB). The panel is useful for the selection of
CC specific binding members with a desired property such as ability to
CC cross BBB, ability to bind endothelial cells or other brain cell antigen,
CC ability to bind areas of inflammation in the brain or BBB breakdown or
CC ability to bind intracellular adhesion molecules and to bind transferrin
CC receptor. The antibodies are useful in diagnosis, prophylaxis and
CC treatment of human or animal body, including neurological diseases, such
CC as Alzheimer's disease, prion disease, AIDS-related dementia, epilepsy
CC and traumatic brain injury and any diseases involving inflammation
CC occurring within the brain or central nervous system.
XX
SQ Sequence 117 AA;
Alignment Scores:
Pred. No.: 9.74e-44 Length: 117
Score: 569.00 Matches: 107
Percent Similarity: 93.16% Conservative: 2
Best Local Similarity: 91.45% Mismatches: 8
Query Match: 67.26% Indels: 0
DB: 22 Gaps: 0
US-08-728-463B-207 (1-462) x AAG62966 (1-117)
QY 58 GAGGTGAGCTGGTGTGAGTCTGGAGCAGAGGTGAAAGCCCGGGAGTCTCTGAAGATC 117
Db 1 GlnValAsnLeuArgGluSerGlyAlaGluValLysProGlyGluSerLeuLysIle 20
QY 118 TCCTGTAAAGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGTGGCCAGATG 177
Db 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValArgGlnMet 40
QY 178 CCCGGGAAAGGCTGGAGTGGATGAGTCACTATCTCTGGTGAATCTGTATACCATAC 237
Db 41 ProGlyLysGlyLeuGluTrpMetGlyIleTyrProGlyAspSerAspThrArgTyr 60
QY 238 AGCCGTCCTTCAAGCCAGGTGACCATCTCAGCCGACAGTCCATCAGACCCGCTAC 297
Db 61 SerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80
QY 298 CTGCACTGGAGCGCTGAGGCTCGGACACCGCATGTATTAATCTGTCGAGAGACCAA 357
Db 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgArgTrp 100
QY 358 CTGGGCTCTTTGACTACTGGGCGCAGGAAACCTCGTCCCTCTCA 408

Db 101 LysGlyHisPheAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 117
RESULT 15
AAB67623
ID AAB67623 standard; Protein; 245 AA.
XX
AC AAB67623;
XX
DT 29-MAY-2001 (first entry)
XX
DE Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_7.
XX
KW Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;
KW miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.
XX
OS Homo sapiens.
XX
PN WO200114558-A1.
XX
PD 01-MAR-2001.
XX
PF 28-AUG-2000; 2000WO-EP08388.
XX
PR 26-AUG-1999; 99EP-0116691.
XX
PA (MORP-) MORPHOSYS AG.
XX
PI Kretzschmar T, Tesar M, Marget M, Kroenke M;
XX WPI: 2001-218451/22.
XX
PT Novel isolated human immunoglobulin or functional immunoglobulin
PT fragment specific for human leukocyte antigen Cw6, useful for treatment
PT of humans and for human leukocyte antigen phenotyping -
XX
PS Claim 3; Fig 1; 23pp; English.
XX
CC AAB67617-23 represent single chain antibody (scFv) fragments which
CC are specific for human leukocyte antigen (HLA)-Cw6. The fragments are
CC derived from a synthetic human combinatorial antibody library based on
CC molecular consensus frameworks and CDRs randomised with trinucleotides.
CC The specification describes a human immunoglobulin fragments specific
CC for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in
CC studies of natural killer cell silencing as well as miscarriages.
CC HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions.
CC Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin
CC fragments are useful for the preparation of a pharmaceutical for the
CC treatment of humans. They are also useful for HLA phenotyping.
XX
SQ Sequence 245 AA;
Alignment Scores:
Pred. No.: 1.66e-43 Length: 245
Score: 567.00 Matches: 109
Percent Similarity: 92.37% Conservative: 0
Best Local Similarity: 92.37% Mismatches: 9
Query Match: 67.02% Indels: 0
DB: 22 Gaps: 0
US-08-728-463B-207 (1-462) x AAB67623 (1-245)
QY 58 GAGTGCAGCTGGTGTGAGTCTGGAGCAGAGGTGAAAGCCCGGGAGTCTCTGAAGATC 117
Db 1 GluValGlnLeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuLysIle 20
QY 118 TCCTGTAAAGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGTGGCCAGATG 177
Db 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValArgGlnMet 40
QY 178 CCCGGGAAAGGCTGGAGTGGATGAGTCACTATCTCTGGTGAATCTGTATACCATAC 237
Db 41 ProGlyLysGlyLeuGluTrpMetGlyIleTyrProGlyAspSerAspThrArgTyr 60

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QY 238 AGCCGCTCTTCCAGGCCAGGTACCATCTCAGCCGACAAGTCCATCAGCAGCCCTAC 297
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61 SerProSerPheGlnGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80
QY 298 CTGCAGTGGAGCAGCTGAAGGCTCGGACACCGCCATCTATTACTGTGCGAGAGACCAA 357
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrCysAlaArgPheVal 100
QY 358 CTGGCCCTCTTTGACTCTGGGGCCAGGGAACCTGGTCACCGCTCTCCTCAGCC 411
Db ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
101 ProTyrTyrMetAspAsnTrpGlyGlnGlyThrLeuValThrValSerSerAla 118

Search completed: June 3, 2003, 09:02:21
Job time : 33.0494 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 09:04:15 ; Search time 19.6297 Seconds
(without alignments)
4764.744 Million cell updates/sec

Title: US-08-728-463b-207

Perfect score: 846

Sequence: 1 ATGGGCTCAACGGCATCTT.....CACCTCTCCAGAGCTT 462

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

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Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 767038

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Database : Published Applications AA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	577	68.2	121	9 US-10-078-958-6	Sequence 6, Appli
2	572.5	67.7	120	9 US-10-125-687-6	Sequence 6, Appli
3	572.5	67.7	120	12 US-10-025-687-6	Sequence 6, Appli
4	567	67.0	252	9 US-09-880-748-1537	Sequence 1537, Ap

5	558.5	66.0	116	9	US-10-035-637-4	Sequence 4, Appli
6	551.5	65.2	249	9	US-09-880-748-1312	Sequence 1312, Ap
7	530	62.6	269	10	US-09-888-721-36	Sequence 36, Appl
8	530	62.6	282	10	US-09-888-721-38	Sequence 38, Appl
9	530	62.6	287	10	US-09-888-721-40	Sequence 40, Appl
10	530	62.6	291	10	US-09-888-721-44	Sequence 44, Appl
11	530	62.6	296	10	US-09-888-721-42	Sequence 42, Appl
12	527	62.3	282	9	US-09-985-442-7	Sequence 7, Appli
13	527	62.3	282	10	US-09-983-580-7	Sequence 7, Appli
14	524	61.9	255	10	US-09-888-721-34	Sequence 34, Appl
15	523.5	61.9	515	10	US-09-825-012-66	Sequence 66, Appl
16	523.5	61.9	517	10	US-09-825-012-38	Sequence 38, Appl
17	523.5	61.9	519	10	US-09-825-012-76	Sequence 76, Appl
18	523.5	61.9	519	10	US-09-825-012-80	Sequence 80, Appl
19	523.5	61.9	521	10	US-09-825-012-71	Sequence 71, Appl
20	523.5	61.9	525	10	US-09-825-012-85	Sequence 85, Appl
21	523.5	61.9	527	10	US-09-825-012-43	Sequence 43, Appl
22	523.5	61.9	529	10	US-09-825-012-95	Sequence 95, Appl
23	523.5	61.9	531	10	US-09-825-012-90	Sequence 90, Appl
24	523.5	61.9	729	10	US-09-825-012-52	Sequence 52, Appl
25	523.5	61.9	730	10	US-09-825-012-49	Sequence 49, Appl
26	523.5	61.9	731	10	US-09-825-012-46	Sequence 46, Appl
27	523.5	61.9	739	10	US-09-825-012-61	Sequence 61, Appl
28	523.5	61.9	740	10	US-09-825-012-58	Sequence 58, Appl
29	523.5	61.9	741	10	US-09-825-012-55	Sequence 55, Appl
30	523	61.8	262	9	US-09-956-086-4	Sequence 4, Appli
31	523	61.8	262	9	US-09-956-087-4	Sequence 4, Appli
32	513	60.6	98	9	US-10-194-975-45	Sequence 45, Appl
33	513	60.6	98	9	US-10-125-687-16	Sequence 16, Appl
34	513	60.6	98	12	US-10-025-687-16	Sequence 16, Appl
35	513	60.6	248	9	US-09-880-748-1995	Sequence 1995, Ap
36	509	60.2	249	9	US-09-880-748-1957	Sequence 1957, Ap
37	508.5	60.1	248	9	US-09-880-748-2088	Sequence 2088, Ap
38	506.5	59.9	248	9	US-09-880-748-1	Sequence 1, Appli
39	503	59.3	180	10	US-09-748-960-6	Sequence 6, Appli
40	502	59.3	98	10	US-09-850-165-89	Sequence 89, Appl
41	497	58.7	247	9	US-09-880-748-2103	Sequence 2103, Ap
42	490	57.9	470	10	US-09-859-053-28	Sequence 28, Appl
43	487	57.6	448	10	US-09-917-410-6	Sequence 6, Appli
44	485.5	57.4	461	9	US-09-249-011A-24	Sequence 24, Appli
45	479	56.6	470	9	US-10-020-786-9	Sequence 9, Appli

ALIGNMENTS

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RESULT 1
US-10-078-958-6
; Sequence 6, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AVA
; APPLICANT: KUCHERLAPATI, RAJU
; APPLICANT: KLAPHOLZ, SUSAN
; APPLICANT: MENDEZ, MICHAEL J.
; APPLICANT: GREEN, LARRY
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING PLURAL Vh AND Vh REGIONS AND ANTIBODIES PRODUCED THEREFROM
; TITLE OF INVENTION: THEREFROM
; FILE REFERENCE: CELL 4.18 CON
; CURRENT APPLICATION NUMBER: US/10/078,958
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 08/759,620
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-078-958-6
Alignment Scores: 7e-39 Length: 121
Pred. No.:

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Score: 577.00 Matches: 108
 Percent Similarity: 93.16% Conservative: 1
 Best Local Similarity: 92.31% Mismatches: 8
 Query Match: 68.20% Indels: 0
 DB: 9 Gaps: 0

US-08-728-463B-207 (1-462) x US-10-078-958-6 (1-121)

QY 106 TCCTGAAGATCTCTCTGAAGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGG 165
 Db 1 SerLeuValSerCysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrp 20
 QY 166 GTGCGCCAGATCGCCGGGAAAGCCCTGGAGTGGATCGGATCATCTATCTCTGGTACTCT 225
 Db 21 ValArgGlnMetProGlyLysGlyLeuGlnTrpMetGlyLleIleTyrProGlyAspSer 40
 QY 226 GATACACATACAGCCCGCTTCCAGGCCAGCTCAGCATCTCAGCCGACAACTCCATC 285
 Db 41 AspThrArgTyrSerProSerPheGlnGlnValThrIleSerAlaAspLysSerIle 60
 QY 286 AGACCGCTACTCTGAGTGGAGCAGCTCGAGGCTCGGACACCGCCATCTATCTACTGT 345
 Db 61 SerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSerPheThrAlaMetTyrTyrCys 80
 QY 346 GCGAGAGACCAACTGGGCTCTTTGACTACTGGGCGCAGGAAACCTGGTCAACGCTCC 405
 Db 81 AlaArgGlnAspGlyAspSerPheAspTyrTrpGlyGlnGlyThrLeuValThrValSer 100
 QY 406 TCAGCTCCACCAAGGGCCCATCGGTCTTCCCTCGCACCTCTCTCCAAG 456
 Db 101 SerAlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArg 117

RESULT 2

US-10-125-687-6
 ; Sequence 6, Application US/10125687
 ; Publication No. US20030054407A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Luo, Peter
 ; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
 ; FILE REFERENCE: 26050-705
 ; CURRENT APPLICATION NUMBER: US/10/125,687
 ; CURRENT FILING DATE: 2002-04-17
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 120
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Human consensus antibody heavy chain variable region
 US-10-125-687-6

Alignment Scores:
 Pred. No.: 1.62e-38 Length: 120
 Score: 572.50 Matches: 110
 Percent Similarity: 91.67% Conservative: 0
 Best Local Similarity: 91.67% Mismatches: 7
 Query Match: 67.67% Indels: 3
 DB: 9 Gaps: 1

US-08-728-463B-207 (1-462) x US-10-125-687-6 (1-120)

QY 58 GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAGCCCGGGAGTCTCTGAAGATC 117
 Db 1 GluValGlnLeuValGlnSerGlyAlaGluValLysProGlyGlySerLeuLysIle 20
 QY 118 TCCTGTAAAGGTTCTGGATACAGCTTACCGGCTACTGGATCGGCTGGTGGCCAGATG 177
 Db 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTyrValArgGlnMet 40
 QY 278 CCCGGGAAAGGCTCGAGTGGATGGGATCATCTATCTCTGGTACTCTGATACCATAC 237
 Db 41 ProGlyLysGlyLeuGlnTrpMetGlyLleIleTyrProGlyAspSerAspThrArgTyr 60

QY 238 AGCCCTCTCTTCCAGGCCAGGTCACATCTCAGCGCAAGTCCATCAGCACCCGCTAC 297
 Db 61 SerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80
 QY 298 CTCAGTGGAGCAGCTGAAGCCTCGGACACCGCCATGTATTACTGTCCGAGA----- 351
 Db 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgTrpGly 100
 QY 352 ---GACCAACTGGGCTCTTTGACTACTCGGCGCAGGAAACCTGGTCAACGCTCTCTCA 408
 Db 101 GlyAspGlyPheTyrAlaMetAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 120

RESULT 3

US-10-025-687-6
 ; Sequence 6, Application US/10025687
 ; Patent No. US20020142255A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Luo, Peter
 ; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
 ; FILE REFERENCE: 26050-705
 ; CURRENT APPLICATION NUMBER: US/10/025,687
 ; CURRENT FILING DATE: 2002-04-17
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 120
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Human consensus antibody heavy chain variable region
 US-10-025-687-6

Alignment Scores:
 Pred. No.: 1.62e-38 Length: 120
 Score: 572.50 Matches: 110
 Percent Similarity: 91.67% Conservative: 0
 Best Local Similarity: 91.67% Mismatches: 7
 Query Match: 67.67% Indels: 3
 DB: 12 Gaps: 1

US-08-728-463B-207 (1-462) x US-10-025-687-6 (1-120)

QY 58 GAGGTGCAGTGGTGCAGTCTGGAGCAGAGGTGAAAGCCCGGGAGTCTCTGAAGATC 117
 Db 1 GluValGlnLeuValGlnSerGlyAlaGluValLysProGlyGlySerLeuLysIle 20
 QY 118 TCCTGTAAAGGTTCTGGATACAGCTTACCGGCTACTGGATCGGCTGGTGGCCAGATG 177
 Db 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValArgGlnMet 40
 QY 178 CCCGGGAAAGGCTCGAGTGGATGGGATCATCTATCTCTGGTACTCTGATACCATAC 237
 Db 41 ProGlyLysGlyLeuGlnTrpMetGlyLleIleTyrProGlyAspSerAspThrArgTyr 60
 QY 238 AGCCCTCTCTTCCAGGCCAGGTCACATCTCAGCGCAAGTCCATCAGCACCCGCTAC 297
 Db 61 SerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80
 QY 298 CTCAGTGGAGCAGCTGAAGCCTCGGACACCGCCATGTATTACTGTCCGAGA----- 351
 Db 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgTrpGly 100
 QY 352 ---GACCAACTGGGCTCTTTGACTACTCGGCGCAGGAAACCTGGTCAACGCTCTCTCA 408
 Db 101 GlyAspGlyPheTyrAlaMetAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 120

RESULT 4

US-09-880-748-1537
 ; Sequence 1537, Application US/09880748
 ; Publication No. US20030059937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PFS23

; CURRENT APPLICATION NUMBER: US/09/880,748

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/212,210

; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 3239

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1537

; LENGTH: 252

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-880-748-1537

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Best Local Similarity:	86.40%	Mismatches:	6
Query Match:	67.02%	Indels:	8
DB:	9	Gaps:	1

US-08-728-463B-207 (1-462) x US-09-880-748-1537 (1-252)

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QY 118 TCCTGTAGGCTTCTGGATACAGCTTTACCGCTACTGATCGGCTGGTGGCCAGATG 177

Db 21 SerCysLysGlySerGlyThrPheThrSerTyrTrpIleGlyTrpValArgGlnMet 40

QY 178 CCGGGAAGGCTGGAGTGGATCATCTATCTCTGGTGCATCTCATACCATAC 237

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QY 238 AGCCGCTCTTCAAGCCAGGTCCATCTCAGCCGACCAAGTCCATCAGCCGCTAC 297

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QY 298 CTGCACTGAGCAGCTGAAGGCTCGGACACCGCCATGTATCTGTCGAGAGACCAA 357

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QY 358 CTGGGCTC-----TTTGACTCTGGGCCGAGGAAACCCCTG 393

Db 101 TyrAspIleLeuThrGlyTyrTyrProSerGlyPheAspTyrTrpGlyGlnGlyThrMet 120

QY 394 GTCACCGTCTCTCTCA 408

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RESULT 5

US-10-035-637-4

; Sequence 4, Application US/10035637

; Publication No. US20030031667A1

; GENERAL INFORMATION:

; APPLICANT: Deo, Yashwant M.

; APPLICANT: Reifer, Tibor

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC

; FILE REFERENCE: MXI-166CP

; CURRENT APPLICATION NUMBER: US/10/035,637

; CURRENT FILING DATE: 2001-11-07

; PRIOR APPLICATION NUMBER: 09/851,614

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: USSN 60/203,126

; PRIOR FILING DATE: 2000-05-08

; PRIOR APPLICATION NUMBER: USSN 60/230,739

; PRIOR FILING DATE: 2000-09-07

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: FastSeq for Windows Version 4.0.

; SEQ ID NO 4

; LENGTH: 116

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-035-637-4

Alignment Scores:

Pred. No.:	2,19e-37	Length:	116
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Percent Similarity:	93.16%	Conservative:	2
Best Local Similarity:	91.45%	Mismatches:	7
Query Match:	66.02%	Indels:	1
DB:	9	Gaps:	1

US-08-728-463B-207 (1-462) x US-10-035-637-4 (1-116)

QY 58 GAGGTGCAGCTGGTGCAGTCTCGAGCAGAGGTGAAAGCCCGGGAGTCTCTGAAGATC 117

Db 1 GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIle 20

QY 118 TCCTGTAGGCTTCTGGATACAGCTTTACCGCTACTGATCGGCTGGTGGCCAGATG 177

Db 21 SerCysLysGlySerGlyAspSerPheThrThrTyrTrpIleGlyTrpValArgGlnMet 40

QY 178 CCGGGAAGGCTGGAGTGGATCATCTATCTCTGGTGCATCTCATACCATAC 237

Db 41 ProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSerAspThrIleTyr 60

QY 238 AGCCGCTCTTCAAGCCAGGTCCATCTCAGCCGACCAAGTCCATCAGCCGCTAC 297

Db 61 SerProSerPheGlnGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80

QY 298 CTGCACTGAGCAGCTGAAGGCTCGGACACCGCCATGTATCTGTCGAGAGACCAA 357

Db 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysThrArgGlyAsp 100

QY 358 CTGGGCTCTTTGACTCTGACTTCTGGGCCGAGGAAACCCCTGGTCCCTCTCA 408

Db 101 ArgGlyVal---AspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 116

RESULT 6

US-09-880-748-1312

; Sequence 1312, Application US/09880748

; Publication No. US20030059937A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PFS23

; CURRENT APPLICATION NUMBER: US/09/880,748

; CURRENT FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/212,210

; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 3239

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1312

; LENGTH: 249

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-880-748-1312

Alignment Scores:		
Pred. No.:	8,296-37	Length:
Score:	551.50	Matches:
Percent Similarity:	77.3%	Conservative:
Best Local Similarity:	74.6%	Mismatches:
Query Match:	65.1%	Indels:
DB:	9	Gaps:
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US-08-728-463B-207 (1-462) x US-09-880-748-1312 (1-249)

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Db	1		117
QY	118	TCTCTGAAGGTTCTGGATACAGCTTTACCGGCTACTCGGATCGCGTGGGTGGCCGACGATG	177
Db	21		177
QY	178	CCCGGGAAGCCCTGGAGTGGATGGGATCATCTATCTCTGTGCACCTCATACCACATAC	237
Db	41		237
QY	238	AGCCCGCTTCCAGGCGCAGGTCCATCTCAGCCGACCAAGTCCATCAGCACCGCCTAC	297
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QY	298	CTGCAGTGGAGCAGCCTGAAGGCTCGGACACCGCCATGTATTACTGTGCGGAGA	351
Db	81		351
QY	352	---GACCAACTG---GCGCTTTTGACTCTGGGGCCAGGAACCCCTG	393
Db	101		393
QY	394	GTACACCGTCTCCTCAGCCTCC-----	414
Db	121		414
QY	415	-----ACCAAGGCCCATCGGTC	432
Db	141		432
QY	141	GlnSerValLeuThrGlnProProSerVal	150
Db			150

RESULT 7

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US-09-888-721-36
; Sequence 36, Application US/09888721
; Patent No. US20020132990A1.
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Wils, Pierre
; APPLICANT: Zhu, Quan
; APPLICANT: Laurent, Olivier
; APPLICANT: Marasco, Wayne A.
; APPLICANT: Scherman, Daniel
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
; FILE REFERENCE: 23611-A USA
; CURRENT APPLICATION NUMBER: US/09/888, 721
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/213,653
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Human/murine
; OTHER INFORMATION: chimeric single chain binding polypeptide (C6ML3-9
; OTHER INFORMATION: gFv')
US-09-888-721-36

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Alignment Scores:		
Pred. No.:	4,559-35	Length:
Scores:	\$30.00	Matches:
Percent Similarity:	71.60%	Conservative:
Best Local Similarity:	65.43%	Mismatches:
Query Match:	62.65%	Indels:
DB:	10	Gaps:
		3

US-08-728-463B-207 (1-462) x US-09-888-721-36 (1-269)

58	QY	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGAGTCTCTGAAGATC	117
	Db		
1	Db	GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIle	20
	QY		
118	QY	TCCTCTAAGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGTGGGTGCGCCAGATG	177
	Db		
21	Db	SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet	40
	QY		
178	QY	CCCGGGAAAGCCCTGGAGTGGATGGGATCATCTATCTCTGGTGCATCTGTATCCACATAC	237
	Db		
41	Db	ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr	60
	QY		
238	QY	AGCCCGCTCTCCAAAGCCAGGTCCACCATCTCAGCCGACCAAGTCCATCAGCACCCGCTAC	297
	Db		
61	Db	SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr	80
	QY		
298	QY	CTGCAGTGGAGCAGCTGAAGGCTCGGCACACCGCCATGTATTACTGTCCGAGAGACCA	357
	Db		
81	Db	LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp	100
	QY		
358	QY	CTGGGC-----CTCTTTTGACTACTGGGCG	381
	Db		
101	Db	ValGlyTyrCysSerSerSerAenCysAlaLysTrpProGluTyrPheGlnHisTrpGly	120
	QY		
382	QY	CAGGGAACCTTGCTCACCCTCTCTCCAGCCTCC-----	414
	Db		
121	Db	GlnGlyThrLeuValThrValSerSerGlyGlyGlySerGlyGlyGlySerGly	140
	QY		
415	QY	-----ACCAAGGCCCATCGGTCTTCCCCCTCGCACCCCTCC	450
	Db		
141	Db	GlyGlyGlySerGlnSerValLeuThrGlnProProSerVal---SerAlaAlaProGly	159
	QY		
451	QY	TCCAAAG	456
	Db		
160	Db	GlnLys	161

RESULT 8

RESOLUT 8
US-09-888-721-38
; Sequence 38, Application US/09888721
; Patent No. US20020132990A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Wills, Pierre
; APPLICANT: Zhu, Quan
; APPLICANT: Laurent, Olivier
; APPLICANT: Marasco, Wayne A.
; APPLICANT: Scherman, Daniel
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
; TITLE OF INVENTION: DELIVERY
; FILE REFERENCE: 23611-A USA
; CURRENT APPLICATION NUMBER: US/09/888,721
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/213,653
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 38
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human/murine

; OTHER INFORMATION: chimeric single chain binding polypeptide
; OTHER INFORMATION: (C6ML3-98FV'-L1-KDEL)
US-09-888-721-38

Alignment Scores:
Pred. No.: 4.56e-35 Length: 282
Score: 530.00 Matches: 106
Percent Similarity: 71.60% Conservative: 10
Best Local Similarity: 65.43% Mismatches: 16
Query Match: 62.65% Indels: 30
DB: 10 Gaps: 3

US-08-728-463B-207 (1-462) x US-09-888-721-38 (1-282)

QY 58 GAGGTGACGCTGGTGCAGTCTGGAGCAGAGGTGAAAGCCCGGGGAGTCTCTGAAGATC 117
Db 1 GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGlnSerLeuLys 20
QY 118 TCCTGTAAAGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGGTGGCCAGATG 177
Db 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
QY 178 CCGGGAAGGCTGGAGTGGATGGGATCATCTATCTGTGACTCTGATACCATAC 237
Db 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
QY 238 ACCCGCTCTTCAAGGCGAGTCAACATCTCAGCGCAGCAAGTCCATCAGCACCCGCTAC 297
Db 61 SerProSerPheGlnGlnValThrLysSerValAspLysSerValSerThrAlaTyr 80
QY 298 CTGCAGTGGAGCAGCTGAAGCCCTCGGACACCGCATGATATCTGTCGAGAGACCA 357
Db 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
QY 358 CTGGGC-----CTCTTTGACTCTGGGC 381
Db 101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGluTyrPheGlnHisTrpGly 120
QY 382 CAGGAACCTGGTCACTCTCTCAGCCTCC----- 414
Db 121 GlnGlyThrLeuValThrValSerSerGlyGlyGlySerGlyGlyGlySerGly 140
QY 415 -----ACCAAGGCCCATCGGTCTTCCCTCGCACCTCC 450
Db 141 GlyGlyGlySerGlnSerValLeuThrGlnProProSerVal---SerAlaAlaProGly 159
QY 451 TCCAAG 456
Db 160 GlnLys 161

RESULT 9

US-09-888-721-40
; Sequence 40, Application US/09888721
; Patent No. US20020132990A1

GENERAL INFORMATION:

; APPLICANT: Huston, James S.

; APPLICANT: Wils, Pierre

; APPLICANT: Zhu, Quan

; APPLICANT: Laurent, Olivier

; APPLICANT: Marasco, Wayne A.

; APPLICANT: Scherman, Daniel

; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID

; FILE REFERENCE: 23611-A USA

; CURRENT APPLICATION NUMBER: US/09/888, 721

; CURRENT FILING DATE: 2001-06-25

; PRIOR FILING DATE: 2001-06-25

; PRIOR APPLICATION NUMBER: 60/213,653

; NUMBER OF SEQ ID NOS: 45

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 40

; LENGTH: 287

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Human/murine

; OTHER INFORMATION: chimeric single chain binding polypeptide

; OTHER INFORMATION: (C6ML3-98FV'-L2-KDEL)

US-09-888-721-40

Alignment Scores:

Pred. No.: 4.56e-35 Length: 287
Score: 530.00 Matches: 106
Percent Similarity: 71.60% Conservative: 10
Best Local Similarity: 65.43% Mismatches: 16
Query Match: 62.65% Indels: 30
DB: 10 Gaps: 3

US-08-728-463B-207 (1-462) x US-09-888-721-40 (1-287)

QY 58 GAGGTGACGCTGGTGCAGTCTGGAGCAGAGGTGAAAGCCCGGGGAGTCTCTGAAGATC 117
Db 1 GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGlnSerLeuLys 20
QY 118 TCCTGTAAAGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGGTGGCCAGATG 177
Db 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
QY 178 CCGGGAAGGCTGGAGTGGATGGGATCATCTATCTGTGACTCTGATACCATAC 237
Db 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
QY 238 ACCCGCTCTTCAAGGCGAGTCAACATCTCAGCGCAGCAAGTCCATCAGCACCCGCTAC 297
Db 61 SerProSerPheGlnGlnValThrLysSerValAspLysSerValSerThrAlaTyr 80
QY 298 CTGCAGTGGAGCAGCTGAAGCCCTCGGACACCGCATGATATCTGTCGAGAGACCA 357
Db 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
QY 358 CTGGGC-----CTCTTTGACTCTGGGC 381
Db 101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGluTyrPheGlnHisTrpGly 120
QY 382 CAGGAACCTGGTCACTCTCTCAGCCTCC----- 414
Db 121 GlnGlyThrLeuValThrValSerSerGlyGlyGlySerGlyGlyGlySerGly 140
QY 415 -----ACCAAGGCCCATCGGTCTTCCCTCGCACCTCC 450
Db 141 GlyGlyGlySerGlnSerValLeuThrGlnProProSerVal---SerAlaAlaProGly 159
QY 451 TCCAAG 456
Db 160 GlnLys 161

RESULT 10

US-09-888-721-44

; Sequence 44, Application US/09888721

; Patent No. US20020132990A1

GENERAL INFORMATION:

; APPLICANT: Huston, James S.

; APPLICANT: Wils, Pierre

; APPLICANT: Zhu, Quan

; APPLICANT: Laurent, Olivier

; APPLICANT: Marasco, Wayne A.

; APPLICANT: Scherman, Daniel

; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID

; FILE REFERENCE: 23611-A USA

; CURRENT APPLICATION NUMBER: US/09/888, 721

; CURRENT FILING DATE: 2001-06-25

; PRIOR FILING DATE: 2001-06-25

; PRIOR APPLICATION NUMBER: 60/213,653

; NUMBER OF SEQ ID NOS: 45

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 44

; LENGTH: 287

; TYPE: PRT

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; SEQ ID NO 44
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Human/murine
; OTHER INFORMATION: chimeric single chain binding polypeptide
; OTHER INFORMATION: (C6WL3-9sfv'-L2-nls)
US-09-888-721-44

Alignment Scores:
Pred. No.: 4,56e-35 Length: 291
Score: 530.00 Matches: 106
Percent Similarity: 71.60% Conservative: 10
Best Local Similarity: 65.43% Mismatches: 16
Query Match: 62.65% Indels: 30
DB: 10 Gaps: 3

US-08-728-463B-207 (1-462) x US-09-888-721-44 (1-291)
QY 58 GAGGTGACGCTGCTGACGCTGAGCAGAGTGAAGCCCGGGGAGTCTCTGAAGATC 117
Db 1 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuLysIle 20
QY 118 TCCTGTAAGGTTCTCGATACAGCTTTACCGGCTACTGGATCGGCTGGTGGCCAGATG 177
Db 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
QY 178 CCCGGGAAAGCCCTGGAGTGGATGGGATCATCTCTGCTGACTCTGATACCATAC 237
Db 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
QY 238 AGCCCGTCCTTCCAAAGCCAGGTCACCATCTCAGCCGACAAAGTCCATCAGACCCGCTAC 297
Db 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
QY 298 CTGCAGTGGAGCAGCCCTGAGGCTCGGACACCGCCATGATTACTGTCGAGAGACCAA 357
Db 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
QY 358 CTGGGC-----CTCTTTGACTACTGGGC 381
Db 101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGluTyrPheGlnHisTrpGly 120
QY 382 CAGGGAACCTGTGTCACCGCTCTCTCAGCCTCC-----414
Db 121 GlnGlyThrLeuValThrValSerSerGlyGlyGlySerGlyGlyGlySerGly 140
QY 415 -----ACCAAGGCCCATCGGCTCTTCCCTGGCAGCCTCC 450
Db 141 GlyGlySerGlnSerValLeuThrGlnProProSerVal---SerAlaAlaProGly 159
QY 451 TCCAAG 456
Db 160 GlnLys 161

RESULT 11
US-09-888-721-42
; Sequence 42, Application US/09888721
; Patent No. US20020132990A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Wils, Pierre
; APPLICANT: Zhu, Quan
; APPLICANT: Laurent, Olivier
; APPLICANT: Marasco, Wayne A.
; APPLICANT: Scherman, Daniel
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
; FILE REFERENCE: 23611-A USA
; CURRENT APPLICATION NUMBER: US/09/888,721
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/213,653
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; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Human/murine
; OTHER INFORMATION: chimeric single chain binding polypeptide
; OTHER INFORMATION: (C6WL3-9sfv'-L2-H14)
US-09-888-721-42

Alignment Scores:
Pred. No.: 4,57e-35 Length: 296
Score: 530.00 Matches: 106
Percent Similarity: 71.60% Conservative: 10
Best Local Similarity: 65.43% Mismatches: 16
Query Match: 62.65% Indels: 30
DB: 10 Gaps: 3

US-08-728-463B-207 (1-462) x US-09-888-721-42 (1-296)
QY 58 GAGGTGACGCTGCTGACGCTGAGCAGAGTGAAGCCCGGGGAGTCTCTGAAGATC 117
Db 1 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuLysIle 20
QY 118 TCCTGTAAGGTTCTCGATACAGCTTTACCGGCTACTGGATCGGCTGGTGGCCAGATG 177
Db 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
QY 178 CCCGGGAAAGCCCTGGAGTGGATGGGATCATCTCTGCTGACTCTGATACCATAC 237
Db 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
QY 238 AGCCCGTCCTTCCAAAGCCAGGTCACCATCTCAGCCGACAAAGTCCATCAGACCCGCTAC 297
Db 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
QY 298 CTGCAGTGGAGCAGCCCTGAGGCTCGGACACCGCCATGATTACTGTCGAGAGACCAA 357
Db 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
QY 358 CTGGGC-----CTCTTTGACTACTGGGC 381
Db 101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGluTyrPheGlnHisTrpGly 120
QY 382 CAGGGAACCTGTGTCACCGCTCTCTCAGCCTCC-----414
Db 121 GlnGlyThrLeuValThrValSerSerGlyGlyGlySerGlyGlyGlySerGly 140
QY 415 -----ACCAAGGCCCATCGGCTCTTCCCTGGCAGCCTCC 450
Db 141 GlyGlySerGlnSerValLeuThrGlnProProSerVal---SerAlaAlaProGly 159
QY 451 TCCAAG 456
Db 160 GlnLys 161

RESULT 12
US-09-985-442-7
; Sequence 7, Application US/09985442
; Patent No. US20020156248A1
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. US20020156248A1 Method for Targeted Delivery of Nucleic Ac
; FILE REFERENCE: 0977.2300003
; CURRENT APPLICATION NUMBER: US/09/985,442
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
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PRIOR APPLICATION NUMBER: 60/104,949
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7

LENGTH: 282
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: C6.5/218 sFv
US-09-985-442-7

Alignment Scores:
Pred. No.: 7,97e-35 Length: 282
Score: 527.00 Matches: 100
Percent Similarity: 77.40% Conservative: 13
Best Local Similarity: 68.49% Mismatches: 21
Query Match: 62.29% Indels: 12
DB: 9 Gaps: 1

US-08-728-463B-207 (1-462) x US-09-985-442-7 (1-282)

QY 58 GAGGTGACGTGGTGCAGTCTGGAGCAGAGGTGAAAGCCCGGGGAGTCTCTGAAGATC 117
DB 130 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysLysProGlyGlnSerLeuLysIle 149
QY 118 TCCTGTAAGGGTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGGCGCCAGATG 177
DB 150 SerCysLysGlySerGlyTyrSerPheThrSerTyrTriPleAlaTrpValArgGlnMet 169
QY 178 CCGGGAAAGGCTGGAGTGGGATCATCTACCGGCTACTGGATCGGCTGGGCGCCAGATG 237
DB 170 ProGlyLysGlyLeuGlnLysMetGlyLeuLysTyrProGlyAspSerAspThrLysTyr 189
QY 238 AGCCGCTCTTCCAAAGCCAGGTCCACCATCTCAGCCGACCAAGTCCATCAGCCGCTAC 297
DB 190 SerProSerPheGlnGlnValThrLysSerValAspLysSerValSerThrAlaTyr 209
QY 298 CTGCACTGGAGCAGCTGAAGGCTCGGACACCGCATCTATTACTGTCCGAGAGACCAA 357
DB 210 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 229
QY 358 CTGGGC-----CTCTTGACTACTGGGC 381
DB 230 ValGlyTyrCysSerSerAsnCysAlaLysTrpProGluTyrPheGlnHisTrpGly 249
QY 382 CAGGGAACCTGTCACCGTCTCTCAGCTCCACCAAGGCCCATCGGTCTTCCCCCTG 441
DB 250 GlnGlyThrLeuValThrValSerSerLysLysLysLysLysLysValThrVal 269
QY 442 GCACCTCTCTCCAAAG 459
DB 270 SerLysLysLysLysLysLys 275

RESULT 13

US-09-983-580-7
Sequence 7, Application US/09983580
Patent No. US20020151061A1

GENERAL INFORMATION:

APPLICANT: Filpula, David R..
APPLICANT: Wang, MaoLiang
APPLICANT: Whitlow, Marc D.
TITLE OF INVENTION: No. US20020151061A1
FILE REFERENCE: 0977.2300002
CURRENT APPLICATION NUMBER: US/09/983,580
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 09/420,592
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/104,949
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7

LENGTH: 282

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: C6.5/218 sFv
US-09-983-580-7

Alignment Scores:
Pred. No.: 7,97e-35 Length: 282
Score: 527.00 Matches: 100
Percent Similarity: 77.40% Conservative: 13
Best Local Similarity: 68.49% Mismatches: 21
Query Match: 62.29% Indels: 12
DB: 10 Gaps: 1

US-08-728-463B-207 (1-462) x US-09-983-580-7 (1-282)

QY 58 GAGGTGACGTGGTGCAGTCTGGAGCAGAGGTGAAAGCCCGGGGAGTCTCTGAAGATC 117
DB 130 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysLysProGlyGlnSerLeuLysIle 149
QY 118 TCCTGTAAGGGTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGGCGCCAGATG 177
DB 150 SerCysLysGlySerGlyTyrSerPheThrSerTyrTriPleAlaTrpValArgGlnMet 169
QY 178 CCGGGAAAGGCTGGAGTGGGATCATCTACCGGCTACTGGATCGGCTGGGCGCCAGATG 237
DB 170 ProGlyLysGlyLeuGlnLysMetGlyLeuLysTyrProGlyAspSerAspThrLysTyr 189
QY 238 AGCCGCTCTTCCAAAGCCAGGTCCACCATCTCAGCCGACCAAGTCCATCAGCCGCTAC 297
DB 190 SerProSerPheGlnGlnValThrLysSerValAspLysSerValSerThrAlaTyr 209
QY 298 CTGCACTGGAGCAGCTGAAGGCTCGGACACCGCATCTATTACTGTCCGAGAGACCAA 357
DB 210 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 229
QY 358 CTGGGC-----CTCTTGACTACTGGGC 381
DB 230 ValGlyTyrCysSerSerAsnCysAlaLysTrpProGluTyrPheGlnHisTrpGly 249
QY 382 CAGGGAACCTGTCACCGTCTCTCAGCTCCACCAAGGCCCATCGGTCTTCCCCCTG 441
DB 250 GlnGlyThrLeuValThrValSerSerLysLysLysLysLysLysValThrVal 269
QY 442 GCACCTCTCTCCAAAG 459
DB 270 SerLysLysLysLysLysLys 275

RESULT 14

US-09-888-721-34
Sequence 34, Application US/09888721
Patent No. US20020132990A1

GENERAL INFORMATION:

APPLICANT: Huston, James S..
APPLICANT: Wils, Pierre
APPLICANT: Zhu, Quan
APPLICANT: Laurent, Olivier
APPLICANT: Marasco, Wayne A.
APPLICANT: Scherman, Daniel
TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
FILE REFERENCE: 23611-A USA
CURRENT APPLICATION NUMBER: US/09/888,721
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: 60/213,653
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 34
LENGTH: 255
TYPE: PRT
ORGANISM: Artificial Sequence

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OM nucleic - protein search, using frame_plus_n2p model

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(without alignments)
2585.294 Million cell updates/sec

Title: US-08-728-463B-207
Perfect score: 846
Sequence: 1 ATGGGGTCAACCGCATCTT.....CACCTCTCTCCAGAGCTT 462

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Ygapop 10.0 , Ygapext 0.5
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Delop 6.0 , Delext 7.0

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Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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SUMMARIES

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2	576	68.1	119	4	US-09-025-769B-26
3	572.5	67.7	120	4	US-09-025-769B-40
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5	553.5	65.4	147	1	US-08-259-372A-8
6	553.5	65.4	147	1	US-08-468-671-8
7	527	62.3	282	4	US-09-420-592A-7
8	524	61.9	258	2	US-08-665-202-5
9	523	61.8	262	4	US-09-069-821-4
10	520	61.5	129	2	US-08-665-202-32
11	513	60.6	98	2	US-08-665-202-33
12	508	60.0	98	1	US-08-478-039-81

13	508	60.0	98	1	US-08-476-349A-81	Sequence 81, Appl
14	503	59.5	125	2	US-08-665-202-44	Sequence 44, Appl
15	501	59.2	125	2	US-08-665-202-53	Sequence 53, Appl
16	501	59.2	125	2	US-08-665-202-54	Sequence 54, Appl
17	501	59.2	125	2	US-08-665-202-59	Sequence 59, Appl
18	500	59.1	222	1	US-08-458-516-22	Sequence 22, Appl
19	500	59.1	235	1	US-08-458-516-23	Sequence 23, Appl
20	500	59.1	449	1	US-08-458-516-13	Sequence 13, Appl
21	499	59.0	125	2	US-08-665-202-45	Sequence 45, Appl
22	499	59.0	125	2	US-08-665-202-46	Sequence 46, Appl
23	499	59.0	125	2	US-08-665-202-48	Sequence 48, Appl
24	499	59.0	125	2	US-08-665-202-55	Sequence 55, Appl
25	497	58.7	125	2	US-08-665-202-58	Sequence 58, Appl
26	496	58.6	125	2	US-08-665-202-51	Sequence 51, Appl
27	496	58.6	125	2	US-08-665-202-52	Sequence 52, Appl
28	496	58.6	125	2	US-08-665-202-56	Sequence 56, Appl
29	492	58.2	125	2	US-08-665-202-50	Sequence 50, Appl
30	492	58.2	125	2	US-08-665-202-57	Sequence 57, Appl
31	489	57.8	98	2	US-08-428-197-17	Sequence 17, Appl
32	489	57.8	98	5	PCT-US93-10555-17	Sequence 17, Appl
33	488	57.7	125	2	US-08-665-202-49	Sequence 49, Appl
34	487.5	57.6	122	4	US-08-983-607-30	Sequence 30, Appl
35	483	57.1	125	2	US-08-665-202-47	Sequence 47, Appl
36	483	57.1	249	4	US-08-918-148-74	Sequence 74, Appl
37	477	56.4	476	2	US-08-378-939-10	Sequence 10, Appl
38	468.5	55.4	467	2	US-07-916-098A-45	Sequence 45, Appl
39	462	54.6	468	4	US-09-485-737B-67	Sequence 67, Appl
40	462	54.6	711	4	US-09-485-737B-90	Sequence 90, Appl
41	461.5	54.6	253	3	US-09-027-449-52	Sequence 52, Appl
42	461.5	54.6	253	3	US-08-804-444A-52	Sequence 52, Appl
43	461.5	54.6	253	4	US-09-026-985-52	Sequence 52, Appl
44	461.5	54.6	253	4	US-09-121-952A-52	Sequence 52, Appl
45	461.5	54.6	253	4	US-09-234-340A-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-08-545-809A-133
; Sequence 133, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiro
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: Fast-SEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545.809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154

;; ZIP: 10021
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/025,769B
;; FILING DATE: 18-FEB-1998
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 95 11 3021.0
;; FILING DATE: 18-AUG-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: James F. Haley, Jr., Esq.
;; REGISTRATION NUMBER: 27,794
;; REFERENCE/DOCKET NUMBER: MORPHO/5
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)596-9000
;; TELEFAX: (212)596-9090
;; INFORMATION FOR SEQ ID NO: 40:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 120 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-025-769B-40

Alignment Scores:
Pred. No.: Length: 120
Score: 572.50 Matches: 110
Percent Similarity: 91.67% Conservative: 0
Best Local Similarity: 91.67% Mismatches: 7
Query Match: 67.67% Indels: 3
DB: 4 Gaps: 1

US-08-728-463B-207 (1-462) x US-09-025-769B-40 (1-120)

QY 58 GAGGTGACGTGGTGGATGCGGATCATCTCTGGAGAGGCGGAGGAGTCTCTGAAGATC 117
Db 1 GluValGlnLeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuLysile 20
QY 118 TCCTGTAAAGGTTCTGGATACAGCTTTACCGGCTACTGATCGGCTGGTGGCGCAGATG 177
Db 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValArgGlnMet 40
QY 178 CCGGGAAGGCTGGAGTGGATGGGATCATCTCTCTGGTGGACTCTGTATACCATAC 237
Db 41 ProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSerAspThrArgTyr 60
QY 238 AGCCCGTCTCTCCAAAGGCCAGGTCAACCATCTCAGCCGCAAGTCCATCAGCACCGCCTAC 297
Db 61 SerProSerPheGlnGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80
QY 298 CTGCACTGAGAGCGCTGAAGCCTCGGACACCGCATGTATATCTGCGGAGA----- 351
Db 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgTrpGly 100
QY 352 ---GACCAACTGGGCTCTTTGACTACTGGGCGGAGAACCTGTACCGCTCTCCCTCA 408
Db 101 GlyAspGlyPheTyrAlaMetAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 120

RESULT 4

US-09-025-769B-67
; Sequence 67, Application US/09025769B
; Patent No. 630064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas

;; TITLE OF INVENTION: Protein/(Poly)peptide libraries
;; NUMBER OF SEQUENCES: 373
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;; STREET: 1251 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10021
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/025,769B
;; FILING DATE: 18-FEB-1998
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 95 11 3021.0
;; FILING DATE: 18-AUG-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: James F. Haley, Jr., Esq.
;; REGISTRATION NUMBER: 27,794
;; REFERENCE/DOCKET NUMBER: MORPHO/5
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)596-9000
;; TELEFAX: (212)596-9090
;; INFORMATION FOR SEQ ID NO: 67:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 120 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-025-769B-67

Alignment Scores:
Pred. No.: Length: 120
Score: 572.50 Matches: 110
Percent Similarity: 91.67% Conservative: 0
Best Local Similarity: 91.67% Mismatches: 7
Query Match: 67.67% Indels: 3
DB: 4 Gaps: 1

US-08-728-463B-207 (1-462) x US-09-025-769B-67 (1-120)

QY 58 GAGGTGACGTGGTGGATGCGGATCATCTCTGGAGAGGCGGAGGAGTCTCTGAAGATC 117
Db 1 GluValGlnLeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuLysile 20
QY 118 TCCTGTAAAGGTTCTGGATACAGCTTTACCGGCTACTGATCGGCTGGTGGCGCAGATG 177
Db 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValArgGlnMet 40
QY 178 CCGGGAAGGCTGGAGTGGATGGGATCATCTCTCTGGTGGACTCTGTATACCATAC 237
Db 41 ProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSerAspThrArgTyr 60
QY 238 AGCCCGTCTCTCCAAAGGCCAGGTCAACCATCTCAGCCGCAAGTCCATCAGCACCGCCTAC 297
Db 61 SerProSerPheGlnGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80
QY 298 CTGCACTGAGAGCGCTGAAGCCTCGGACACCGCATGTATATCTGCGGAGA----- 351
Db 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgTrpGly 100
QY 352 ---GACCAACTGGGCTCTTTGACTACTGGGCGGAGAACCTGTACCGCTCTCCCTCA 408
Db 101 GlyAspGlyPheTyrAlaMetAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 120

RESULT 5

US-08-259-372A-8
; Sequence 8, Application US/08259372A
; Patent No. 5565354

```

; GENERAL INFORMATION:
; APPLICANT: Ostberg, Lars G.
; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,372A
; FILING DATE: 14-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/871,426
; FILING DATE: 21-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,036
; FILING DATE: 27-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/538,796
; FILING DATE: 15-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/925,196
; FILING DATE: 31-OCT-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/904,517
; FILING DATE: 05-SEP-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-50-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 147 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-259-372A-8

Alignment Scores:
Pred. No.: 1,09e-46 Length: 147
Score: 553.50 Matches: 109
Percent Similarity: 78.23% Conservative: 6
Best Local Similarity: 74.15% Mismatches: 21
Query Match: 65.43% Indels: 11
DB: 1 Gaps: 1

US-08-728-463B-207 (1-462) x US-08-259-372A-8 (1-147)
QY 1 ATGGGTCAACGGCCATCTCCCTCTCTGCTTCTCCAGGAGTCTGTGCGGAG 60
Db 1 MetGlySerThrAlaIleLeuGlyLeuLeuAlaValLeuGlnGlyValCysAlaGlu 20
QY 61 GTGCAGCTGGTCTGAGTCAGGAGGCTGAAAGCCCGGGAGTCTCTGAAGATCTCC 120
Db 21 ValGlnLeuValGlnSerGlyAlaGluValIleLeuProGlyGluSerLeuArgIleSer 40
QY 12* TGTAAAGGTTCTTGGATACAGCTTTTACCGGCTACTGGATCGGCTGGTGGCGCAGATGCC 180

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Db 41 CyLySgLySerGlyTyrSerPheThrSerTyrTTPileSerTTPValArgInMetPro 60
QY 181 GGAAGAGGCTGGAGTGGATGGGATCATCTATCTCTGGTGGTACTCTGATACCATACAGC 240
Db 61 GlyLySgLyLeuGlnTyrMetGlyArgLeuAppProSerAlaSerSerAlaIlePheSer 80
QY 241 CGTCTCTTCAAGGCCAGGTCACCATCTCAGCCGCAAGTCCATCAGCAGCCGCTTACCTG 300
Db 81 ProSerLeuGlnGlyHisValThrIleSerValAspLysSerMetArgThrAlaTyrVal 100
QY 301 CAGTGGAGGAGCTGAAGCCCTCGGACACCCGCTATGTTACTGTGCGAGAGACCAAA--- 357
Db 101 GlnTyrArgSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgHisValArg 120
QY 358 -----CTGGGCGCTCTTTGACTACTGGGCGCAGGGA 387
Db 121 GluLysSerMetValGlnGlyValIleIleLysAlaPheAspIleTTPGlyGlnGly 140
QY 388 ACCCTGGTCAACGCTCTCTCTCA 408
Db 141 ThrMetValThrValSerSer 147

RESULT 6
US-08-468-671-8
; Sequence 8, Application US/08468671
; Patent No. 5648077
; GENERAL INFORMATION:
; APPLICANT: Ostberg, Lars G.
; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,671
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/259,372
; FILING DATE: 14-JUN-1994
; APPLICATION NUMBER: US 07/871,426
; FILING DATE: 21-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,036
; FILING DATE: 27-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/538,796
; FILING DATE: 15-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/192,754
; FILING DATE: 11-MAY-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/925,196
; FILING DATE: 31-OCT-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/904,517
; FILING DATE: 05-SEP-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-50-7
; TELECOMMUNICATION INFORMATION:

```


Db 190 SerProSerPheGlnGlyValThrIleSerValAspLysSerValSerThrAlaTyr 209
QY 298 CTGAGTGGAGCAGCTGAAGCCCTCGGACACCGCATGTATTCTGCGAGAGACCAA 357
Db 210 LeuGlnTrpSerSerLeuLysProSerAspAlaValTyrPheCysAlaArgHisAsp 229
QY 358 CTGGGC-----CTCTTTGACTACTGGGGC 381
Db 230 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGluTyrPheGlnHisTrpGly 249
QY 382 CAGGGAACCTGGTCAACCTCTCCCTCAGCCTCCACC 417
Db 250 GlnGlyThrLeuValThrValSerSerAsnLysThr 261

RESULT 10

US-08-665-202-32
; Sequence 32, Application US/08665202
; Patent No. 5977322

GENERAL INFORMATION:

; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/665,202

; FILING DATE: 13-JUN-1996

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/000,238

; FILING DATE: 14-JUN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/000,250

; FILING DATE: 15-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Hunter, Tom

; REGISTRATION NUMBER: 38,498

; REFERENCE/DOCKET NUMBER: 02307E-061410

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 129 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-665-202-32

Alignment Scores:

Pred. No.: 2,08e-43 Length: 129
Score: 520.00 Matches: 97
Percent Similarity: 83.72% Conservative: 11
Best Local Similarity: 75.19% Mismatches: 9
Query Match: 61.47% Indels: 12
DB: 2 Gaps: 1

US-08-728-463b-207 (1-462) x US-08-665-202-32 (1-129)

QY 58 GAGGTGCAGCTGGTGCAGTCTGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTGAGATC 117

Db 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysLysProGlyGluSerLeuLysIle 20
QY 118 TCCTGTAAGGGTCTTGATACAGCTTTTACCGGCTACTGGATCGGTGGTGGCCAGATG 177
Db 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
QY 178 CCCGGGAAGCGCTGGAGTGGATGGGATCATCTATCTCTGCTGACTCTGATACCATAC 237
Db 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
QY 238 AGCCCGTCTCTCCAGGCGCAGTCAACCATCTCAGCCGACCAAGTCCATCAGCACCAGCTAC 297
Db 61 SerProSerPheGlnGlyValThrIleSerValAspLysSerValSerThrAlaLys 80
QY 298 CTGAGTGGAGCAGCCTGAAGCCCTCGGACACCGCATGTATTCTGCGAGAGACCAA 357
Db 81 LeuGlnTrpSerSerLeuLysProSerAspAlaValTyrPheCysAlaArgHisAsp 100
QY 358 CTGGGC-----CTCTTTGACTACTGGGGC 381
Db 101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGluTyrPheGlnHisTrpGly 120
QY 382 CAGGGAACCTGGTCAACCTCTCCCTCA 408
Db 121 GlnGlyThrLeuValThrValSerSer 129

RESULT 11
US-08-665-202-33
; Sequence 33, Application US/08665202
; Patent No. 5977322

; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-665-202-33

Alignment Scores:

Pred. No.: 9,4e-43 Length: 98
Score: 513.00 Matches: 96
Percent Similarity: 97.96% Conservative: 0
Best Local Similarity: 97.96% Mismatches: 2
Query Match: 60.64% Indels: 0
DB: 2 Gaps: 0

US-08-728-463B-207 (1-462) x US-08-665-202-33 (1-98)

QY 58 GAGTGCAGCTGTGAGTCTGAGCAGAGGTGAAAAAGCCCGGGAGTCTCTGAAGATC 117
Db 1 GluValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysile 20
QY 118 TCCTGAAGGTTCTCGATACAGCTTTACCGCTACTGATCGCTGGTGGCCGAGATG 177
Db 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValArgGlnMet 40
QY 178 CCGGGAAGGCTGAGTGGATGGGATCATCTATCTCTGTGACTCTGTATACCATAC 237
Db 41 ProGlyLysGlyLeuGlnTrpMetGlyIleIleTyrProGlyAspSerAspThrArgTyr 60
QY 238 AGCCCGTCTCTCAAGGCGAGTCCACCATCTCAGCGGCAAGTCCATCAGCAGCCCTAC 297
Db 61 SerProSerPheGlnGlyValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80
QY 298 CTGCAGTGCAGAGCTGAAGGCTCGACACCGCCATGTATTACTGTGCGAGA 351
Db 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArg 98

RESULT 12

US-08-478-039-81

Sequence 81, Application US/08478039

Patent No. 5681722

GENERAL INFORMATION:

APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA

COUNTRY: USA

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/478,039

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/379,072

FILING DATE: 25-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/912,292

FILING DATE: 10-JUL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/856,281

FILING DATE: 23-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/735,064

FILING DATE: 25-JUL-1991

ATTORNEY/AGENT INFORMATION:

NAME: Teskin Esq., Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-160

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6620

TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 81:

SEQUENCE CHARACTERISTICS:

LENGTH: 98 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

POSITION IN GENOME:

CHROMOSOME/SEGMENT: VHS consensus

US-08-478-039-81

Alignment Scores:

Pred. No.: 2,92e-42 Length: 98
Score: 508.00 Matches: 95
Percent Similarity: 96.94% Conservative: 0
Best Local Similarity: 96.94% Mismatches: 3
Query Match: 60.05% Indels: 0
DB: 1 Gaps: 0

US-08-728-463B-207 (1-462) x US-08-478-039-81 (1-98)

QY 58 GAGTGCAGCTGTGAGTCTGAGCAGAGGTGAAAAAGCCCGGGAGTCTCTGAAGATC 117
Db 1 GluValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysile 20
QY 118 TCCTGAAGGTTCTCGATACAGCTTTACCGCTACTGATCGCTGGTGGCCGAGATG 177
Db 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValArgGlnMet 40
QY 178 CCGGGAAGGCTGAGTGGATGGGATCATCTATCTCTGTGACTCTGTATACCATAC 237
Db 41 ProGlyLysGlyLeuGlnTrpMetGlyIleIleTyrProGlyAspSerAspThrArgTyr 60
QY 238 AGCCCGTCTCTCAAGGCGAGTCCACCATCTCAGCGGCAAGTCCATCAGCAGCCCTAC 297
Db 61 SerProSerPheGlnGlyValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80
QY 298 CTGCAGTGCAGAGCTGAAGGCTCGACACCGCCATGTATTACTGTGCGAGA 351
Db 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArg 98

RESULT 13

US-08-476-349A-81

Sequence 81, Application US/08476349A

Patent No. 5750105

GENERAL INFORMATION:

APPLICANT: Newman, Roland A.

APPLICANT: Hanna, Nabil

APPLICANT: Raab, Ronald W.

TITLE OF INVENTION: Recombinant Antibodies for Human Therapy

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince St.

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/476,349A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/379,072
;; FILING DATE: 25-JAN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/912,292
;; FILING DATE: 10-JUL-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/856,281
;; FILING DATE: 23-MAR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/735,064
;; FILING DATE: 25-JUL-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Teskin Esq., Robin L.
;; REGISTRATION NUMBER: 35,030
;; REFERENCE/DOCKET NUMBER: 012712-161
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-836-6620
;; TELEFAX: 703-836-2021
;; INFORMATION FOR SEQ ID NO: 81:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 98 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: peptide
;; ORIGINAL SOURCE:
;; ORGANISM: Homo sapiens
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT: VH5 consensus
US-08-476-349A-81

Alignment Scores:
Pred. No.: 2,92e-42 Length: 98
Score: 508.00 Matches: 95
Percent Similarity: 96.94% Conservative: 0
Best Local Similarity: 96.94% Mismatches: 3
Query Match: 60.05% Indels: 0
DB: 1 Gaps: 0

US-08-728-463B-207 (1-462) x US-08-476-349A-81 (1-98)

QY 58 GAGGTGACGCTGTCAGTCTGGAGCAGAGGTGAAAGCCCGGGAGTCTCTGAAGATC 117
DB 1 GluValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIle 20
QY 118 TCCTGTAAGGGTCTCGATACAGCTTTACCGCTACTGCTGCTGGGTGGGCCAGATG 177
DB 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValargGlnMet 40
QY 178 CCCGGAAGGCTCGAGTGGATGGGATCATCTATCTGTGACTCTGATACCATAC 237
DB 41 ProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSerAspThrargTyr 60
QY 238 ACCCGTCTCTCCAGGCCAGGTACCATCTCAGCCGACAAAGTCATCAGCCGCTAC 297
DB 61 SerProSerPheGlnGlyHisValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80
QY 298 CTGCACTGAGCAGCTGAAGGCTCGGACCGCCATCTATTACTGTCCGAGA 351
DB 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaarg 98

RESULT 14

US-08-665-202-44
; Sequence 44, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, Eighth Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94111-3834
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/665,202
;; FILING DATE: 13-JUN-1996
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/000,238
;; FILING DATE: 14-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/000,250
;; FILING DATE: 15-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hunter, Tom
;; REGISTRATION NUMBER: 38,498
;; REFERENCE/DOCKET NUMBER: 02307E-061410
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 44:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 125 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-665-202-44

Alignment Scores:
Pred. No.: 9,7e-42 Length: 125
Score: 503.00 Matches: 93
Percent Similarity: 83.20% Conservative: 11
Best Local Similarity: 74.40% Mismatches: 9
Query Match: 59.46% Indels: 12
DB: 2 Gaps: 1

US-08-728-463B-207 (1-462) x US-08-665-202-44 (1-125)

QY 58 GAGGTGACGCTGTCAGTCTGGAGCAGAGGTGAAAGCCCGGGAGTCTCTGAAGATC 117
DB 1 GluValGlnLeuLeuGlnSerGlyAlaGluLeuLysLysProGlyGluSerLeuLysIle 20
QY 118 TCCTGTAAGGGTCTCGATACAGCTTTACCGCTACTGCTGCTGGGTGGGCCAGATG 177
DB 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValargGlnMet 40
QY 178 CCCGGAAGGCTCGAGTGGATGGGATCATCTATCTGTGACTCTGATACCATAC 237
DB 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
QY 238 ACCCGTCTCTCCAGGCCAGGTACCATCTCAGCCGACAAAGTCATCAGCCGCTAC 297
DB 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
QY 298 CTGCACTGAGCAGCTGAAGGCTCGGACCGCCATCTATTACTGTCCGAGAGACCAA 357
DB 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaargHisAsp 100
QY 358 CTGGGC-----CTCTTGTACTACTGGGC 381
DB 101 ValGlyTyrCysSerSerSerAsnCysAlaLysTyrProGluTyrPheGlnHisTyrGly 120
QY 382 CAGGGAACCTGGTC 396

Db 121 GlnGlyThrLeuVal 125

RESULT 15
US-08-665-202-53
; Sequence 53, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 125 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-53

Alignment Scores:
Pred. No.: 1.53e-41 Length: 125
Score: 501.00 Matches: 94
Percent Similarity: 82.40% Conservative: 9
Best Local Similarity: 75.20% Mismatches: 10
Query Match: 59.22% Indels: 12
DB: 2 Gaps: 1

US-08-728-463b-207 (1-462) x US-08-665-202-53 (1-125)

QY 58 GAGTGCAGCTGCTGAGTCTGGAGCAGAGTGAAGCCCGGGAGTCTCTGAAGATC 117
Db 1 GlnValGlnLeuValGlnSerGlyGlyGluMetLysLysProGlyGluSerLeuLysile 20
QY 118 TCCTGTAAAGGGTCTCGATACAGCTTTACCGGCTACTGGATCGGCTGGTGGCCAGATG 177
Db 21 SerCysLysGlyLeuGlyTyrAspPheSerThrTyrTrpIlealaTrpValArgGlnMet 40
QY 178 CCGGGAAAGGCTGGAGTGGATGGGATCATCTATCTGTGACTCTGTATACCATAC 237
Db 41 ProGlyLysGlyLeuGlyTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
QY 248 AGCCCGCTCTTCCAAAGGCGAGTCCACCATCTCAGCGGACAAAGTCCATCAGCAGCCGCTAC 297

Db 61 SerProSerPheGlnGlyGlnValThrIleSerAlaAspGluSerIleSerThrAlaTyr 80
QY 298 CTGCAGTGGAGCAGCCTGAGGCTCGGACACCGCCATGTATTACTGTCCGAGACACCAA 357
Db 81 LeuGluTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgHisApp 100
QY 358 CTGGGC-----CTCTTTGACTACTGGGC 381
Db 101 ValGlyTyrCysSerSerSerAanCysAlaLysTrpProGluTyrPheGlnHisTrpGly 120
QY 382 CAGGGAACCTGGTC 396
Db 121 GlnGlyThrLeuVal 125

Search completed: June 3, 2003, 09:47:28
Job time : 13.5159 secs

A:Molecule type: mRNA

A:Residues: 1-132 <KLE>

A:Cross-references: EMBL:X72444

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:37-111/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	2,7e-44	Length:	132
Score:	577.00	Matches:	110
Percent Similarity:	92.42%	Conservative:	12
Best Local Similarity:	83.33%	Mismatches:	10
Query Match:	72.95%	Indels:	0
DB:	2	Gaps:	0

US-08-728-463B-208 (1-439) x S40334 (1-132)

```

QY 4 GACATGGAGTTCCTCCGCTCAGCTCCTGGGCTCCTGCTCTGTTTCCAGGTGCCAGA 63
Db 1 AspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpLeuProGlyAlaArg 20

QY 64 TGTGATCCAGATGACCCAGTCTCCATCTCAGTCTGTCATCTGTAGGAGACAGATC 123
Db 21 CysAspIleGlnLeuThrGlnSerProSerPheLeuSerAlaSerIleGlyAspArgVal 40

QY 124 ACATCACTTGTCCGGCAGTCAGGTATTAGCAGCTGTTAGCTGTATCAGCAGAAA 183
Db 41 ThrIleThrCysArgAlaSerGlnGlyIleAsnSerTyLeuAlaTrpTyGlnGlnLys 60

QY 184 CCAGAGAAGCCCTCAAGTCCCTGATCTATTCTGCATCCAGTTGCAAGTGGGTCCA 243
Db 61 ProGlyLysAlaProLysLeuLeuIleTyValAlaSerThrLeuGlnSerGlyValPro 80

QY 244 TCAAGTTTCAGCGCAGTGGATCTGGGACAGATTTTCATCTCACCATCAGCAGCTGCAG 303
Db 81 SerArgPheSerGlySerGlyThrGluPheThrLeuThrIleSerSerLeuGln 100

QY 304 CTGGAAGATTTTGCATTTATTACTGCGCAACAGTAGTAGTATACCGTACACTTTTGGC 363
Db 101 ProGluAspPheAlaSerTyTyCysGlnGlnPheAsnSerTyProPheThrPheGly 120

QY 364 CAGGGGACCAAGCTGAGATCAACGAACTGTGGCT 399
Db 121 GlyGlyThrLysValGluIleArgThrValAla 132

```

RESULT 5

S40333

Ig kappa chain V-J region - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40333

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40333

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-125 <KLE>

A:Cross-references: EMBL:X72443; NID:9441354; PIDN:CAA51111.1; PID:9441355

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-108/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	4.13e-44	Length:	125
Score:	575.00	Matches:	109
Percent Similarity:	94.35%	Conservative:	8
Best Local Similarity:	87.90%	Mismatches:	7
Query Match:	72.69%	Indels:	0
DB:	2	Gaps:	0

US-08-728-463B-208 (1-439) x S40333 (1-125)

```

QY 16 CCCGTTAGCTCCTCGGGCTCCTGCTGCTCTGTTTCCAGGTGCCAGATGTCATCCAG 75
Db 2 ProAlaGlnLeuLeuGlyLeuLeuLeuTrpLeuProGlyAlaLysCysAspIleGln 21

QY 76 ATGACCCAGTCTCCATCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 135
Db 22 MetThrGlnSerProSerThrLeuSerAlaSerValGlyAspArgValThrIleThrCys 41

QY 136 CGGCGAGCTCAGGCTATTAGCAGCTGGTTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 195
Db 42 ArgAlaSerGlnSerIleSerSerTrpLeuAlaTrpTyGlnGlnLysProGlyLysAla 61

QY 196 CTTAAGTCCCTGATCTATTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 255
Db 62 ProLysLeuLeuIleTyLysAlaSerSerLeuGluSerGlyValProSerArgPheSer 81

QY 256 GGCAGTGTGATCTGGGACAGATTCTACTCTCACCATCAGCAGCTCAGCTGCAAGATTTT 315
Db 82 GlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeuGlnProAspPhe 101

QY 316 GCACTTATTACTGCCAACAGTATGATAGTTACCCGTACACTTTTGGCCAGGGACCAAG 375
Db 102 AlaThrTyTyCysGlnGlnTyAsnSerTyProTrpThrPheGlyGlnGlyThrLys 121

QY 376 CTGGAGATCAAA 387
Db 122 ValGluIleLys 125

```

RESULT 6

KIHU11

Ig kappa chain precursor V-I region (HK101) - human

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1981 #sequence_revision 31-Mar-1981 #text_change 24-Sep-1999

C:Accession: A01881; A21056

R:Bentley, D.L.; Rabbitts, T.H.

Nature 288, 730-733, 1980

A:Title: Human immunoglobulin variable region genes - DNA sequences of two V-kappa gene.

A:Reference number: A33241; MUID:81098966; PMID:6779204

A:Accession: A01881

A:Molecule type: DNA

A:Residues: 1-117 <BEN1>

A:Cross-references: GB:V00558; GB:J00244; GB:J00246; NID:933176; PIDN:CAA23824.1; PID:933176

A>Note: the sequence was determined from the germline gene

R:Bentley, D.L.; Rabbitts, T.H.

Cell 32, 181-189, 1983

A:Title: Evolution of immunoglobulin V genes: evidence indicating that recently duplicated

A:Reference number: A21056; MUID:83129397; PMID:6402305

A:Accession: A21056

A:Molecule type: DNA

A:Residues: 1-117 <BEN2>

A:Cross-references: GB:K01322; NID:9185993; PIDN:AAA58930.1; PID:9185994

C:Genetics:

A:Gene: GDB:IGKV1

A:Cross-references: GDB:J36264

A:Map position: 2p12-2p12

A:Introns: 19/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka)

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1-

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-117/Product: Ig kappa chain V-I region (HK101) #status predicted <MAT>

F:38-112/Domain: immunoglobulin homology <IMM>

F:45-110/Disulfide bonds: #status predicted

Alignment Scores:

Pred. No.:	6.32e-44	Length:	117
Score:	573.00	Matches:	110
Percent Similarity:	95.73%	Conservative:	2
Best Local Similarity:	94.02%	Mismatches:	5
Query Match:	72.44%	Indels:	0
DB:	1	Gaps:	0

US-08-728-463B-208 (1-439) x KIHU11 (1-117)

QY 1 ATGGACATCGAGTTCCTCCGTTCCAGCTCCTGGGCTCTGTCTGCTCTGTCTTCCAGGTGCC 60
Db |||||MetArgValLeuAlaGlnLeuLeuGlyLeuLeuLeuCysPheProGlyAla 20

QY 61 AGATGTGACATCCAGATGACCAGTCTCCACTCTCATCTGTGCATCTGTAGGAGACAGA 120
Db |||||AArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArg 40

QY 121 GTCACCATCACATTGTCGGCGAGTCNAGGTTATTAGCAGCTGGTAGCTGGTATCACGAG 180
Db |||||ValThrIleThrCysArgAlaArgGlnGlyIleSerSerTrpLeuAlaTrpTyrgInGln 60

QY 181 AAACAGAGAAAGCCCCTTAAGTCCCTGATCTATTCTGCATCCAGTTCGAAGTGGGTC 240
Db |||||LysProGluLysAlaProLysSerLeuIleTyralaalaSerSerLeuGlnSerGlyVal 80

QY 241 CCATCAAGGTCACGGGAGTGATCTGGGACAGATTCTCACTCTCACCATCAGCCTG 300
Db |||||ProSerArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100

QY 301 CAGCCTGAAGATTTGCAACTTATTACTGCAACAGTATCATAGTTACCG 351
Db |||||GlnProGluAspPheAlaThrTy-Tyr-CysGlnGlnTyrsnSertYrPro 117

RESULT 7
S40368
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
R:Accession: S40368
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40368
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-130 <KLE>
A:Cross-references: EMBL:X72478
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:33-107/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 3.3e-43 Length: 130
Score: 565.00 Matches: 108
Percent Similarity: 90.77% Conservative: 10
Best Local Similarity: 83.08% Mismatches: 12
Query Match: 71.43% Indels: 0
DB: 2 Gaps: 0

US-08-728-463B-208 (1-439) x S40368 (1-130)

QY 16 CCGGTCAGCTCTGGGCTCTGCT 75
Db |||||ProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpPheProGlySerArgCysAspIleGln 20

QY 76 ATGACCCAGTCTCCATCTCACTGCTGCATCTGTAGGAGACAGATCACCATCACATTGT 135
Db |||||MetThrGlnSerProSerSerValSerAlaSerValGlyAspArgValIleIleThrCys 40

QY 136 CGGGCGAGTCAGGGTATTAGCAGCTGGTAGCTGTATTCAGCAGAAACCCAGAAAGCC 195
Db |||||ArgAlaSerGlnAspValAlaGlyTrpLeuAlaTrpTyrgInGlnLysProGlyAlaAla 60

QY 196 CTAGTCCCTGATCTATTCTGCATCCAGTTCGAAGTGGGTCCTCCATCAAGGTTCCAGC 255
Db |||||ProLysLeuLeuIleTyraalaSerSerLeuGlnSerGluValProProArgPheSer 80

QY 256 GSCAGTGGATCTGGACAGATTTCACTCTACCATCAGCAGCTTCGACGCTGAAGATTTT 315

US-08-728-463B-208 (1-439) x S40316 (1-125)

QY 22 CAGCTCTCTGGGCTCTGCTGCTCTGTTTCCAGGTGCCAGATGTGATCCAGATGACC 81
Db |||||GlnLeuLeuGlyLeuLeuLeuLeuTrpPheProGlySerArgCysAspIleGlnLeuThr 20

QY 82 CAGTCTCCATCTCACTCTGTCATCTGTAGGACAGAGTCACCATCACTTGTGGCGC 141
Db |||||GlnSerProSerSerValSerAlaSerValGlyAspArgValThrIleThrCysArgAla 40

QY 142 AGTCAGGCTATTAGCAGCTGGTAGCTGGTATCAGCAGAACCCAGAGAAGCCCCCTAAG 201
Db |||||SerGlnGlyIleSerSerTrpLeuAlaTrpTyrgInGlnLysProGlyLysAlaProAsn 60

QY 202 TCCCTGATCTATTCTGCATCCAGTTCGAAAGTGGGTCCCATCAAGGTTCCAGCGCAGT 261
Db |||||LeuLeuIleTyrielleSerSerLeuGlnThrGlyValProSerArgPheSerGlySer 80

QY 262 GSATCTGGAGCAGATTTCATCTCACCATCAGCAGCTCGAGCCTGAAGATTTTGAACCT 321
Db |||||GlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPheAlaIle 100

QY 322 TATTACTGCCAACAGTATGATGATTTACCCGTACACTTTTGGCCAGGGGACCAAGCTGGAG 381
Db |||||TyrTyrcysGlnGlnAlaAspSerPheProLeuThrPheGlyGlyThrLysValGlu 120

QY 382 ATCAAACGNACTGG 396
Db |||||IleLysargthrVal 125

RESULT 9
S38646
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995#text change 21-Jan-2000

C:Accession: S38646
 R:Bensimon, C.; Chastagner, P.; Zouali, M.
 submitted to the EMBL Data Library, November 1993
 A:Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.
 A:Reference number: S38643
 A:Accession: S38646
 A>Status: preliminary
 A:Molecule type: mRNA

A:Residues: 1-132 <BEN>
 A:Cross-references: EMBL:227173; NID:g415961; PIDN:CAA81697.1; PID:g415962
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:40-114/Domain: immunoglobulin homology <IMM>

Alignment Scores:
 Pred. No.: 9.32e-43 Length: 132
 Score: 560.00 Matches: 110
 Percent Similarity: 89.23% Conservative: 6
 Best Local Similarity: 84.62% Mismatches: 14
 Query Match: 70.80% Indels: 0
 DB: 2 Gaps: 0

US-08-728-463B-208 (1-439) x S38646 (1-132)

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QY 1 ATGGACATGAGTTCCTCCCTTCAGCTCTCGGGCTCCTGCTCTGTTTCCAGGTGCC 60
DB 3 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuProGlyAla 22
QY 61 AGATGTGACATCCAGATACCCAGTCTCCATCTCACTCTGTCATCTGTAGGAGACAGA 120
DB 23 ArgCysAlaIleArgIleAlaGlnSerProSerLeuSerAlaSerThrGlyAspArg 42
QY 121 GTCACCATCACTGTGGCGAGTCAGGGTATTAGCAGCTGTTAGCCCTGTTATCAGCAG 180
DB 43 ValThrIleThrCysArgAlaSerGlnGlyIleSerSerTyLeuAlaTrpTyrglnGln 62
QY 181 AAACAGAGAAAGCCCTAAGTCCCTGATCTTCTGCAATCCAGTTTGCAGAGTGGGTC 240
DB 63 LysProGlyLysAlaProLysLeuLeuIleTyAlaAlaSerThrLeuGlnSerGlyVal 82
QY 241 CCATCAAGTTCAGCGGAGTCGATCTGGCAGACAGATTTCACTCTCACCATCAGCAGCTG 300
DB 83 ProSerArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerCysLeu 102
QY 301 CAGCCCTGAAGATTTTGCAACTATTACTCCCAACAGATGATGATGATGATGATGATGAT 360
DB 103 GlnSerGluAspPheAlaThrTyrcysGlnGlnTyrcysGlnGlnTyrcysGlnGln 122
QY 361 GCCCAGGGACCAAGCTGGAGATCAACGA 390
DB 123 GlyGlnGlyThrLysValGluIleLysArg 132

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RESULT 10

S40349
 Ig kappa chain V-J region - human
 C:Species: Homo sapiens (man)
 C>Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
 C:Accession: S40349
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A:Reference number: S40312; MUID:94080891; PMID:8258341
 A:Accession: S40349
 A>Status: preliminary; translation not shown
 A:Molecule type: mRNA

A:Residues: 1-125 <KLE>
 A:Cross-references: EMBL:X72459; NID:g441386; PIDN:CAA51127.1; PID:g441387
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:33-107/Domain: immunoglobulin homology <IMM>

Alignment Scores:
 Pred. No.: 1.75e-42 Length: 125

Score: 557.00 Matches: 109
 Percent Similarity: 92.00% Conservative: 6
 Best Local Similarity: 87.20% Mismatches: 10
 Query Match: 70.42% Indels: 0
 DB: 2 Gaps: 0

US-08-728-463B-208 (1-439) x S40349 (1-125)

```

QY 16 CCCGTTACGTCCTGGGGCTCCTGCTCTGTTTCCAGGTGCCAGATGACATCCAG 75
DB 1 ProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuProGlyAlaArgCysAlaIleGln 20
QY 76 ATGACCCAGTCTCCATCTCCTGCTCTGCACTCTGTAGGAGACAGAGTACCACATCTGT 135
DB 21 LeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThrCys 40
QY 136 CGGCGAGTCAGGGTATTAGCAGCTGGTTAGCTGGTATCAGCAAAACACAGAAAGCC 195
DB 41 ArgAlaSerGlnGlyIleSerSerAlaLeuAlaTrpTyrglnGlnLysProGlyLysAla 60
QY 196 CTTAAGTCCCTGATCTATTCTGCACTCCAGTTTGCAAGTGGGGTCCCATCAAGGTTACAG 255
DB 61 ProlysLeuLeuIleTyrcysGlnGlnPheAsnThrTyrcysGlnGlnValProSerArgPheSer 80
QY 256 GGCAGTGCATCTGGGAGACAGATTCTCTCACCATCAGCAGCTGCAGCTGCAAGATTTT 315
DB 81 GlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPhe 100
QY 316 GCAACTTATTACTGCAACAGTATGATAGTTACCGGTACACTTTTGGCCAGGGGACCAAG 375
DB 101 AlaThrTyrcysGlnGlnPheAsnThrTyrcysGlnGlnValProSerArgPheSer 120
QY 376 CTGGAGATCAACGA 390
DB 121 ValGluIleLysArg 125

```

RESULT 11

C21056
 Ig kappa chain precursor V region (HK137) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 21-Jan-2000
 C:Accession: C21056
 R:Bentley, D.L.; Rabbitts, T.H.
 Cell 32, 181-189, 1983
 A:Title: Evolution of immunoglobulin V genes: evidence indicating that recently duplicated
 A:Reference number: A21056; MUID:83129397; PMID:6402305
 A:Accession: C21056
 A>Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-117 <BEN>
 A:Cross-references: GB:J00248; NID:g185991; PIDN:AAA59094.1; PID:g185992
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:38-112/Domain: immunoglobulin homology <IMM>

Alignment Scores:
 Pred. No.: 2.68e-42 Length: 117
 Score: 555.00 Matches: 107
 Percent Similarity: 95.73% Conservative: 5
 Best Local Similarity: 91.45% Mismatches: 5
 Query Match: 70.16% Indels: 0
 DB: 2 Gaps: 0

US-08-728-463B-208 (1-439) x C21056 (1-117)

```

QY 1 ATGGACATGAGTTCCTCCCTTCAGCTCTCGGGCTCCTGCTCTGTTTCCAGGTGCC 60
DB 1 MetAspMetArgValLeuAlaGlnLeuLeuGlyLeuLeuLeuLeuCysPheProGlyAla 20
QY 61 AGATGTGACATCCAGATACCCAGTCTCCATCTCCTCAGTCTGTCATCTGTAGGAGACAGA 120
DB 21 ArgCysAspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArg 40

```

QY	121	GTCA	CCATCA	CTTCTCGGCGG	CAGTCAGG	TATTAG	CAGCTGGT	TAGCTGTAT	CAGCAG	180
Db	41	Vai	Thr	Ile	Thr	Cys	A	G	A	180
QY	181	AAAC	CA	GAG	AAAGCCCT	TA	GTCCCT	GATCTAT	TCTGC	240
Db	61	Lys	Pro	Gly	lys	Ala	Pro	Lys	Ser	240
QY	241	CCAT	CAAG	TTCTAG	CGCGCAG	TGGAT	CTGG	ACACAG	ATTTTCA	300
Db	81	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	300
QY	301	CAGC	CTG	AGAT	TTTGC	AACTTAT	TACTG	CCAA	CAGTAT	351
Db	101	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	351

```

RESULT 12
S46372
IG light chain variable region (VJ) - human
C:Species: Homo sapiens (man)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S46372
R:Bensimon, C.; Chastagner, P.; Zouali, M.
A:EMBO J. 13, 2951-2962, 1994
A>Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re-
A:Accession: S46369, MUID:94313975; PMID:8039491
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-128 <BEN>
A:Cross-references: EMBL:Z27173
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:336-110/Domain: immunoglobulin homology <IMM>

```

Alignment Scores:	
Align. No.:	
Score:	3.269-42
Percent Similarity:	554.00
Percent Local Similarity:	89.84%
Query Match:	85.16%
DB:	70.04%
	2
Length:	128
Matches:	109
Conservative:	6
Mismatches:	13
Indels:	0
Gaps:	0
US-08-728-463B-208 (1-433) x S46372 (1-128)	

7 ATGAGTGTCCCGCTTCAGCTCCTGGGGCTCTGCTGCTCTGTTCCTCCAGGTGCAGAGTG 66
| | | | |
1 MetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuProGlyAlaArgCys 20
| | | | |
67 GACATCCAGATGACCCAGTCTCCATCTCTCACTGTCTGATCTGTAGGAGACAGAGTCCACC 126
| : : : : :
21 AlaIleArgIleThrGlnSerProSerLeuSerAlaSerThrGlyAspArgValThr 40
| | | | |
127 ATCATTTGTCCGGCGACTCAGGTATTAGCACGTGGTTAGCCTGATATCAGCAAACCA 186
| : : : : :
41 IleThrCysArgAlaSerGlnGlyIleSerSerThrLeuAlaTrpTyrlGlnGlnLysPro 60
| | | | |
187 GAGAAACCCCCTAAGTCCCTCATCTATTCTGCATCCAGTTGCCAAAGTGGGTCCCCATCA 246
| : : : : :
61 GlyLysAlaProLysLeuLeuIleTyrAlaAlaSerThrLeuGlnSerGlyValProSer 80
| | | | |
247 AGGTTTCAGCGGCAGTGATCTGGACAGATTCTCACTCTCACATCAGCAGCCCTGCACGCT 306
| | | | |
81 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerCysLeuGlnSer 100
| | | | |
307 GAAGATTTTGCCAATTATTACTGCCAACAGTATGATAGTTTACCCGTACACTTTTGGCCAG 366
| | | | |
101 GluAspPheAlaThrTyrTyrCysGlnGlnTyrTyrrSerTyrProArgThrPheGlyGln 120
| | | | |
367 GGGACCAAGCTGGAGATCAACGA 390
| | | : : : | | | | |
121 GlyThrLysValGluIleLysArg 128

Ig kappa c
C;Species:

R; Klein, J. Im
Eur. J. Im
A: Title: E

A;Status:
A;Molecule

Keywords: 36-110/D

ered. No.:
Score:
Percent sin

B:

9

9

9

2

3

30

0367 . kappa cha

Accession:
Klein, R.;

Accession: pr
Status: pr

Cross-referenced
Superfamily

Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)

Kirklein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin

A; Status: preliminary; translation not shown
Molecule type: mRNA

Keywords: immunoglobulin V region; immunoglobulin homology; heterotetramer; immunoglobulin; 36-110/Domain; immunoglobulin homology <IMM>

red. No.:	6.08e-42	Length:	131
core:	551.00	Matches:	107
percent	90.00		
Similarity:			

В: 2
Гарс: 0

[illegible]

b

21 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAsnArgValThr 40

41 IleThrCysArgAlaSerGlnGlnGlyIleSerAsnTyrLeuAlaTrpTyrGlnGlnLysPro 60

[illegible]

307 GAAGATTTTGGAACTTATTACTGCCAACAGTATGATAGTTACCCCGTACACTTTTGGCCAG 366

367 GGGACCAAGCTGGAGATCAAACGAACTGTG 396

0367
SOMI 14
kappa chain V-J-C region - human

Accession: S40367
Klein, R.; Jaenichen, R.; Zachau, H.G.

Accession: S40367
Status: preliminary; translation not shown
MW: 10000; MD: 10000; MWID: 8238341

Superfamily: immunoglobulin V region; immunoglobulin homology

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C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 7,52e-42 Length: 127
Score: 550.00 Matches: 109
Percent Similarity: 91.34% Conservative: 7
Best Local Similarity: 85.83% Mismatches: 11
Query Match: 69.53% Indels: 0
DB: 2 Gaps: 0

US-08-728-463B-208 (1-439) x S40367 (1-127)

```

QY 16 CCAGTTCAGCTCTCTGGGCTCTGCTCTGTTCCAGGTGCCAGATGTGACATCCAG 75
Db 1 ProAlaGlnLeuLeuGlyLeuLeuLeuTrpLeuArgGlyAlaArgCysAspIleGln 20
QY 76 ATGACCCAGTCTCCATCTCTGCTCTGCTCTGTTAGGAGACAGATCCATCCTGTT 135
Db 21 MetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThrCys 40
QY 136 CGGCGAGTCAAGGTATTAGCAGCTGTTAGCCTGTTAGCCTGATCAGCAAAACAGAGAACGCC 195
Db 41 ArgAlaSerGlnSerIleSerAsnTyrLeuAsnTrpTyrGlnArgLysProGlyLysAla 60
QY 196 CTAAGTCCCTGATCTATTCTGTCATCCAGTTCGATTTGCAAGTGGGTCCCATCAAGTTTCAGC 255
Db 61 ProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgPheSer 80
QY 256 GGCAGTGCATCTGGAGCAGATTCTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTC 315
Db 81 GlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPhe 100
QY 316 GCAACTTATTACTGCCAACAGTAGTAGTTACCCGTACACTTTTGGCCAGGGGACCAAG 375
Db 101 AlaThrTyrTyrCysGlnGlnSerTyrAsnThrProTrpThrPheGlyGlnGlyThrLys 120
QY 376 CTGAGATCAACGAACTGTG 396
Db 121 ValGluIleLysArgThrVal 127

```

RESULT 15

S40353
Ig kappa chain V-J-C region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40353
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40353
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-125 <MLE>
A;Cross-references: EMBL:X72463
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;30-104/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 1.14e-41 Length: 125
Score: 548.00 Matches: 107
Percent Similarity: 91.20% Conservative: 7
Best Local Similarity: 85.60% Mismatches: 11
Query Match: 69.28% Indels: 0
DB: 2 Gaps: 0

US-08-728-463B-208 (1-439) x S40353 (1-125)

```

QY 25 CTCCTGGGCTCTGCTCTGTTCCAGGTGCCAGATGTGACATCCAGATGACCCAG 84
Db 1 LeuLeuGlyLeuLeuLeuTrpPheProGlyAlaArgCysAspIleGlnMetThrGln 20

```

```

QY 85 TCTCCATCTCTCACTGCTCTGATCTGTAGGAGACAGATCACCATCACTTGTGGGCGAGT 144
Db 21 SerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAlaSer 40
QY 145 CAGGGTATTAGCAGCTGGTTAGCCTGTTAGCCTGATCAGCAGAAACAGAGAAAGCCCTAAGTCC 204
Db 41 GlnGlyIleGlyAsnAspLeuGlyTrpTyrGlnGlnLysProGlyLysAlaProLysArg 60
QY 205 CTGATCTATTCTGCATCCAGTTTCAAAAGTGGGTCCCATCAAGGTTTCAGCGGCGAGTGA 264
Db 61 LeuIleTyrAlaAlaSerSerPheGlnSerGlyValProSerArgPheSerGlySerGly 80
QY 265 TCTGGGACAGATTCTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCACATTAT 324
Db 81 SerGlyThrGluPheThrLeuThrIleSerGlyLeuGlnProGluAspPheAlaThrTyr 100
QY 325 TACTGCCAACAGTAGTAGTTACCCGTACACTTTTGGCCAGGGGACCAAGCTGGAGATC 384
Db 101 TyrCysLeuGlnHisAsnSerTyrProLeuThrPheGlyGlyThrArgValGluIle 120
QY 385 AAACGAACTGTGGCT 399
Db 121 LysArgThrValAla 125

```

Search completed: June 3, 2003, 09:07:57
Job time : 20.5692 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 8.32701 Seconds

(without alignments)
4373.264 Million cell updates/sec

Title: US-08-728-463B-208

Perfect score: 791

Sequence: 1 ATGCACATGGAGTTCCTCCGTT.....CCCGCCATCTCATGAAGCTT 439

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 225784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USPTO spo01/US08728463/runat 03062003 085614 16804/app query.fasta 1.3690
-DB=SwissProt 40 -OPMT=fastan -SUFFIX=rep -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=bloms62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08728463 @CGN 1.1 76 @runat 03062003 085614 16804 -NCPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOF=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	573	72.4	117	1 KVI1 HUMAN	P01601 homo sapien
2	529	66.9	129	1 KVI1 HUMAN	P04431 homo sapien
3	528	66.8	117	1 KVI1 HUMAN	P01602 homo sapien
4	489	61.8	108	1 KVI1 HUMAN	P01604 homo sapien
5	487	61.6	108	1 KVI1 HUMAN	P04430 homo sapien
6	486	61.4	129	1 KVI1 HUMAN	P04432 homo sapien
7	476	60.2	108	1 KVI1 HUMAN	P01610 homo sapien
8	470.5	59.5	107	1 KVI1 HUMAN	P01596 homo sapien
9	468	59.2	108	1 KVI1 HUMAN	P01599 homo sapien
10	465	58.8	108	1 KVI1 HUMAN	P01600 homo sapien
11	465	58.8	128	1 KVI1 HUMAN	P01637 mus musculu
12	463	58.5	108	1 KVI1 HUMAN	P01598 homo sapien
13	460	58.2	108	1 KVI1 HUMAN	P01594 homo sapien
14	460	58.2	108	1 KVI1 HUMAN	P01607 homo sapien
15	460	58.2	108	1 KVI1 HUMAN	P01611 homo sapien
16	457	57.8	108	1 KVI1 HUMAN	P01593 homo sapien
17	454	57.4	130	1 KVI1 HUMAN	P01639 mus musculu
18	449	56.8	108	1 KVI1 HUMAN	P01605 homo sapien

19	448	56.6	108	1 KVI1 HUMAN	P01608 homo sapien
20	448	56.6	108	1 KVI1 HUMAN	P03162 homo sapien
21	445	56.3	108	1 KVI1 HUMAN	P01595 homo sapien
22	442.5	55.9	129	1 KVI1 HUMAN	P18136 homo sapien
23	441.5	55.8	129	1 KVI1 HUMAN	P18135 homo sapien
24	441	55.8	108	1 KVI1 HUMAN	P01597 homo sapien
25	441	55.8	108	1 KVI1 HUMAN	P01606 homo sapien
26	438	55.4	108	1 KVI1 HUMAN	P01603 homo sapien
27	433	54.7	108	1 KVI1 HUMAN	P01609 homo sapien
28	428.5	54.2	129	1 KVI1 HUMAN	P04207 homo sapien
29	426	53.9	128	1 KVI1 HUMAN	P06311 homo sapien
30	417	52.7	115	1 KVI1 HUMAN	P01638 mus musculu
31	413	52.2	112	1 KVI1 HUMAN	P01613 homo sapien
32	409	51.7	108	1 KVI1 HUMAN	P01643 mus musculu
33	409	51.7	134	1 KVI1 HUMAN	P06314 homo sapien
34	408.5	51.6	109	1 KVI1 HUMAN	P01612 homo sapien
35	402	50.8	136	1 KVI1 HUMAN	P01634 mus musculu
36	399	50.4	108	1 KVI1 HUMAN	P01636 mus musculu
37	399	50.4	108	1 KVI1 HUMAN	P01644 mus musculu
38	399	50.4	108	1 KVI1 HUMAN	P01652 mus musculu
39	398.5	50.4	109	1 KVI1 HUMAN	P01622 homo sapien
40	398	50.3	114	1 KVI1 HUMAN	P01625 homo sapien
41	397.5	50.3	133	1 KVI1 HUMAN	P06320 homo sapien
42	397.5	50.3	133	1 KVI1 HUMAN	P06313 homo sapien
43	396	50.1	108	1 KVI1 HUMAN	P01650 mus musculu
44	396	50.1	115	1 KVI1 HUMAN	P04433 homo sapien
45	395.5	50.0	109	1 KVI1 HUMAN	P01624 homo sapien

ALIGNMENTS

RESULT 1

ID	KVI1 HUMAN	STANDARD;	PRT;	117 AA.
AC	P01601;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig kappa chain V-I region HK101 precursor (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81098966; PubMed=6779204;			
RA	Bentley D.L., Rabbitts T.H.;			
RT	"Human immunoglobulin variable region genes -- DNA sequences of two V			
RT	kappa genes and a pseudogene.";			
RL	Nature 288:730-733(1980).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=83129397; PubMed=6402305;			
RA	Bentley D.L., Rabbitts T.H.;			
RT	"Evolution of immunoglobulin V genes: evidence indicating that			
RT	recently duplicated human V kappa sequences have diverged by gene			
RT	conversion.";			
RL	Cell 32:181-189(1983).			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; K01322; AAA58930.1; -			
DR	EMBL; K01324; AAA58932.1; -			
DR	EMBL; V00558; CAA23824.1; -			
DR	PIR; A01881; K1HUI1.			
DR	PIR; A21056; A21056.			
DR	HSSP; P01607; 1REI.			


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Db 101 GlyThrLysLeuAspIleLysArg 108
|||||
RESULT 5
KV1V_HUMAN
ID KV1V_HUMAN STANDARD; PRT; 108 AA.
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human)
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240;
RA Dwulet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR FIR; A01878; KIHUBN.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Amyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 93 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Alignment Scores:
Pred. No.: 8.77e-44 Length: 108
Score: 487.00 Matches: 91
Percent Similarity: 94.44% Conservative: 11
Best Local Similarity: 84.26% Mismatches: 6
Query Match: 61.57% Indels: 0
DB: 1 Gaps: 0

US-08-728-463B-208 (1-439) x KV1V_HUMAN (1-108)
QY 67 GACATCAGATGACCCAGTCTCCATCTCTGCTGCTAGGACAGAGTCACC 126
Db 1 AspIleGlnLeuThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThr 20
QY 127 ATCACTTGTCGGCGAGTCAGGTATATACAGCTGTTAGCTGTATCAGCAGAAACCA 186
Db 21 IleThrCysArgAlaSerGlnSerValTyrAsnTyrValAlaTyrPheGlnGlnLysPro 40
QY 187 GAGAAAGCCCTTAAGTCTCTGATCTATCTGTCAGTTCGAAAGTGGGTCCCATCA 246
Db 41 GlyLysAlaProLysSerLeuLeuTyrAspAlaSerThrLeuGlnSerGlyValProSer 60
QY 247 AGGTTGAGCGGCGAGTCGATCTGCGAGAGATTTCACTCTCACCATCAGCAGCTCGAGCT 306
Db 61 AsnPheThrGlySerGlySerGlyThrAspPheLeuThrLeuSerSerLeuGlnPro 80
QY 307 GAAGATTTTGCACATATTACTGCCAACAGATGATAGTACCGGTACACTTTTGGCCAG 366
Db 81 GluAspPheAlaThrTyrTyrCysGlnGlnTyrAsnSerTyrProTyrPheGlyGln 100
QY 367 GGGACCAAGCTGAGATCAACCA 390
Db 101 GlyThrLysValGlnIleLysArg 108
|||||
US-08-728-463B-208 (1-439) x KV1X_HUMAN (1-129)
QY 1 ATGGACATGGAGTCTCCCGTTCAGCTCTCGGGCTCTGCTGCTCTGTTCCAGGTGCC 60
Db 1 MetAspMetCargValProAlaGlnLeuLeuGlyLeuLeuLeuTrpLeuArgVal 20
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTCCTCATCTGTCATCTGTAGGACAGCA 120
Db 21 ArgCysAspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArg 40
QY 121 GTCACCATCATTCTCGGCGAGTCAGGTATTACAGCTGTTAGCTGTATCAGCAG 180
Db 41 ValThrIleThrCysArgAlaGlyHisAsnIleThrAsnPheLeuSerTyrTyrGlnGln 60
QY 181 AAACGAGAGAAAGCCCTTAAGTCTGATCTATTCTGATCCAGTTTGCRAAGTGGGTC 240
|||||
Alignment Scores:
Pred. No.: 1.15e-43 Length: 129
Score: 486.00 Matches: 95
Percent Similarity: 82.95% Conservative: 12
Best Local Similarity: 73.64% Mismatches: 22
Query Match: 61.44% Indels: 0
DB: 1 Gaps: 0

RESULT 6
KV1X_HUMAN
ID KV1X_HUMAN STANDARD; PRT; 129 AA.
AC P04432;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Daudi precursor.
OS Homo sapiens (Human)
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combriato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
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CC -----
EMBL; X00966; CAA25478.1; ALT_TERM.
DR FIR; A01884; KIHUDI.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION DAUDI.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14235 MW; CAF076BC7E5574C8 CRC64;

Alignment Scores:
Pred. No.: 1.15e-43 Length: 129
Score: 486.00 Matches: 95
Percent Similarity: 82.95% Conservative: 12
Best Local Similarity: 73.64% Mismatches: 22
Query Match: 61.44% Indels: 0
DB: 1 Gaps: 0

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Db      61 LysProGlyLysAlaProThrLeuLeuIleTyrAlaValSerAsnLeuGlnValGlyVal 80
QY      241 CCATCAGCTTCAGCGGAGTGGATCTGGACAGATTTCATCTCACCATCAGCAGCCG 300
Db      81 ProSerArgPheSerGlySerGlyAlaGluPheThrLeuThrIleSerLeu 100
QY      301 CAGCCTGAAGATTTGCACTTATTACTCCCAACAGTATGATAGTTACCCGTCACACTTTT 360
Db      101 GlnProGluAspPheAlaThrTyrCysGlnGlnAsnTyrAsnPheSerPheThrPhe 120
QY      361 GCCCAGGGGACCAAGCTGGAGATCAAA 387
Db      121 GlyGlyGlyThrLysValAspAsnLys 129

RESULT 7
KVIR_HUMAN
ID KVIR_HUMAN STANDARD; PRT; 108 AA.
AC P01610;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig kappa chain V-I region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
RT (protein WEA) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33."
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841 (1983).
CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
DR PIR; A01876; KIHWE.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Monoclonal antibody.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Alignment Scores:
Pred. No.: 1,29e-42 Length: 108
Score: 476.00 Matches: 91
Percent Similarity: 91.67% Conservative: 8
Best Local Similarity: 84.26% Mismatches: 9
Query Match: 60.18% Indels: 0
DB: 1 Gaps: 0

US-08-728-463B-208 (1-439) x KVIR_HUMAN (1-108)
QY 67 GACATCCAGATCACCAGTCTCCATCTGCTGCTGCTAGGACAGAGTCACC 126
Db 1 AspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThr 20
QY 127 ATCACTTGTGGCGGAGTCAGGATTTAGCAGCTGGTGTAGCTGCTGCTAGGACAGAAACCA 186
Db 21 IleThrCysArgAlaSerGlnGlyIleArgAsnLeuThrTrpTyrGlnGlnLysPro 40

US-08-728-463B-208 (1-439) x KVID_HUMAN (1-107)
QY 67 GACATCCAGATCACCAGTCTCCATCTGCTGCTGCTAGGACAGAGTCACC 126
Db 1 AspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArgValAla 20
QY 127 ATCACTTGTGGCGGAGTCAGGATTTAGCAGCTGGTGTAGCTGCTGCTAGGACAGAAACCA 186
Db 21 IleThrCysArgAlaSerGlnGlyIleArgAsnLeuThrTrpTyrGlnGlnLysPro 40

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QY 187 GGAAGAGCCCTAAGTCCCTGATCTATCTGTCATCCAGTTTCGAAAGTGGGTCCCATCA 246
Db 41 GlyThrAlaProLysArgLeuIleTyrGlyAlaThrSerLeuGlnSerGlyValProSer 60
QY 247 AGGTTTCAGCGGAGTGGATCTGGGACAGATTTCTCTCACCATCAGCAGCCTGCAGCCT 306
Db 61 ArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIleAsnSerLeuGlnPro 80
QY 307 GAAGATTTGCACTTATTACTGCGCAACAGTATGATAGTTACCCGTCACACTTTTGGCCAG 366
Db 81 GluAspPheAlaThrTyrTyrCysLeuGlnTyrSerSerPheProTrpThrPheGlyGln 100
QY 367 GCGACCAAGCTGGAGATCAACGA 390
Db 101 GlyThrLysValGluValLysArg 108

RESULT 8
KVID_HUMAN
ID KVID_HUMAN STANDARD; PRT; 107 AA.
AC P01596;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig kappa chain V-I region CAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75075135; PubMed=4216454;
RA Milstein C.P., Deverson E.V.;
RT "Primary structure of kappa light chain from a human myeloma
RT protein."
RL Eur. J. Biochem. 49:377-391 (1974).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01864; KIHUAR.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Glycoprotein.
FT CARBOHYD 28
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11703 MW; E1BF0DF9844C3346 CRC64;

Alignment Scores:
Pred. No.: 4,94e-42 Length: 107
Score: 470.50 Matches: 89
Percent Similarity: 93.52% Conservative: 12
Best Local Similarity: 82.41% Mismatches: 6
Query Match: 59.48% Indels: 1
DB: 1 Gaps: 1

US-08-728-463B-208 (1-439) x KVID_HUMAN (1-107)
QY 67 GACATCCAGATCACCAGTCTCCATCTGCTGCTGCTAGGACAGAGTCACC 126
Db 1 AspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArgValAla 20
QY 127 ATCACTTGTGGCGGAGTCAGGATTTAGCAGCTGGTGTAGCTGCTGCTAGGACAGAAACCA 186
Db 21 IleThrCysArgAlaSerGlnGlyIleArgAsnLeuThrTrpTyrGlnGlnLysPro 40
QY 187 GGAAGAGCCCTAAGTCCCTGATCTATCTGTCATCCAGTTTCGAAAGTGGGTCCCATCA 246
Db 41 GlyLysAlaProLysValLeuIleTyrLysSerSerLeuGlnSerGlyValProSer 60
QY 247 AGGTTTCAGCGGAGTGGATCTGGGACAGATTTCTCTCACCATCAGCAGCCTGCAGCCT 306

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Db 61 ArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu***Pro 80
 QY 307 GAAGATTTCGCACTTATTACTCCCAACAGATGATAGTACCGTACACTTTTGGCCAG 366
 Db 81 *****PheAlaThrTyTyCysGlnGlnTyAsnThrPhe---PheThrPheGlyPro 99
 QY 367 GGGACCAAGCTGGAGATCAACGA 390
 Db 100 GlyThrLysValAspIleLysarg 107

RESULT 9
 KVIH_HUMAN STANDARD; PRT; 108 AA.
 AC P01559;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region GHL.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=75059122; PubMed=4215718;
 RA Laure C.J., Watanabe S., Hilschmann N.;
 RT "The primary structure of a monoclonal IgM-immunoglobulin
 RT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
 RT kappa-type, subgroup I."
 RL Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504 (1973).
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 CC MACROGLOBULIN
 DR PIR; A01867; KIHUCL.
 DR HSSP; P01607; IREI.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600FF73 CRC64;

Alignment Scores:
 Pred. No.: 9,11e-42 Length: 108
 Score: 468.00 Matches: 91
 Percent Similarity: 91.67% Conservative: 8
 Best Local Similarity: 84.26% Mismatches: 9
 Query Match: 59.17% Indels: 0
 DB: 1 Gaps: 0

US-08-728-463b-208 (1-439) x KVIH_HUMAN (1-108)

QY 67 GACATCCAGATGACCCAGTCTCCATCTCTGTCATCTGTAGGACAGAGTCACC 126
 Db 1 AspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThr 20
 QY 127 ATCACTTGTGGGCGAGTCAGGCTATTACACCTGGTACCTGGTATCAGCAGAAACCA 186
 Db 21 IleIleCysArgAlaSerGlnGlyIleArgAsnAspLeuThrTrpTyGlnGlnLysPro 40
 QY 187 GAGAAAGCCCTAAGTCCCTGATCTATTCTGCATCCAGTTTGCAGAGTGGGTCCCATCA 246
 Db 41 GlyLysAlaProGlyGluLeuIleTyAlaAlaSerAsnLeuGlnSerGlyValProSer 60

QY 247 AGTTTCAGCGCAGTGGATCTGGACAGATTTCACTCTCACCATCAGCAGCTTCAGCCT 306
 Db 61 ArgPheSerGlySerGlyAlaGlyThrGluPheThrLeuThrIleSerSerLeuGlnPro 80
 QY 307 GAAGATTTCGCACTTATTACTCCCAACAGATGATAGTACCGTACACTTTTGGCCAG 366
 Db 81 GLUAspPheAlaThrTyTyCysLeuGlnGlnAsnSerTyProArgSerPheGlyGln 100
 QY 367 GGGACCAAGCTGGAGATCAACGA 390
 Db 101 GlyThrLysValGluIleLysarg 108

RESULT 10
 KVIH_HUMAN STANDARD; PRT; 108 AA.
 AC P01600;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Hau.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=71032830; PubMed=4097974;
 RA Watanabe S., Hilschmann N.;
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
 RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
 RT subgroups.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295 (1970).
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01868; KIHUHU.
 DR HSSP; P80362; 1WTL.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Alignment Scores:
 Pred. No.: 1,9e-41 Length: 108
 Score: 465.00 Matches: 92
 Percent Similarity: 91.67% Conservative: 7
 Best Local Similarity: 85.19% Mismatches: 9
 Query Match: 58.79% Indels: 0
 DB: 1 Gaps: 0

US-08-728-463b-208 (1-439) x KVIH_HUMAN (1-108)

QY 67 GACATCCAGATGACCCAGTCTCCATCTCTGTCATCTGTAGGACAGAGTCACC 126
 Db 1 AspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThr 20
 QY 127 ATCACTTGTGGGCGAGTCAGGCTATTACACCTGGTACCTGGTATCAGCAGAAACCA 186
 Db 21 IleThrCysArgAlaSerGlnSerIleSerSerTyLeuSerTrpTyGlnGlnLysPro 40
 QY 187 GAGAAAGCCCTAAGTCCCTGATCTATTCTGCATCCAGTTTGCAGAGTGGGTCCCATCA 246
 Db 41 GlyLysAlaProGlnValLeuIleTyAlaAlaSerSerLeuProSerGlyValProSer 60

QY 247 AGGTTACGGGACGTCAGTCTGGACAGATTTTCACTCTCACCATCAGCAGCCTGCAGCCT 306
 DB 61 ArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80
 QY 307 GAAGATTGTCACCTATTACTGCGCAACAGTAGTATGATGTTACCCGTACACATTTTGGCCAG 366
 DB 81 GluAspPheAlaThrTyTyCysGlnGlnAsnTyIleThrProThrSerPheGlyGln 100
 QY 367 GGGACCAAGCTGGAGATCAACAGA 390
 DB 101 GlyThrArgValGluIleLysArg 108

RESULT 11
 KV5E_MOUSE
 ID KV5E_MOUSE STANDARD; PRT; 128 AA.
 AC P01637;

DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-V region 11 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81052342; PubMed=6776411;
 RA Altenburger W., Steinmetz M., Zachau H.G.;
 RT "Functional and non-functional joining in immunoglobulin light chain
 genes of a mouse myeloma.";
 RL Nature 287:603-607(1980).
 CC -----
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 CC -----

DR EMBL; V00772; CAA24150.1; -.
 DR PIR; A01920; KVMST1.
 DR HSP; P80382; LWL.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IgV; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 128 IG KAPPA CHAIN V-V REGION T1.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 69 FRAMEWORK-2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 77 108 FRAMEWORK-3.
 FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 118 127 FRAMEWORK-4.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON_TER 128 128
 SQ SEQUENCE 128 AA; 14385 MW; AFA5563D31BB7E05 CRC64;

Alignment Scores:
 Pred. No.: 1,94e-41 Length: 128
 Score: 465.00 Matches: 85
 Percent Similarity: 82.03% Conservative: 19
 Best Local Similarity: 67.19% Mismatches: 23
 Query Match: 58.79% Indels: 0
 DB: 1 Gaps: 0

US-08-728-463b-208 (1-439) x KV5E_MOUSE (1-128)

QY 7 ATGGAGTCCCGGTTCAGCTCTCTGGGCTCTGTGCTGTGTTCACGAGTCCAGATGT 66

DB 1 MetArgThrProAlaGlnPheLeuGlyIleLeuLeuLeuTrpPheProGlyIleLysCys 20
 QY 67 GACATCCAGTACGACCCAGTCTCCATCTCCTCATCTGTGTCATCTGTAGGACAGAGTCCACC 126
 DB 21 AspileLysMetThrGlnSerProSerSerMetTyAlaSerLeuGlyGluArgValThr 40
 QY 127 ATCACTTCTGGCGAGTCAGGTTATTAGCAGCTGTTAGCTGTGATCAGCAGAAACCA 186
 DB 41 IleSerCysLysAlaSerGlnAspIleAsnSerTyLeuThrTrpPheGlnGlnLysPro 60
 QY 187 GAGAAAGCCCTAAGTCCCTGATCTATTCTGCATCCAGTTTCAAGTGGGTCCCATCA 246
 DB 61 GlyLysSerProLysThrLeuLeuTyArgAlaAsnArgLeuValAspGlyValProSer 80
 QY 247 AGGTTACGCGCAGTGGTCTCTGGACAGATTTTCACTCTCACCATCAGCAGCCTGCAGCCT 306
 DB 81 ArgPheSerGlySerGlyGlnAspPheSerLeuThrIleSerSerLeuGluTy 100
 QY 307 GAAGATTGTCACCTATTACTGCGCAACAGTAGTATGATGTTACCCGTACACATTTTGGCCAG 366
 DB 101 GluAspMetGlyIleTyTyCysLeuGlnTyAspGluPheProLeuThrPheGlyAla 120
 QY 367 GGGACCAAGCTGGAGATCAACAGA 390
 DB 121 GlyThrLysLeuGluLeuLysArg 128

RESULT 12
 KV1F_HUMAN

ID KV1F_HUMAN STANDARD; PRT; 108 AA.

AC P01598;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-1 region EU.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=71064023; PubMed=5489770;

RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;

RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino

acid sequence of the light chain.";

RL Biochemistry 9:3155-3161(1970).

RN [2]

RP DISULFIDE BOND.

RX MEDLINE=71064027; PubMed=4923144;

RA Gall W.E., Edelman G.M.;

RT "The covalent structure of a human gamma G-immunoglobulin. X.

RT Intrachain disulfide bonds.";

RL Biochemistry 9:3188-3196(1970).

CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.

DR PIR; A01866; KIHUEU.

DR HSP; P01607; IREI.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig_1.

DR SMART; SM00406; IgV; 1.

KW Immunoglobulin V region.

FT DOMAIN 1 23

FT DOMAIN 24 34 FRAMEWORK-1.

FT DOMAIN 35 49 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 50 56 FRAMEWORK-2.

FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 89 97 FRAMEWORK-3.

FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.

FT DISULFID 23 88

FT NON_TER 108 108

SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;

X MEDLINE=76039968; PubMed=1182131;
A Epp O., Lattman E.E., Schiffer M., Huber P.

Db 81 GluAspPheAlaThrTyrPheCysGlnGlnAlaHisSerValProLeuThrPheGlyGly 100
Qy 367 GGGACCAAGCTGGAGATCAAACGA 390
Db 101 GlyThrThrValAspIleIysArg 108
||||| :|||||
||||| :|||||

Search completed: June 3, 2003, 09:04:07
Job time : 10.327 secs

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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 38.9704 Seconds

(without alignments)
4642.224 Million cell updates/sec

Title: US-08-728-463B-208

Perfect score: 791

Sequence: 1 ATGCATGGAGTTCCTCCCGT.....CCCGCATCTGATGAGCTT 439

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1343160

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q/cgn2 1/USPTO spool/US08728463/runat 03062003 085614 16815/app query.fasta_1.3690
-DB=SPTREMBL 21 -QWMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZES=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08728463 @CEN 1 1.380 @runat 03062003 085614 16815 -NCPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

SPTREMBL 21:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phase:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	539	68.1	234	11 Q8R062	Q8R062 mus musculus

2	523	66.1	234	11 Q8VCP0	Q8VCP0 mus musculus
3	510	64.5	233	11 Q1W8S9	Q1W8S9 mus musculus
4	506	64.0	234	11 Q91WF8	Q91WF8 mus musculus
5	492	62.2	108	4 Q9UL70	Q9UL70 homo sapien
6	473	59.8	108	4 Q9UL77	Q9UL77 homo sapien
7	464	58.7	108	4 Q9UL79	Q9UL79 homo sapien
8	463.5	58.6	107	4 Q96SA9	Q96SA9 homo sapien
9	459	58.0	214	11 Q9RIA5	Q9RIA5 mus musculus
10	453	57.3	116	4 Q96PF6	Q96PF6 homo sapien
11	445	56.3	127	11 Q925S9	Q925S9 mus musculus
12	444.5	56.2	239	4 Q8TCD0	Q8TCD0 homo sapien
13	438.5	55.4	107	4 Q9UL81	Q9UL81 homo sapien
14	411	52.0	238	11 Q99M37	Q99M37 mus musculus
15	405	51.2	108	11 Q8V1J0	Q8V1J0 mus musculus
16	404	51.1	298	11 Q9QYF0	Q9QYF0 mus musculus
17	400	50.6	107	11 Q9JL84	Q9JL84 mus musculus
18	399	50.4	109	11 Q920E6	Q920E6 mus musculus
19	397	50.2	108	4 Q9UL83	Q9UL83 homo sapien
20	395	49.9	238	11 Q8VCT6	Q8VCT6 mus musculus
21	391.5	49.5	235	11 Q91W12	Q91W12 mus musculus
22	390.5	49.4	239	11 Q8VC55	Q8VC55 mus musculus
23	389.5	49.2	109	4 Q9UL78	Q9UL78 homo sapien
24	385.5	48.7	134	11 Q8VDD0	Q8VDD0 mus musculus
25	385	48.7	234	11 Q8R028	Q8R028 mus musculus
26	383.5	48.5	109	4 Q9UL85	Q9UL85 homo sapien
27	371.5	47.0	109	4 Q9UL86	Q9UL86 homo sapien
28	364	46.0	111	11 Q920E9	Q920E9 mus musculus
29	357.5	45.2	241	11 Q921A6	Q921A6 mus musculus
30	344.5	43.6	106	5 Q9U410	Q9U410 schistosoma
31	341	43.1	107	11 Q9ER29	Q9ER29 mus musculus
32	328	41.5	99	11 Q9JL74	Q9JL74 mus musculus
33	325	41.1	97	11 Q9JL76	Q9JL76 mus musculus
34	321	40.6	101	11 Q9JL78	Q9JL78 mus musculus
35	313	39.6	103	11 Q9JL80	Q9JL80 mus musculus
36	303	38.3	114	4 Q9UL80	Q9UL80 homo sapien
37	299	37.8	109	6 Q9N0W5	Q9N0W5 oryctolagus
38	297.5	37.6	104	11 Q9JL82	Q9JL82 mus musculus
39	295.5	37.4	233	4 Q8TBC9	Q8TBC9 homo sapien
40	288.5	36.5	237	4 Q8WUK4	Q8WUK4 homo sapien
41	288.5	36.5	237	4 Q8WTU6	Q8WTU6 homo sapien
42	258	32.6	236	4 Q96E61	Q96E61 homo sapien
43	248	31.4	130	4 Q9NP29	Q9NP29 homo sapien
44	242	30.6	235	11 Q99M11	Q99M11 mus musculus
45	237.5	30.0	112	4 Q96JDI	Q96JDI homo sapien

ALIGNMENTS

RESULT 1

Q8R062	PRELIMINARY;	PRT;	234 AA.
ID Q8R062			
AC Q8R062			
DT 01-JUN-2002 (TRENBLrel. 21, Created)			
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)			
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)			
DE Hypothetical 25.9 kDa protein.			
OS Mus musculus (Mouse).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX NCBI_TaxID=10090;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=COLON;			
RA Strausberg R.;			
RL Submitted (APR-2002) to the EMBL/GenBank/DBSJ databases.			
DR EMBL; BC027418; AAH27418.1; -			
KW Hypothetical protein.			
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426ABAB1 CRC64;			

Alignment Scores:

Pred. No.:	1.71e-52	Length:	234
Score:	539.00	Matches:	103
Percent Similarity:	84.06%	Conservative:	13


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Db      30 LeuSerAlaSerLeuGlyAspArgValThrIleSerCysSerGlySerGlnGlyLeuAla 49
      157 AGCTGGTGTAGCTGTATCAGCAGAAACAGAGAAAGCCCTAAGTCCCTGATCTATTCT 216
      50 AsnTyrLeuAsnTrpTyrGlnGlnLysProAspGlyThrValLysLeuLeuIleTyrTyr 69
      217 GCATCCAGTTTCCAAAGTGGGTCCCATCAAGGTTTCAGGGCAGTGGATCTGGGACAGAT 276
      70 ThrSerSerLeuHisSerGlyValProSerArgPheSerGlySerGlySerGlyThrAsp 89
      277 TTCACTCTCACCATCAGCAGCTGCAGCCTGAAGATTTTGGCAACTTATTACTGCCAACAG 336
      90 TyrSerLeuThrIleSerAsnLeuGluProGluAspIleAlaThrTyrTyrCysGlnGln 109
      337 TATGATAGTTACCGGTACACTTTTGGCCAGGGGCAAGCTGGAGATCAACAAAGTGTG 396
      110 TyrArgTyrLeuProTrpTrpPheGlyGlyGlyThrLysLeuGluIleLysArgAlaAsp 129
      397 GCTGCACCATCTGTCTTCATCTCTCCGCCCATCTGTGAA 435
      130 AlaAlaProThrValSerIlePheProSerSerGlu 142

RESULT 4
Q91WF8
ID Q91WF8 PRELIMINARY; PRT; 234 AA.
AC Q91WF8;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015292; AAH15292.1; -.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B085EB7812D2 CRC64;

Alignment Scores:
Pred. No.: 9.69e-49 Length: 234
Score: 506.00 Matches: 98
Percent Similarity: 82.61% Conservative: 16
Best Local Similarity: 71.01% Mismatches: 24
Query Match: 63.97% Indels: 0
DB: 11 Gaps: 0

US-08-728-463B-208 (1-439) x Q91WF8 (1-234)

QY 22 CAGCTCTGGGGCTCTGCTGCTCTGTTTCCAGGTGCCAGATGTGATCCAGATGACC 81
Db 6 GlnPheLeuGlyLeuLeuLeuLeuCysPheGlnGlyThrArgCysAspIleGlnMetThr 25
QY 82 CAGTCTCCATCTCCTACTGTCTGATCTGTAGGAGCAGAGTCCACATCACTTGTGGGGG 141
Db 26 GlnThrThrSerSerLeuSerAlaSerLeuGlyAspArgValThrIleSerCysArgAla 45
QY 142 ACTCAGGGTATTAGCAGCTGGTGTAGCTGTATCAGCAGAAACAGAGAAAGCCCTAAG 201
Db 46 SerGlnAspIleSerAsnTyrLeuAsnTrpTyrGlnGlnLysProAspGlyThrValLys 65
QY 202 TCCTGTATCTATTCTGCATCCAGTTTGCAAAGTGGGTGCCATCAAGGTTTCAGCGCAGT 261

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Db      66 LeuLeuIleTyrTyrThrSerArgLeuTyrLeuGlyValProSerArgPheSerGlySer 85
      262 GGATCTGGGACAGATTCTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCACCT 321
      86 GlySerGlyThrAspTyrSerLeuThrIleSerAsnLeuGlnGluAspIleAlaThr 105
      322 TATTACTGCCAACAGTATGATGTTACCGGTACACTTTTGGCCAGGGGACCAAGCTGGAG 381
      106 TyrPheCysGlnGlnGlyAsnThrProPheThrPheGlySerGlyThrLysLeuGlu 125
      382 ATCAAAACCAACTGTGCTGCACCATCTGTCTTCATCTTCCCGCCCATCTGATGAA 435
      126 ValLysArgAlaAspAlaAlaProThrValSerIlePheProSerSerGlu 143

RESULT 5
Q9UL70
ID Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035044; RAD56280.1; -.
DR HSP; F01607; IREI.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1 108
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Alignment Scores:
Pred. No.: 3.31e-47 Length: 108
Score: 492.00 Matches: 96
Percent Similarity: 94.44% Conservative: 6
Best Local Similarity: 88.89% Mismatches: 6
Query Match: 62.20% Indels: 0
DB: 4 Gaps: 0

US-08-728-463B-208 (1-439) x Q9UL70 (1-108)

QY 67 GACATCCAGATGACCCAGTCTCCATCTCCTCACTGTCTGATCTGTAGGAGACAGATCACC 126
Db 1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
QY 127 ATCACTTCTGGGCGAGTCAGGTTATTAGCAGCTGGTATTAGCTGTATCAGCAGAAACCA 186
Db 21 IleThrCysArgAlaSerGlnGlyIleSerAsnTyrLeuAlaTrpTyrGlnGlnLysPro 40
QY 187 GAGAAAGCCCTCACTGCTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGTGCCATCA 246
Db 41 GlyLysValProLysSerLeuIleTyrAlaAlaSerThrLeuGlnSerGlyValProSer 60
QY 247 AGGTTTCAGCGCAGTGGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCTGCAGCT 306
Db 61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80
QY 307 GAAGATTTTGCACACTTATTACTTGCACACAGTATGATAGTTACCCCTTACACTTTTGGCCAG 366

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Db 81 GluAspValAlaThrTyrTyrCysGlnLysTyrAsnSerAlaProArgThrPheGlyPro 100
 QY 367 GGGACCAAGCTGGAGATCAACGA 390
 |||||
 Db 101 GlyThrLysLeuGluIleLysArg 108

RESULT 6

Q9UL77 PRELIMINARY; PRT; 108 AA.
 AC Q9UL77;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
 DR EMBL; AF035037; AAD56273.1; -;
 DR HSSP; P01607; IREI.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 108
 FT NON_TER 108
 SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Alignment Scores:

Pred. No.: 4, 78e-45 Length: 108
 Score: 473.00 Matches: 94
 Percent Similarity: 91.67% Conservative: 5
 Best Local Similarity: 87.04% Mismatches: 9
 Query Match: 59.80% Indels: 0
 DB: 4 Gaps: 0

US-08-728-463B-208 (1-439) x Q9UL77 (1-108)

QY 67 GACATCCAGATGCCAGTCCATCTCTGTCATCTGTAGGACAGAGTCACC 126
 |||||
 Db 1 AspileGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThr 20
 |||||
 QY 127 ATCACTTGTGGCGAGTCAGGTATTAGCAGCTGTTAGCTGTATCAGCAGAAACCA 186
 |||||
 Db 21 IleThrCysArgAlaSerGlnSerIleSerSerTyrLeuAsnTrpTyrGlnGlnLysPro 40
 |||||
 QY 187 GAGAAAGCCCTTAAGTCCCTGATCTATTCTGCATCCAGTTTCCAAAGTGGGTCCCATCA 246
 |||||
 Db 41 GlyLysAlaProAsnLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSer 60
 |||||
 QY 247 AGGTTACGGCGAGTCGGACAGATTTCACTCTCACCATCAGCAGCTCGAGCCT 306
 |||||
 Db 61 ArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80
 |||||
 QY 307 GAAGATTTTGCAACTATTACTGCCAACAGATGATAGTACCCTGACACTTTTGCCAG 366
 |||||
 Db 81 GluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerThrTrpThrPheGlyGlu 100
 |||||
 QY 367 GGGACCAAGCTGGAGATCAACGA 390
 |||||
 Db 101 GlyThrLysValGluIleLysArg 108

RESULT 7

Q9UL79 PRELIMINARY; PRT; 107 AA.
 AC Q9UL79;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
 DE variable region (Fragment).
 OS Homo sapiens (Human).

ID Q9UL79 PRELIMINARY; PRT; 108 AA.
 AC Q9UL79;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
 DR EMBL; AF035035; AAD56271.1; -;
 DR HSSP; P01607; IREI.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 108
 FT NON_TER 108
 SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Alignment Scores:

Pred. No.: 5, 05e-44 Length: 108
 Score: 464.00 Matches: 91
 Percent Similarity: 90.74% Conservative: 7
 Best Local Similarity: 84.26% Mismatches: 10
 Query Match: 58.66% Indels: 0
 DB: 4 Gaps: 0

US-08-728-463B-208 (1-439) x Q9UL79 (1-108)

QY 67 GACATCCAGATGCCAGTCCATCTCTGTCATCTGTAGGACAGAGTCACC 126
 |||||
 Db 1 AspileValMetThrGlnSerProSerLeuSerAlaSerThrGlyAspArgValThr 20
 |||||
 QY 127 ATCACTTGTGGCGAGTCAGGTATTAGCAGCTGTTAGCTGTATCAGCAGAAACCA 186
 |||||
 Db 21 IleSerCysArgMetSerGlnGlyIleSerSerTyrLeuAlaTrpTyrGlnGlnLysPro 40
 |||||
 QY 187 GAGAAAGCCCTTAAGTCCCTGATCTATTCTGCATCCAGTTTCCAAAGTGGGTCCCATCA 246
 |||||
 Db 41 GlyLysAlaProGluLeuLeuIleTyrAlaAlaSerThrLeuGlnSerGlyValProSer 60
 |||||
 QY 247 AGGTTACGGCGAGTCGGACAGATTTCACTCTCACCATCAGCAGCTCGAGCCT 306
 |||||
 Db 61 ArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerCysLeuGlnSer 80
 |||||
 QY 307 GAAGATTTTGCAACTATTACTGCCAACAGATGATAGTACCCTGACACTTTTGCCAG 366
 |||||
 Db 81 GluAspPheAlaThrTyrTyrCysGlnGlnTyrSerPheProThrPheGlyGln 100
 |||||
 QY 367 GGGACCAAGCTGGAGATCAACGA 390
 |||||
 Db 101 GlyThrLysValGluIleLysArg 108

RESULT 8

Q96SA9 PRELIMINARY; PRT; 107 AA.
 ID Q96SA9;
 AC Q96SA9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
 DE variable region (Fragment).
 OS Homo sapiens (Human).

41 IleSerCysArgSerThrGlnSerLeu

41 IleSerCysArgSerThrGlnSerLeuValTyrSerAspGlyAsnThr

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QY 172 TATCAGCAGAACACAGAACCCCTAAGTCCCTGATCTATCTGTCATCCAGTTGGCAA 231
Db 61 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLysValSerAsnArgAsp 80
QY 232 AGTGGGGTCCCATCAAGGTTACGGCGCAGTGGGACAGATTTCTCCTCACCACATC 291
Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 100
QY 292 AGCAGCTGACGCTGAGAGATTTTGCACATTTACTGTCACACAGATGATGATGATGAT 351
Db 101 ThrArgValGluAlaGluAspValGlyValTyrPheCysMetGlnGlyThrHisTrpPro 120
QY 352 TACATCTTTTGGCCAGGGACCAAGCTGGAGATCAACAGACTGCTGGTGCACCATCTGTC 411
Db 121 SerThrPheGlyGlnGlyThrLysLeuGluIleLysArgThrValAlaAlaProSerVal 140
QY 412 TTCACTCTTCCCGCCATCTGATCAA 435
Db 141 PheIlePheProProSerAspGlu 148

RESULT 13
Q9UL81
ID Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe F.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035033; RAD56269.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1 107
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

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Alignment Scores:

Pred. No.:	48-41	Length:	107
Score:	438.50	Matches:	90
Percent Similarity:	88.07%	Conservative:	6
Best Local Similarity:	82.57%	Mismatches:	10
Query Match:	55.44%	Indels:	3
DB:	4	Gaps:	2

US-08-728-463B-208 (1-439) x Q9UL81 (1-107)

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QY 67 GACATCCAGATGACCCAGTCTCCATCTCTGTCATCTGTAGGAGACAGATGACC 126
Db 1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
QY 127 ATCACTTGTGGCGGAGTCAGGATTTAGCAGCTGGTGGCTGATCAGCAGAAACA 186
Db 21 IleThrCysArgAlaSerGlnSerIleSerAsnTyrLeuAsnTrpTyrGlnGlnLysPro 40
QY 187 GAGAAGCCCTCAAGTCCCTGATCTATCTGTCAGTTTCGAAAGTGGGTCCCATCA 246
Db 41 GlyLysAlaProAsnLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSer 60

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QY 247 AGTTTCAGCGCAGTGGATCTGGGACAGATTTCTACTCTCAGCATCAGAGCTGAGCCT 306
Db 61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerGlyLeuGlnAla 80
QY 307 GAAGATTTTGAACACTTATTACTGCGCAACAGATGATGATGATGATGATGATGATG 363
Db 81 GluAspPheAlaThrTyrTyrCysGlnGln-----SerTyrSerAlaLeuThrPheGly 98
QY 364 CAGGGACCAAGCTGGAGATCAAAACGA 390
Db 99 ProGlyThrLysValAspIleArgArg 107

RESULT 14
Q99M37
ID Q99M37 PRELIMINARY; PRT; 238 AA.
AC Q99M37;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002035; AA02035.1; -.
DR HSP; P01679; 2FBJ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003600; IG_Like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG_C1; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Alignment Scores:
Pred. No.: 6,17e-38 Length: 238
Score: 411.00 Matches: 83
Percent Similarity: 70.27% Conservative: 21
Best Local Similarity: 56.08% Mismatches: 38
Query Match: 51.96% Indels: 6
DB: 11 Gaps: 2

US-08-728-463B-208 (1-439) x Q99M37 (1-238)
QY 7 ATGGAGTTCCCGTTACGTCCTGGGGCTCTGTCGTCTGTTCCTCCAGGTGCCAGATGT 66
Db 1 MetLysLeuProValArgLeuLeu---ValLeuMetPheTrpIleProAlaSerSerSer 19
QY 67 GACATCCAGATGACCCAGTCTCCATCTGTCATCTGTGTCATCTGTAGGAGACAGATCACC 126
Db 20 AspValValMetThrGlnThrProLeuSerLeuProValSerLeuGlyAspGlnAlaSer 39
QY 127 ATCACTTGTGGCGGAGTCAGGATTTAGCAGCTGGTGGCTGATCAGCAGAAACA 171
Db 40 IleSerCysArgSerSerGlnSerIleValHisSerAsnGlyAsnThrTyrLeuGluTrp 59
QY 172 TATCAGCAGAAACACAGAAAGCCCTAAGTCCCTGATCTATCTGTCATCCAGTTGGCAA 231
Db 60 TyrLeuGlnLysProGlyGlnSerProLysLeuLeuIleTyrLysValSerAsnArgPhe 79
QY 232 AGTGGGTCCCATCAAGTTCAGGGCAGTGGATCTGGGACAGATTTCTACTCTCACCATC 291

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Db      81  GluAspLeuAlaGluTyrPheCysGlnGlnTyrAsnSeryTyrProTyrThrPheGlyGly 100
      |||||  |||  |||:::|||||||:::|||||||:::|||||||
Qy      367  GGGACCAAGCTGGAGATCAACGA 390
      |||||  |||||  |||||  |||||  |||||  |||||
Db      101  GlyThrLysLeuGluLeuLysArg 108
      |||||  |||||  |||||  |||||  |||||  |||||

Search completed: June 3, 2003, 09:15:55
Job time : 40.9704 secs

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Search completed: June 3, 2003, 09:15:55
Job time : 40.9704 sec8

PRT; 108 AA.

OS *Mus musculus* (Mouse).
OC Eukaryota; Metazoa;
OC Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria;
OC Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI TaxID=10090.

RP SEQUENCE FROM N.A.

EUR: J. Immunol. 26:2225-2233 (1995)

SMART; SMO0406; IGV: 1.

SEQUENCE 108 AA; 11859 MW; 68506D75613DBFBE CRC64;

Player	Goals	Assists	Minutes	Matches
David Beckham	10	15	1,200	76

Best Local Locksmith
Call 1-800-251-1222
Competitive: 16

Query Match:

5'-TGGTGGGCTGACCAAGTCTCCATCTGCTGGCATCTGTG-3'

[illegible]

DATA ENTRY TRAINING

Y
127 ATCACTTGTGGGCGAGTCACGCATATTACACACACACACAC

[illegible][illegible]

41 GLVGLNSGQPDVALVQALVFQVLTFLM...

.....

7
24 / AGGTTTCAGCGGCAGTGGATCTGGACAGATTTCATCTCCACCA

THE UNIVERSITY OF CHICAGO

207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160 1161 1162 1163 1164 1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 11

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model
Run on: June 3, 2003, 08:56:21 ; Search time 28.3951 Seconds
(without alignments)
4120.219 Million cell updates/sec

Title: US-08-728-463B-208
Perfect score: 791
Sequence: 1 ATGGACATGGAGTTCCTCCGT.....CCGGCCATCTGATGAAGCTT 439

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 1816940

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USPTO.spool/US08728463/runat.03062003.085613.16797/app.query.fasta_1.3690
-DB=A_Geneseq.101002 -OPMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -MINLEN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ext -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08728463 @CWN 1.1.353 @runat.03062003.085613.16797 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORE=0 -WAIT -DSPELOCK=100 -LONGLOG
-DRV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq.101002.*

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	661	83.6	236	23	AAU74297	Anti-human AILIM m
2	656.5	83.0	241	22	AA82912	Human immune respo
3	651	82.3	236	21	AA96297	Human IGFAM-9 immu
4	638	80.7	260	23	ABP41164	Human ovarian anti
5	637.5	80.6	237	21	AA96298	Human IGFAM-10 imm
6	634	80.2	146	22	AA899115	Human protein SEQ
7	633.5	80.1	237	21	AA96289	Human IGFAM-1 immu
8	632.5	80.0	234	14	AA838162	Sequence of the ka
9	630	79.6	234	13	AA820058	Light chain of 306
10	629.5	79.6	237	21	AA96301	Human IGFAM-13 imm
11	624.5	79.0	237	21	AA815546	Human immune syste
12	623	78.8	236	14	AA842065	Human anti-HBs lig
13	617	78.0	139	22	ABP43157	Human ovarian anti
14	609	77.0	224	22	AA875040	TRO005 HuMab kappa
15	606	76.6	224	22	AA875044	TRO005 HuMab kappa
16	604	76.4	236	21	AA96293	Human IGFAM-5 immu
17	592	74.8	234	18	AAW11638	Human anti-RSV mon
18	590	74.6	236	16	AA877614	Humanised SGI.1 VL
19	590	74.6	236	23	ABP51696	SGI.1 light chain
20	589	74.5	224	22	AA875043	TRO005 HuMab kappa
21	588	74.3	164	20	AA934317	IGG antibody 2.6.1
22	585.5	74.0	235	18	AAW11640	Human anti-RSV mon
23	584	73.8	235	21	AA803684	Immunoglobulin kap
24	579	73.2	129	21	AA956722	Amino acid sequenc
25	578	73.1	117	14	AA838651	Human V-kappa frag
26	578	73.1	117	15	AA862931	Human V-kappa vk65
27	578	73.1	117	17	AAW03949	DNA fragment vk65.
28	578	73.1	117	18	AAW41147	Human vkappa65.15
29	578	73.1	117	19	AAW62185	Human DNA vkappa65
30	578	73.1	117	20	AA940432	Amino acid sequenc
31	577	72.9	130	21	AA956737	Amino acid sequenc
32	576	72.8	234	18	AAW10233	TF8-S69 CDR-grafte
33	576	72.8	236	21	AA96300	Human IGFAM-12 imm
34	574	72.6	214	20	AA908600	JP11127855 Seq ID
35	573	72.4	233	21	AA803713	Immunoglobulin kap
36	573	72.4	363	22	AAU14228	Human novel protei
37	572	72.3	124	21	AA956723	Amino acid sequenc
38	572	72.3	134	23	AAW47645	Human protein sequ
39	572	72.3	367	22	AAU14556	Human novel protei
40	571	72.2	132	18	AAW25842	Human anti-tumour
41	568	71.8	224	22	AA875041	TRO005 HuMab kappa
42	568	71.8	234	12	AA813050	CD4-specific CDR-g
43	567	71.7	129	23	ABG33326	Thrombopoietin ego
44	567	71.7	214	21	AA993735	The kappa chain of
45	566	71.6	129	16	AA865018	93KA9 anti-Varicel

ALIGNMENTS

RESULT 1

AAU74297
ID AAU74297 standard; Protein; 236 AA.

XX
AC AAU74297;

XX
DT 12-MAR-2002 (first entry)

XX
DE Anti-human AILIM monoclonal antibody clone Jmab-136, light chain.

XX
KW Human; antirheumatic; antiarthritis; antidiabetic; antipsoriatic;
KW antiallergic; antitumor; neuroprotective; antithyroid; vasotropic;
KW immunosuppressive; dermatological; antiinflammatory; hepatotropic;
KW activation inducible lymphocyte immunomodulatory molecule; AILIM;
KW monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;
KW multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;
KW allergic contact-type dermatitis; chronic inflammatory dermatosis;
KW systemic lupus erythematosus; autoimmune disorder; inflammation;
KW graft versus host reaction; immune rejection; intestinal immunity;

KW ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.
 OS Homo sapiens.
 XX WO200187981-A2.
 XX PD 22-NOV-2001.
 XX PF 15-MAY-2001; 2001WO-JP04035.
 XX PR 18-MAY-2000; 2000JP-0147116.
 XX PR 30-MAR-2001; 2001JP-0099508.
 XX PA (NISR) JAPAN TOBACCO INC.
 XX PI Tsuji T, Tezuka K, Hori N;
 XX WPI; 2002-075313/10.
 XX DR N-PSDB; AAS99473.
 XX PT New human monoclonal antibody that binds to activation inducible
 PT lymphocyte immunomodulatory molecule, useful for treating rheumatoid
 PT arthritis, multiple sclerosis and inflammation
 XX Claim 30; Page 270-271; 300pp; English.
 XX The invention relates to a novel human antibody (I), preferably a human
 CC monoclonal antibody which binds to an activation inducible lymphocyte
 CC immunomodulatory molecule (Ailim). (I) is useful for modulating signal
 CC transduction into a cell mediated by Ailim, for modulating proliferation
 CC of Ailim-expressing cells, for modulating production of a cytokine from
 CC Ailim-expressing cells, and for inducing antibody-dependent cytotoxicity
 CC against Ailim-expressing cells and/or immune cytotoxicity or apoptosis of
 CC Ailim-expressing cells. (I) is useful for treating, preventing or
 CC prophylaxis of delayed type allergy. (I) is useful for treating and
 CC preventing various diseases associated with Ailim-mediated
 CC costimulatory transduction, and for inhibiting the onset and/or
 CC advancement of the diseases. (I) is useful for suppression,
 CC prevention and/or treatment of rheumatoid arthritis, multiple
 CC sclerosis, autoimmune thyroiditis, allergic contact-type dermatitis,
 CC chronic inflammatory dermatitis, systemic lupus erythematosus,
 CC insulin-dependent diabetes mellitus, psoriasis, autoimmune or allergic
 CC disorders, inflammation, graft versus host reaction, graft versus host
 CC disease, immune rejection, disorders caused by abnormal intestinal
 CC immunity, specifically inflammatory intestinal disorders such as
 CC ulcerative colitis, pneumonia, hepatitis, nephritis, vasculitis, and
 CC pancreatitis. (I) induces no serious immunorejection due to antigenicity
 CC to human i.e., human anti-mouse immunorejection due to antigenicity
 CC AAU74296-AAU74301 represent anti-human Ailim monoclonal antibody amino
 CC acid sequences of the invention.

SQ Sequence 236 AA;

Alignment Scores:

Pred. No.: 1.34e-60 Length: 236
 Score: 661.00 Matches: 129
 Percent Similarity: 93.10% Conservative: 6
 Best Local Similarity: 88.97% Mismatches: 10
 Query Match: 83.57% Indels: 0
 DB: 23 Gaps: 0

US-08-728-463B-208 (1-439) x AAU74297 (1-236)

QY 1 ATGGACATGAGTCCCGTTCAGTCTCTGGGGCTCTGCTGCTGTTTCCAGTGCC 60
 Db 1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpPheProGlySer 20
 QY 61 AGATGTGACATCCAGTACCCAGTCTCCATCTCCTGCTGTGATCTGTAGGAGACAGA 120
 Db 21 ArGcYsAspIleGlnMetThrGlnSerProSerValSerAlaSerValGlyAspArg 40
 QY 121 GTCCACATCAGTCTGTGGGCGAGTCCAGGTATTACACCTGGTTAGCTGGTATCAGCAG 180
 †|||||

Db 41 ValThrIleThrCysArgAlaSerGlnGlyIleSerArgLeuLeuAlaTrpTrpGlnGln 60
 QY 181 AAACACAGAGAACCCCTAAGTCCCTGATCTATTCTGTCATCCAGTTTGCAAGTGGGTC 240
 Db 61 LysProGlyLysAlaProLysLeuLeuIleTrpValAlaSerSerLeuGlnSerGlyVal 80
 QY 241 CCATCAAGTTTCAGCGCAGTGGATCGGACAGATTTTCACCTCCTCACCATCAGCAGCCTG 300
 Db 81 ProSerArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100
 QY 301 CAGCCTGAAGATTTTCGAATCTATTACTGCGCAACAGATGATAGTATACCCGTACACTTT 360
 Db 101 GlnProGluAspPheAlaThrTrpTrpCysGlnGlnAlaAenSerPheProTrpThrPhe 120
 QY 361 GGCCAGGGACCAAGCTGGAGATCAAAAGCACTGGTGGCTGCACCATCTGTCTTCATCTTC 420
 Db 121 GlyGlnGlyThrLysValGluIleLysArgThrValAlaAlaProSerValPheIlePhe 140
 QY 421 CGCCCATCTCTGATGAA 435
 Db 141 ProProSerAspGlu 145
 RESULT 2
 AAB82912
 ID AAB82912 standard; Protein; 241 AA.
 XX AC AAB82912;
 XX DT 26-NOV-2001 (first entry)
 XX DE Human immune response protein HIRP1.
 XX KW Immune response protein; HIRP1; human; immunological disease;
 KW cell proliferation; cancer; anti-HIV; anti-allergic;
 KW antianemic; antianasthmatic; antiarteriosclerotic; antipsoriatic;
 KW immunosuppressive; dermatologic; antidiabetic; antiinflammatory;
 KW neuroprotective; osteopathic; antirheumatic; antiarthritic;
 KW antitumor; virucide; antibacterial; fungicide; protozoacide;
 KW antihelminthic; vulnerary; hepatotropic; cytostatic; therapy;
 KW diagnosis; vaccine; immunoglobulin.
 XX OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..22 /label= Signal_peptide
 FT Protein 22..241 /label= Mature_protein
 FT Modified-site 36 /note= "O-phosphorylated"
 FT Modified-site 44 /note= "O-phosphorylated"
 FT Modified-site 79 /note= "O-phosphorylated"
 FT Modified-site 80 /note= "O-phosphorylated"
 FT Modified-site 94 /note= "O-phosphorylated"
 FT Modified-site 129 /note= "O-phosphorylated"
 FT Modified-site 189 /note= "O-phosphorylated"
 FT Modified-site 191 /note= "O-phosphorylated"
 FT Modified-site 209 /note= "O-phosphorylated"
 FT Domain 38..117 /note= "O-phosphorylated"
 FT Region 98..134 /note= "immunoglobulin domain motif"
 FT Region 123..240 /note= "T-cell glycoprotein CD8 motif"
 FT Domain 154..223 /note= "immunoglobulin kappa complex motif"

PT protein is useful for preventing and treating disorders associated with altered levels of the protein such as cancer, immune system disorders

Claim 1; Page 85; 105pp; English.

The present sequence is the human immunoglobulin superfamily protein IGFAW-9. Its gene was isolated from a cDNA library of breast tumour tissue. It is expressed in reproductive, gastrointestinal and immune and haematopoietic tissue, where cancer and inflammation are common. The gene, protein, its antibodies, agonists and antagonists are suitable for diagnosing and treating many diseases, including cancer, immune system disorders (such as inflammation, AIDS, allergies, anaemia, arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's disease, diabetes mellitus, emphysema, Graves' disease, hepatitis, multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus and ulcerative colitis), complications of cancer, haemodialysis and extracorporeal circulation, trauma and haematopoietic cancer (such as leukaemia) and infections caused by bacteria, viruses, fungi or parasites.

Sequence 236 AA;

Alignment Scores:

Pred. No.:	1.48e-59	Length:	236
Score:	651.00	Matches:	126
Percent Similarity:	91.72%	Conservative:	7
Local Similarity:	86.90%	Mismatches:	12
Query Match:	82.30%	Indels:	0
JB:	21	Gaps:	0

JS-08-728-463B-208 (1-439) x AAY96297 (1-236)

1	ATGGACATGGAGTTC	CCCGTTCAGCTCCTGGGGCTCTGCTGCTCTGTGTTTCC	CAGGTGCC	60																	
1	Met	Asp	Met	Arg	Val	Leu	Ala	Gln	Leu	Gly	Leu	Leu	Leu	Cys	Phe	Pro	Gly	Ala	20		
61	AGATGTGACATCCAGATGACCCAGTCTCCATCTCTCATCTGTCTGCATCTCTGTAGGAGACAGA	120																			
21	Arg	Cys	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	40
121	GTCCACCATCACTTGTTCGGGCGAGTCAGGGTATTAGCAGCTGGTGTAGCTGGTGTATCAGCAG	180																			
41	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Ser	Asn	Tyr	Ileu	Ala	Trp	Phe	Gln	60	
181	AAACCACAGAGAAGCCCTAAGTCCCTGATCTATTCTGCATCCAGTTGCAAGTGGGGTTC	240																			
61	Lys	Pro	Gly	Thr	Ala	Pro	Lys	Ser	Leu	Ile	Tyr	Asp	Thr	Ser	Ser	Leu	Gln	Ser	Gly	Val	80
241	CCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGATTTCACCTCACCATCAGCAGCCTTG	300																			
81	Pro	Ser	Lys	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Asn	Ser	Leu	100
301	CAGCCTGAAGATTTGCAACTTATTACTGCCAACAGTAGTAGTTACCCGTACACTTTT	360																			
101	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	His	Ser	Tyr	Pro	Leu	Thr	Phe	120	
361	GGCCAGGGACCACCAAGCTGGAGATCAACGCAACTGTGGCTGGACACCATCTGTCTTCATCTTC	420																			
121	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	140
421	CCGCCATCTGATGAA	435																			
141	Pro	Pro	Ser	Asp	Glu	145															

RESULT 4

BP41164 ABP41164 standard; Protein; 260 AA.

ABP41164;

23-AUG-2002 (first entry)

24

DE Human ovarian antigen HRACW30, SEQ ID NO:2296.

Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
ovarian cancer; breast cancer; reproductive system disorder;
infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
inflammatory condition; immune disorder; blood disorder;
cardiovascular disorder; respiratory disorder; neurological disorder;
gastrointestinal disorder; urinary system disorder; drug screening;
gene therapy; chromosome mapping; forensic analysis;
antibody preparation; cytostatic; immunomodulatory; neuroprotective;
antiinflammatory; gynaecological; reproductive; chromosome 2p12.

Homo sapiens.

WO200200677-A1.

03-JAN-2002

07-JUN-2001; 2001WO-US18569.

07-JUN-2000; 2000US-209467P.

(HUMA-) HUMAN GENOME SCI INC.

Birse CE, Rosen CA;

WPI; 2002-147878/19.

N-PSDB; ABQ54241.

Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases -

Claim 11; SEQ ID No 2296; 2922pp; English.

The invention relates to 2175 novel human ovarian antigens (ABP411054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis), and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published/pct sequences.

sequence 260 AA;

Alignment Scores:

Pred. No.:	3,460-58	Length:	260
Score:	638.00	Matches:	125
Percent Similarity:	89.66%	Conservative:	5


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Db      141 PheProSerAspGlu 146
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RESULT 6
AAB99115
ID AAB99115 standard; Protein; 146 AA.
XX
AC AAB99115;
XX
DT 22-AUG-2001 (first entry)
XX
DE Human protein SEQ ID 12.
XX
KW Human; antiarthritic; cardiant; monoclonal antibody; keloid; arthritis;
KW Tumour Growth Factor-beta II receptor; TGF-beta II receptor; atopy;
KW signal transduction inhibition; tissue fibrosis; atherosclerosis.
XX
OS Homo sapiens.
XX
PN WO200136642-A1.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000NO-JP08129.
XX
PR 18-NOV-1999; 99JP-0328681.
PR 08-NOV-2000; 2000JP-0340216.
XX
PA (NISR) JAPAN TOBACCO INC.
XX
PI Sakamoto S, Kanada M;
XX
DR WPI; 2001-343825/36.
DR N-PSDB; AAH41157.
XX
PT Human monoclonal antibodies recognizing human TGF-beta II receptor,
PT useful for treating TGF-beta associated diseases such as tissue
PT fibrosis.
XX
PS Claim 11; Page 104-105; 118pp; Japanese.
XX
CC The present invention relates to novel human monoclonal antibodies. The
CC antibodies can bind to human Tumour Growth Factor-beta (TGF-beta) II
CC receptor, resulting in the inhibition of the signal transduction of human
CC TGF-beta into cells. The antibodies can be used for the prevention and
CC treatment of diseases associated with the production of TGF-beta, such as
CC tissue fibrosis in the lung, liver, skin, kidney or other tissues,
CC atherosclerosis, atopy, keloid and arthritis. The present sequence was
CC used in the present invention.
XX
SQ Sequence 146 AA;

Alignment Scores:
Pred. No.: 8e-58 Length: 146
Score: 634.00 Matches: 125
Percent Similarity: 90.34% Conservative: 6
Best Local Similarity: 86.21% Mismatches: 14
Query Match: 80.15% Indels: 0
DB: 22 Gaps: 0

US-08-728-463B-208 (1-439) x AAB99115 (1-146)

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Db 1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpPheProGlyAla 20
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QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTCTGCTGCTGCTGTGAGGACAGA 120
|||||
Db 21 ArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArg 40
|||||
QY 121 GTACCATCTACTGTTCGGGGAGTACAGGATATAGCAGCTGGTATGCTGTTATCAGCAG 180
|||||
Db 41 ValThrIleThrCysArgAlaSerGlnGlyIleArgAsnAspLeuGlyTrpTyrGlnGln 60
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QY 181 AAACACAGAAAGCCCTAAGTCCCTGATCTATTCTGTCATCCAGTTTGCAGAGTGGGTC 240
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|||||
QY 241 CCATCAAGTTTCAGCGGAGTGGATCTGGGACAGATTTCTACTCTCACCATCAGCAGCTG 300
|||||
Db 81 ProSerArgPheSerGlySerAlaSerGlyThrGluPheThrLeuThrIleSerSerLeu 100
|||||
QY 301 CAGCCTGAAGATTTTGCACACTTATTACTGCCAACAGATATGATGTTACCCGTACACTTTT 360
|||||
Db 101 GlnProGluAspPheAlaThrTyrTyrCysLeuGlnHisAsnSerAsnProLeuThrPhe 120
|||||
QY 361 GGCCAGGGAGACCAAGCTGGAGATCAACCAAGTGTGGTGCACCATCTGTCTTCATCTTC 420
|||||
Db 121 GlyGlyGlyThrLysValGluIleLysArgThrValAlaAlaProSerValPheIlePhe 140
|||||
QY 421 CGCCCATCTGATGAA 435
Db 141 ProProSerAspGlu 145
|||||
RESULT 7
AAY96289
ID AAY96289 standard; protein; 237 AA.
XX
AC AAY96289;
XX
DT 16-AUG-2000 (first entry)
XX
DE Human IGFAM-1 immunoglobulin.
XX
KW Human; immunoglobulin; IGFAM-1; IGFAM; immune disorder; cancer;
KW infection; inflammation; haematopoiesis; AIDS; allergy.
XX
OS Homo sapiens.
XX
FH Key
FT Peptide 1..22 Location/Qualifiers
FT Protein 23..237 /label= signal_peptide
FT Domain 38..112 /label= IGFAM-1
FT Domain 150..219 /label= Ig_domain
FT Region 154..176 /label= Ig_domain
FT Domain 193..236 /label= Ig_signature
FT Region 215..232 /label= Ig_domain
FT Region 215..232 /label= Ig_signature
XX
PN WO200029583-A2.
XX
PD 25-MAY-2000.
XX
PF 19-NOV-1999; 99WO-US27566.
XX
PR 19-NOV-1998; 99US-0113635.
PR 22-DEC-1998; 98US-0113635.
PR 07-APR-1999; 99US-0128194.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Yue H, Tang YT, Corley NC, Quegler KJ, Gorgone GA, Baughn MR;
PI Lu DAM, Lai P, Hillman JL, Yang J;
XX
DR WPI; 2000-387796/33.
DR N-PSDB; AAA27381.
XX
PT Immunoglobulin superfamily proteins, the agonist and antagonist of the
PT protein is useful for preventing and treating disorders associated with
PT altered levels of the protein such as cancer, immune system disorders

```


DB 141 ProProSerAspGlu 145

RESULT 13

ABP43157

ID ABP43157 standard; Protein; 139 AA.

XX AC ABP43157;

XX AC

DT 22-AUG-2002 (first entry)

XX DE Human ovarian antigen HVVIC150, SEQ ID NO:4289.

XX DE Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;

KW ovarian cancer; breast cancer; tumour; reproductive system disorder;

KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;

KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;

KW inflammatory condition; immune disorder; blood disorder;

KW cardiovascular disorder; respiratory disorder; neurological disorder;

KW gastrointestinal disorder; urinary system disorder; drug screening;

KW gene therapy; chromosome mapping; forensic analysis;

KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;

KW antiinflammatory; gynaecological; reproductive.

OS Homo sapiens.

XX

XX WO200200677-A1.

PN 03-JAN-2002.

XX

XX 07-JUN-2001; 2001WO-US18569.

XX

XX 07-JUN-2000; 2000US-209467E.

PR (HUNA-) HUMAN GENOME SCI INC.

XX

PA Birse CE, Rosen CA;

XX

XX WPI; 2002-147878/19.

DR N-PSDB; ABQ56234.

XX

PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,

PT useful in the prevention, treatment and diagnosis of cancer (e.g.

PT ovarian cancer), immune disorders, cardiovascular disorders and

PT neurological diseases -

XX

PS Claim 11; SEQ ID NO 4289; 2922dp; English.

XX

CC The invention relates to 2175 novel human ovarian antigens (ABP41054-

CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also

CC encompasses polypeptides 90% identical and polynucleotides 95% identical

CC to the sequences of the invention. The invention additionally relates to

CC recombinant vectors and host cells comprising human ovarian antigen

CC polynucleotides, antibodies against human ovarian antigens, and the use

CC of ovarian antigen polynucleotides and polypeptides in diagnosing,

CC treating, prognosing or preventing various ovary and/or breast-related

CC disorders. Such conditions include ovarian cancer and breast cancer, and

CC metastatic tumours of ovarian or breast origin, reproductive system

CC disorders (e.g., infertility, disorders of pregnancy, anovulation,

CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine

CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic

CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and

CC vaginitis), immune disorders (e.g., congenital and acquired

CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),

CC blood-related disorders (e.g., anaemia), cardiovascular disorders,

CC respiratory disorders, neurological disorders, gastrointestinal disorders

CC and urinary system disorders. Ovarian antigen polypeptides and

CC polynucleotides may also be used in screening for compounds which

CC modulate ovarian antigen expression or activity. The polynucleotides may

CC further be used for gene therapy, chromosome mapping, in the

CC identification of individuals and in forensic analysis, and the

CC polypeptides may be used as food additives or to prepare antibodies

CC useful in disease diagnosis, drug targeting and phenotyping. The present

CC sequence represents a human ovarian antigen of the invention.

CC

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 139 AA;

Alignment Scores:

Pred. No.: 4,74e-56 Length: 139

Score: 617.00 Matches: 119

Percent Similarity: 89.93% Conservative: 6

Best Local Similarity: 85.61% Mismatches: 12

Query Match: 78.00% Indels: 2

DB: 23 Gaps: 0

US-08-728-463B-208 (1-439) x ABP43157 (1-139)

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QY 76 ATGACCCAGCTCCATCCCTCACTGCTGCTATCTGTAGGAGACAGAGTCCATCATCTGT 135

DB 23 MetThrGln**ProSerThrLeuSerAlaSerValGlyAspArgValThrIleThrCys 42

QY 136 CGGGCAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACAGAGAAAGCC 195

DB 43 ArgAla***GlnSerIleSerSerTrp***AlaTrpTyrGlnGlnLysProGlyLysAla 62

QY 196 CCTAAGTCCCTGATCTATTCTGCATCCAGTTTGGGTTGCAAAAGTGGGTCCTCAAGGTTCCAGC 255

DB 63 ProLysLeuLeuIleTyr**AlaSerSerLeuGluSerGlyValProSerArgPheSer 82

QY 256 GCGAGTGGATCTGGGACAGATTTCACCTCACCATCAGCAGCCTGCAGCCTGAAGATTTT 315

DB 83 GlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeuGlnProAspAspPhe 102

QY 316 GCAACTTATTACTGCCAACAGATGATGATTACCCGTACACTTTTGGCCAGGGGACCAAG 375

DB 103 AlaThrTyrTyrCysGlnHisTyrAsnSerTyrProTyrThrPheGlyGln-GlyProSe 122

QY 376 CTGAGATCAACAACTGGGTGGTGCACCATCTGTCTTCATCTTCCGCCCATC 428

DB 122 rTrpArgSerAsnGluLeuTrpLeuHisLeu-LeuHisLeuProAlaIle 139

RESULT 14

ABP75040

ID AAB75040 standard; Protein; 224 AA.

XX AC AAB75040;

XX

DT 19-JUL-2001 (first entry)

XX DE TR0005 HuMab kappa chain protein sequence 3E2K.

XX

KW Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;

KW human antibody phage display library; immunisation; transgenic animal.

OS Homo sapiens.

OS Synthetic.

XX WO200125492-A1.

XX

XX 12-APR-2001.

XX

XX 02-OCT-2000; 2000WO-US27237.

PF

XX 02-OCT-1999; 99US-0157415.

PR

XX 01-DEC-1999; 99US-0453234.

XX

XX (BIOS-) BIOSITE DIAGNOSTICS INC.

PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.

XX

PI Buechler J, Valkirs G, Gray J, Lonberg N;

THIS PAGE BLANK (USPTO)

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Qy	427	TCTGATCAA	435
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Search completed: June 3, 2003, 09:02:23
 Job time : 30.5618 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 09:04:15 ; Search time 18.6525 Seconds
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Title: US-08-728-463B-208

Perfect score: 791

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Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 767038

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	661	83.6	236	10 US-09-859-053-30	Sequence 30, Appl
2	592	74.8	234	10 US-09-740-002-24	Sequence 24, Appl
3	590	74.6	236	9 US-10-006-593-69	Sequence 69, Appl
4	585.5	74.0	234	10 US-09-740-002-26	Sequence 26, Appl

5	567	71.7	214	9 US-10-153-382-19	Sequence 19, Appl
6	553	69.9	214	9 US-09-875-221A-128	Sequence 128, App
7	553	69.9	214	10 US-09-949-559-128	Sequence 10, Appl
8	553	69.9	237	9 US-10-020-786-10	Sequence 10, Appl
9	550	69.5	237	10 US-09-056-160B-100	Sequence 100, App
10	550	69.5	491	12 US-10-011-125-2	Sequence 2, Appli
11	546.5	69.1	235	10 US-09-800-729-152	Sequence 152, App
12	545	68.9	234	10 US-09-800-729-150	Sequence 150, App
13	540.5	68.3	211	10 US-09-974-449-36	Sequence 36, Appl
14	539	68.1	237	9 US-10-227-694-1	Sequence 1, Appli
15	539	68.1	237	10 US-09-940-166A-6	Sequence 6, Appli
16	538.5	68.1	235	10 US-09-910-059-52	Sequence 52, Appl
17	537	67.9	214	10 US-09-940-166A-2	Sequence 2, Appli
18	537	67.9	214	10 US-09-811-384-11	Sequence 11, Appl
19	537	67.9	218	9 US-09-925-179-9	Sequence 9, Appli
20	537	67.9	218	10 US-09-802-077-9	Sequence 9, Appli
21	537	67.9	218	10 US-09-802-096-9	Sequence 9, Appli
22	537	67.9	218	10 US-09-920-171-13	Sequence 13, Appl
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24	536	67.8	245	9 US-09-797-941A-6	Sequence 6, Appli
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34	529	66.9	239	10 US-09-825-012-9	Sequence 9, Appli
35	528	66.8	128	10 US-09-855-271-26	Sequence 26, Appl
36	528	66.8	218	9 US-09-925-179-67	Sequence 67, Appl
37	527	66.6	107	9 US-10-035-637-2	Sequence 2, Appli
38	522.5	66.1	235	10 US-09-910-059-97	Sequence 97, Appl
39	521	65.9	212	12 US-10-011-125-5	Sequence 5, Appli
40	519.5	65.7	235	9 US-10-153-382-7	Sequence 7, Appli
41	519	65.6	234	9 US-10-153-382-15	Sequence 15, Appl
42	518	65.5	224	9 US-09-453-234-48	Sequence 48, Appl
43	512.5	64.8	242	9 US-09-726-258-51	Sequence 51, Appl
44	512.5	64.8	242	9 US-09-726-258-56	Sequence 56, Appl
45	511.5	64.7	242	9 US-09-726-258-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-09-859-053-30
; Sequence 30, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tezuka, Takashi
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-30

Alignment Scores: 2.22e-51 Length: 236
Pred. No.: 236

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21	ArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArg	40
121	GTCCACCATCACTTGTGGCGCAGTCAGGCTATTAGCAGCTGGTTAGCTGTGATCATGACAG	180
41	ValThrIleThrCysGlyAlaSerGluAsnIleTyrGlyAlaLeuAsnTrpTyrGlnGln	60
181	AAACCGAGAAAGCCCTTAAGTCCCTGATCTATTCTCGATCCAGTTTGCAAGTGGGGTC	240
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101	GlnProGluAspPheAlaThrTyrTyrCysGlnAsnValLeuAsnThrProLeuThrPhe	120
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RESULT 4

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US-09-740-002-26
; Sequence 26, Application US/09740002
; Patent No. US20020001798A1
; GENERAL INFORMATION:
; APPLICANT: BRAMS, PETER
; APPLICANT: MORROW, PHILLIP
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
; TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
; FILE REFERENCE: 037003-0275759
; CURRENT APPLICATION NUMBER: US/09/740,002
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/335,697
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/488,376
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 234
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-740-002-26

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Db	101	GlyThrLysValGluIleLysArgThrValAlaAlaProSerValPheIlePhePro	120
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RESULT 6
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 / Sequence 128, Application US/09875221A
 / Publication No. US20030026805A1
 / GENERAL INFORMATION:
 / APPLICANT: Athwal, Diljeet Singh
 / APPLICANT: Brown, Derek Thomas
 / APPLICANT: Weir, Andrew Neil Charles
 / APPLICANT: Popplewell, Andrew George
 / APPLICANT: Chapman, Andrew Paul
 / APPLICANT: King, David John
 / TITLE OF INVENTION: Biological Products
 / FILE REFERENCE: Carp-0089
 / CURRENT APPLICATION NUMBER: US/09/875,221A
 / CURRENT FILING DATE: 2001-06-06
 / PRIOR APPLICATION NUMBER: GB0013810.7
 / PRIOR FILING DATE: 2000-06-06
 / NUMBER OF SEQ ID NOS: 130
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO 128
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 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Grafted light chain for
 US-09-875-221A-128

Alignment Scores:	
Pred. No.:	1.08e-41
Score:	553.00
Percent Similarity:	93.6%
Best Local Similarity:	86.9%
Query Match:	69.91%
DB:	9
Length:	214
Matches:	107
Conservative:	7
Mismatches:	9
Indels:	0
Gaps:	0
US-08-728-463B-208 (1-439) x US-09-875-421A-128 (1-214)	

67	GACATCCAGATGACCCAGTCTCCACTCTCACTGCTGCATCTCTAGAGACAGAGTCACC	126
bb		
1	AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr	20
yy		
127	ATCACTTGTCGGGGAGTCCAGGTATTAGCAGCTGGTTAGCCCTGGTATCAGCAAAACCA	186
bb		
21	IleThrCysIysAlaSerGlnAsnValGlyThrAsnValAlaIleTrpYrGlnGlnIysPro	40
yy		
187	GAGAAACCCCTTAAGTCCCTGATCTATTTCGCATCCAGTTTGCAAAAGTGGGGTCCCATCA	246
bb		
41	GlyIysAlaProIysAlaLeuIleTyrSerAlaSerPheLeuTyrSerGlyValProTyr	60
yy		
247	AGGTTTCAGCGCAGTGTGATCTGGACAGATTTCACATCTCACATCAGCAGCTGCAGCT	306
bb		
61	ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro	80
yy		
307	GAGATTGTGCAACTTATTACTGCCAACAGTATGATAGTTACCGGTACACTTTTGGCCAG	366
bb		
81	GluAspPheAlaThrTyrTyrCysGlnIleTyrAsnIleTyrProLeuThrPheGlyGln	100
yy		
367	GGGACCAAGCTGAGATCAAAACGAACGTGGCTGCACCATCTGTCTTCATCTTCCCGCCA	426
b		
101	GlyThrLysValGluIleLysArgThrValAlaProSerValPheIlePheProPro	120
yy		
427	TCTGATGAA	435
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Db          121 SerAspGlu 123
RESULT 7
US-09-949-559-128
; Sequence 128, Application US/09949559
; Patent No. US20020151682A1
; GENERAL INFORMATION:
; APPLICANT: Athwal, Diljeet Singh
; APPLICANT: Brown, Derek Thomas
; APPLICANT: Weir, Andrew Neil Charles
; APPLICANT: Popplewell, Andrew George
; APPLICANT: Chapman, Andrew Paul
; APPLICANT: King, David John
; TITLE OF INVENTION: Biological Products
; FILE REFERENCE: Carp-0095
; CURRENT APPLICATION NUMBER: US/09/949,559
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 0013810.7GB
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: 09/875,221
; PRIOR FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 128
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Grafted light chain for fab and modified fab
US-09-949-559-128

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Alignment Scores:			
Pred. No.:	1.08E-41	Length:	214
Score:	553.00	Matches:	107
Percent Similarity:	92.68%	Conservative:	7
Best Local Similarity:	86.99%	Mismatches:	9
Query Match:	69.91%	Indels:	0
DB:	10	Gaps:	0

US-08-728-463B-208 (1-439) x US-09-949-559-128 (1-214)

[illegible]

RESULT 8
US-10-020-786-10
Sequence 10, Application US/10020786
Publication No. US20030073164A1

GENERAL INFORMATION:
APPLICANT: Simmons, Laura C.
APPLICANT: Klimowski, Laura
APPLICANT: Reilly, Dorothea
APPLICANT: Yansura, Daniel G.
TITLE OF INVENTION: PROKARYOTICALLY PRODUCED ANTIBODIES AND USES THEREOF
FILE REFERENCE: P1793R1
CURRENT APPLICATION NUMBER: US/10/020,786
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/256,164
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 10
LENGTH: 237
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: anti-VEGF light chain
US-10-020-786-10

Alignment Scores:
Pred. No.: 1.09e-41 Length: 237
Score: 553.00 Matches: 108
Percent Similarity: 90.48% Conservative: 6
Best Local Similarity: 85.71% Mismatches: 12
Query Match: 69.91% Indels: 0
DB: Gaps: 0

US-08-728-463B-208 (1-439) x US-10-020-786-10 (1-237)

QY 58 GCCAGATGACATCCAGATGACCCAGTCTCCATCTCTGCTGCTGATGAGAGAC 117
Db 21 AlaTyrAlaAspIleGlnLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAsp 40
QY 118 AGAGTCACCATCCTTGTGCGGCGAGTTCAGGGTATTAGCAGCTGGTTCAGCTGGTATCAG 177
Db 41 ArgValThrIleThrCysSerAlaSerGlnAspIleSerAsnTyrLeuAsnTrpTyrGln 60
QY 178 CAGAAACACGAGAAAGCCCTTAAGTCCCTGATCTATTCTGCATCCAGTTTGCAAGTGGG 237
Db 61 GlnLysProGlyLysAlaProLysValLeuIleTyrPheThrSerSerLeuHisSerGly 80
QY 238 GTCCCATCAAGTTTCAGCGGCGAGTTCGGAGATGATTCCTGATCTTACCTCACCATCAGCAGC 297
Db 81 ValProSerArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSer 100
QY 298 CTCGAGCCTGAAGATTTTGCACCTTATTACTGCAACAGTATGATGTTACCGGTACACT 357
Db 101 LeuGlnProGluAspPheAlaThrTyrTyrCysGlnGlnTyrSerThrValProTrpThr 120
QY 358 TTTGCCAGGGGACCAAGCTGGAGATCAAAACGAACTGTGGCTGCACCATCTGCTTTCATC 417
Db 121 PheGlyGlnGlyThrLysValGluIleLysArgThrValAlaAlaProSerValPheIle 140
QY 418 TTCCCGCCCATCTGATGAA 435
Db 141 PheProProSerAspGlu 146

RESULT 9
US-09-056-160B-100
Sequence 100, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way

CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hasek, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-100

Alignment Scores:
Pred. No.: 2.02e-41 Length: 237
Score: 550.00 Matches: 107
Percent Similarity: 90.48% Conservative: 7
Best Local Similarity: 84.92% Mismatches: 12
Query Match: 69.53% Indels: 0
DB: Gaps: 0

US-08-728-463B-208 (1-439) x US-09-056-160B-100 (1-237)

QY 58 GCCAGATGACATCCAGATGACCCAGTCTCCATCTCTGCTGCTGATGAGAGAC 117
Db 21 AlaTyrAlaAspIleGlnLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAsp 40
QY 118 AGAGTCACCATCCTTGTGCGGCGAGTTCAGGGTATTAGCAGCTGGTTCAGCTGGTATCAG 177
Db 41 ArgValThrIleThrCysSerAlaSerGlnAspIleSerAsnTyrLeuAsnTrpTyrGln 60
QY 178 CAGAAACACGAGAAAGCCCTTAAGTCCCTGATCTATTCTGCATCCAGTTTGCAAGTGGG 237
Db 61 GlnLysProGlyLysAlaProLysValLeuIleTyrPheThrSerSerLeuHisSerGly 80
QY 238 GTCCCATCAAGTTTCAGCGGCGAGTTCGGAGATGATTCCTGATCTTACCTCACCATCAGCAGC 297
Db 81 ValProSerArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSer 100
QY 298 CTCGAGCCTGAAGATTTTGCACCTTATTACTGCAACAGTATGATGTTACCGGTACACT 357
Db 101 LeuGlnProGluAspPheAlaThrTyrTyrCysGlnGlnTyrSerThrValProTrpThr 120
QY 358 TTTGCCAGGGGACCAAGCTGGAGATCAAAACGAACTGTGGCTGCACCATCTGCTTTCATC 417
Db 121 PheGlyGlnGlyThrLysValGluIleLysArgThrValAlaAlaProSerValPheIle 140
QY 418 TTCCCGCCCATCTGATGAA 435
Db 141 PheProProSerAspGlu 146

RESULT 10
US-10-011-125-2
Sequence 2, Application US/10011125
Patent No. US20020142386A1
GENERAL INFORMATION:

LENGTH: 23
TYPE: PRT

Alignment Scores:
Pred. No.:

Length: 234

QY 298 CTCGACGCTGAAGATTTCGCACTTATTACTGCAACAGTATGATAGTAGTACCCGTACACT 357
Db |||||||
QY 101 LeuGlnProGluAspPhealaThrTyrCysGlnGlnGlyAsnThrLeuProThr 120
Db |||||||
QY 358 TTGGCCAGGGACCAAGCTGGAGATCAACGAACTGGCTGGCCACATCTGTCTTCATC 417
Db |||||||
QY 121 PheGlyGlnGlyThrLysValGluIleLysArgThrValAlaAlaProSerValPheile 140
Db |||||||
QY 418 TTCCCGCCATCTGATGAA 435
Db |||||||
QY 141 PheProProSerAspGlu 146
Db |||||||

RESULT 15

US-09-940-166A-6

; Sequence 6, Application US/09940166A

; Patent No. US20020058324A1

; GENERAL INFORMATION:

; APPLICANT: Blank, Gregory S.

; Narindray, Daljit S.

; Zapata, Gerardo A.

; TITLE OF INVENTION: Protein Recovery

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/940,166A

; FILING DATE: 27-Aug-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/097,309

; FILING DATE: 13-JUN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Schwartz, Timothy R.

; REGISTRATION NUMBER: 32171

; REFERENCE/DOCKET NUMBER: P1105R1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-7467

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 237 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-940-166A-6

Alignment Scores:
Pred. No.: 1.96e-40 Length: 237
Score: 539.00 Matches: 106
Percent Similarity: 90.48% Conservative: 8
Best Local Similarity: 84.13% Mismatches: 12
Query Match: 68.14% Indels: 0
DB: 10 Gaps: 0

US-08-728-463B-208 (1-439) x US-09-940-166A-6 (1-237)

QY 58 GCCAGATGTGACATCCAGATCCAGTCTCCATCTCTGTCGATCTGTAGGAGAC 117
Db |||||||
QY 21 AlaTyrAlaAspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAsp 40
Db |||||||
QY 118 AGAGTCACCATCACTTGTGGCGGAGTCAGGATATTAGCAGCTGGTGTAGCCTGGTATCAG 177
Db |||||||
QY 41 ArgValThrIleThrCysArgAlaSerGlnAspIleAsnAsnTyrLeuAsnTrpIleGln 60
Db |||||||

QY 178 CAGAAACCAGAGAAAGCCCTTAAGTCCCTGATCTATTCTGTCATCCAGTTTGCAAGTGGG 237
Db |||||||
QY 61 GlnLysProGlyLysAlaProLysLeuLeuIleTyrThrSerThrLeuHisSerGly 80
Db |||||||
QY 238 GTCCCATCAAGGTTTCAGCGGAGTGGATCTGGGACAGATTTCTCTCACCATCAGCAGC 297
Db |||||||
QY 81 ValProSerArgPheSerGlySerGlyThrAspTyrThrLeuThrIleSerSer 100
Db |||||||
QY 298 CTGACGCTCAAGATTTCGCACTTATTACTGCCAACAGATGATAGTACCCGTACACT 357
Db |||||||
QY 101 LeuGlnProGluAspPhealaThrTyrCysGlnGlnGlyAsnThrLeuProThr 120
Db |||||||
QY 358 TTGGCCAGGGACCAAGCTGGAGATCAACGAACTGGCTGGCCACATCTGTCTTCATC 417
Db |||||||
QY 121 PheGlyGlnGlyThrLysValGluIleLysArgThrValAlaAlaProSerValPheile 140
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QY 418 TTCCCGCCATCTGATGAA 435
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QY 141 PheProProSerAspGlu 146
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 09:02:35 ; Search time 9.99241 Seconds

(without alignments)
2585.294 Million cell updates/sec

Title: US-08-728-463B-208

Perfect score: 791

Sequence: 1 ATGGACATGGAGTTCCTCCGT.....CCGGCCATCTGATGAAGCTT 439

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Searched: 262574 seqs, 29422922 residues

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Maximum Match 100%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents AA:**
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	623	78.8	236	1	US-08-157-101A-5
2	594	73.8	235	3	US-08-812-586-16
3	578	73.1	117	4	US-09-042-353-48
4	578	73.1	117	4	US-08-758-417A-313
5	573	72.4	233	3	US-08-812-586-45
6	571	72.2	116	1	US-08-053-131-185
7	571	72.2	116	2	US-08-096-762-185
8	571	72.2	129	1	US-08-217-918-2
9	548.5	69.3	128	1	US-08-372A-14
10	548.5	69.3	128	1	US-08-468-671-14
11	542	68.5	233	2	US-07-934-373C-25
12	542	68.5	233	3	US-08-437-642B-25

13	542	68.5	233	4	US-08-146-206C-25
14	542	68.5	233	5	PCT-US93-07832-25
15	539.5	68.2	232	1	US-08-704-744-80
16	539	68.1	214	2	US-07-934-373C-39
17	539	68.1	214	3	US-08-437-642B-39
18	539	68.1	214	5	PCT-US93-07832-39
19	539	68.1	237	3	US-09-097-309-6
20	539	68.1	237	4	US-09-097-171A-10
21	539	68.1	237	4	US-09-422-712B-2
22	539	68.1	237	4	US-09-607-756-2
23	539	68.1	237	4	US-09-460-587-6
24	538.5	68.1	235	4	US-09-171-945-52
25	538	68.0	214	1	US-08-253-877C-5
26	538	68.0	214	2	US-08-452-164A-5
27	537	67.9	214	2	US-07-934-373C-40
28	537	67.9	214	2	US-08-788-800-11
29	537	67.9	214	3	US-08-437-642B-40
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34	537	67.9	218	2	US-08-887-352B-13
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36	537	67.9	218	4	US-09-109-207C-13
37	537	67.9	218	4	US-09-296-005-13
38	537	67.9	218	4	US-08-466-163B-9
39	537	67.9	237	2	US-08-463-587A-25
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42	537	67.9	237	5	PCT-US91-09133-26
43	536	67.8	218	5	PCT-US96-13152-2
44	535	67.6	214	4	US-09-679-397-1
45	535	67.6	214	4	US-09-680-148-1

ALIGNMENTS

RESULT 1

US-08-157-101A-5

; Sequence 5, Application US/08157101A

; Patent No. 5808032

; GENERAL INFORMATION:

; APPLICANT: KURIHARA, TATSUYA

; APPLICANT: MATSUKURA, SHIGEKAZU

; APPLICANT: TSURUOKA, NOBUO

; APPLICANT: ARIMA, KENJI

; APPLICANT: NISHIHARA, TATSURO

; TITLE OF INVENTION: ANTI-HBs ANTIBODY GENES AND EXPRESSION

; TITLE OF INVENTION: PLASMIDS THEREFOR

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PILLSBURY, MADISON & SUTRO

; STREET: 1100 NEW YORK AVENUE, N.W.

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/157,101A

; FILING DATE: 05-APR-1994

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: TITUS, MARLANA K

; REGISTRATION NUMBER: 35843

; REFERENCE/DOCKET NUMBER: 9437/204199

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-861-3711

; TELEFAX: 202-822-0944

```

; TELEX: 6714627 CUCH
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-157-101A-5

Alignment Scores:
Pred. No.: 1-32e-63 Length: 236
Score: 623.00 Matches: 118
Percent Similarity: 90.34% Conservative: 13
Best Local Similarity: 81.38% Mismatches: 14
Query Match: 78.76% Indels: 0
DB: 1 Gaps: 0

US-08-728-463B-208 (1-439) x US-08-157-101A-5 (1-236)
QY 1 ATGGACATGGAGTCCCGCTCAGCTCTGGGGCTCTGCTGCTCTGTTCCAGGTGCC 60
Db 1 MetaspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTppPheProGlyVala 20
QY 61 AGATGTGACATCCAGATGACCCAGCTCCATCCCTCACTGCTGCTGCTAGGAGACAGA 120
Db 21 ArgCysAspIleGlnMetThrGlnSerProSerAlaMetAlaAAserValGlyAspArg 40
QY 121 GTCACCATCACTTGTGCGGGAGTCAGGCTATTAGCAGCTGTTAGCTGTGATCAGCAG 180
Db 41 ValThrIleThrCysArgAlaSerGlnGlyIleGlyAsnTyrLeuValTppPheGlnGln 60
QY 181 AAACAGAGAAGCCCTTAAGTCCCTGATCTATCTGATCCATCCAGTTCGAAAGTGGGTC 240
Db 61 LysProGlyLysValProLysArgLeuIleTyrAlaAlaSerSerLeuGlnSerGlyVal 80
QY 241 CCATCAAGGTTGAGCGGAGTGGATCGGACAGATTCATCTCCATCCATCAGCAGCCTG 300
Db 81 ProSerArgPheSerGlySerGlyThrGlyThrGlyThrLeuThrIleSerArgLeu 100
QY 301 CAGCTGAAGTTTGGCACTTATTACTGCAACAGTATGATGATACCGTACACTTTT 360
Db 101 GlnProGluAspPheAlaThrTyrTyrCysLeuHisAsnAsnTyrProLeuSerPhe 120
QY 361 GGCCAGGGGACCAAGCTGGAGATCAACAGCACTGCTGGCTGACCATCTGCTTCATCTTC 420
Db 121 GlyGlyThrLysValGluIleLysArgThrValAlaAlaProSerValPheIlePhe 140
QY 421 CCGCCATCTGATGAA 435
Db 141 ProProSerAspGlu 145

RESULT 2
US-08-812-586-16
; Sequence 16, Application US/08812586
; Patent No. 6048704
; GENERAL INFORMATION:
; APPLICANT: Martin David Tilson
; TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURISM (AAA)
; TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,586
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/53862-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-812-586-16

Alignment Scores:
Pred. No.: 4.08e-59 Length: 235
Score: 584.00 Matches: 114
Percent Similarity: 85.52% Conservative: 10
Best Local Similarity: 78.62% Mismatches: 21
Query Match: 73.83% Indels: 0
DB: 3 Gaps: 0

US-08-728-463B-208 (1-439) x US-08-812-586-16 (1-235)
QY 1 ATGGACATGGAGTCCCGCTCAGCTCTGGGGCTCTGCTGCTCTGTTCCAGGTGCC 60
Db 1 MetaspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTppPheProGlyVala 20
QY 61 AGATGTGACATCCAGATGACCCAGCTCTCCATCCCTCACTGCTGCTGCTAGGAGACAGA 120
Db 21 ArgCysAlaIleArgIleAlaGlnSerProSerSerLeuSerAlaSerThrGlyAspArg 40
QY 121 GTCACCATCACTTGTGCGGGAGTCAGGCTATTAGCAGCTGTTAGCTGTGATCAGCAG 180
Db 41 ValThrIleThrCysArgAlaSerGlnGlyIleSerAsnTyrLeuAlaTppTyrGlnGln 60
QY 181 AAACAGAGAAGCCCTTAAGTCCCTGATCTATCTGATCCATCCAGTTCGAAAGTGGGTC 240
Db 61 LysProGlyGlnAlaProArgLeuLeuIleTyrAspAlaSerSerArgAlaThrGlyIle 80
QY 241 CCATCAAGGTTGAGCGGAGTGGATCGGACAGATTCATCTCCATCCATCAGCAGCCTG 300
Db 81 ProAspArgPheSerGlySerGlyThrGlyThrGlyThrLeuThrIleSerArgLeu 100
QY 301 CAGCTGAAGTTTGGCACTTATTACTGCAACAGTATGATGATACCGTACACTTTT 360
Db 101 GluProGluAspPheAlaValTyrTyrGlyGlnGlnTyrGlySerSerProLeuThrPhe 120
QY 361 GGCCAGGGGACCAAGCTGGAGATCAACAGCACTGCTGGCTGACCATCTGCTTCATCTTC 420
Db 121 GlyGlyThrLysValGluIleLysArgThrValAlaAlaProSerValPheIlePhe 140
QY 421 CCGCCATCTGATGAA 435
Db 141 ProProSerAspGlu 145

RESULT 3
US-09-042-353-48
; Sequence 48, Application US/09042353
; Patent No. 6255458
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 421

```


RESULT 5
US-08-812-586-45
; Sequence 45, Application US/08812586
; Patent No. 6048704
; GENERAL INFORMATION:
; APPLICANT: Martin David Tilson
; TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSM (AAA)
; TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF

RESULT 6
US-08-053-131-185

Db 103 PheAlaThrTyrTyrCysGlnGlnAlaAspSerLeuProPheThrPheGlyGlyThr 122
QY 373 AAGCTGGAGATCAACGA 390
|||:|||||
Db 123 LysValAspPheLysArg 128
|||:|||||
RESULT 11
US-07-934-373C-25
; Sequence 25, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-25
Alignment Scores:
Pred. No.: 2,79e-54 Length: 233
Score: 542.00 Matches: 106
Percent Similarity: 89.76% Conservative: 8
Best Local Similarity: 83.46% Mismatches: 13
Query Match: 68.52% Indels: 0
DB: 2 Gaps: 0

US-08-728-463b-208 (1-439) x US-07-934-373C-25 (1-233)

QY 55 GGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTCCATCTGTCATCTGTAGGA 114
|||
Db 16 GlyValHisSerAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGly 35
|||:|||||
QY 115 GACAGATCCACCATCTGTCGGGCGAGTCAGGATTATGACAGCTGGTTCCTGAT 174
|||:|||||
Db 36 AspArgValThrIleThrCysArgAlaSerGlnAspIleAsnAsnTyrLeuAsnTrpTyr 55
|||:|||||
QY '175 CACGAGAAACGAGAAAGCCCTAAGTCCCTCATCTATTCTGCATCCAGTTTGCAAAGT 234
|||:|||||
Db 56 GlnGlnLysProGlyLysAlaProLysLeuLeuIleTyrThrThrSerThrLeuHisSer 75
|||:|||||

QY 235 GGGTCCCATCATAGGTTTCAGGGCAGTGGATCTGGAGACAGATTTTCACTCTCACCATCAGC 294
|||:|||||
Db 76 GlyValProSerArgPheSerGlySerGlyThrAspTyrThrLeuThrIleSer 95
|||:|||||
QY 295 AGCTTCGACAGCTGAAGATTTTGCACACTTATTACTGCCAACAGTATGATAGTTTACCCGTAC 354
|||:|||||
Db 96 SerLeuGlnProGluAspPheAlaThrTyrTyrCysGlnGlnGlyAsnThrLeuProPro 115
|||:|||||
QY 355 ACTTTTGGCCAGGACCAAGCTGGAGATCAAAACAACTGTGGTGACCACTGTCTGTTC 414
|||:|||||
Db 116 ThrPheGlyGlnGlyThrLysValGluIleLysArgThrValAlaAlaProSerValPhe 135
|||:|||||
QY 415 ATCTTCCCGCCATCTGATGAA 435
|||:|||||
Db 136 IlePheProProSerAspGlu 142
|||:|||||
RESULT 12
US-08-437-642B-25
; Sequence 25, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-25
Alignment Scores:
Pred. No.: 2,79e-54 Length: 233
Score: 542.00 Matches: 106
Percent Similarity: 89.76% Conservative: 8
Best Local Similarity: 83.46% Mismatches: 13
Query Match: 68.52% Indels: 0


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; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 7092P2CT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX: 415/952-9881
; TELEFAX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; PCT-US93-07832-25

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Alignment Scores:
Pred. No.: 2,796-54 Length: 233
Score: 542.00 Matches: 106
Percent Similarity: 89.76% Conservative: 8
Best Local Similarity: 83.46% Mismatches: 13
Query Match: 68.52% Indels: 0
DB: 5 Gaps: 0

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US-08-728-463B-208 (1-439) x PCT-US93-07832-25 (1-233)

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QY 55 GGTGCCAGATGTGACATCCAGATGACCCAGCTCCATCTCCATCTGCTGCTGCTGCTAGGA 114
Db 16 GlyValHisSerAspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGly 35
QY 115 GACAGAGTCCACATCCTTGTGGCGAGTCTGAGGTATTAGCAGCTGGTTAGCTGTGTAT 174
Db 36 AspArgValThrIleThrCysArgAlaSerGlnAspIleAsnAenTyLeuAsnTyr 55
QY 175 CAGCAGAAACCCAGAGAAAGCCCTTAAGTCCCTGATCTTCTGATCCATCCAGTTTGCAAGT 234
Db 56 GlnGlnLysProGlyLysAlaProLysLeuLeuIleTyrThrSerThrLeuHisSer 75
QY 235 GGGTCCCATCAAGGTTTCAGCGGAGTGGTCTGGGACAGATTTTCACTCTCCACCATCAGC 294
Db 76 GlyValProSerArgPheSerGlySerGlyThrAspTyrThrLeuThrIleSer 95
QY 295 AGCTTCGAGCTGAAGATTTTGCACCTTATTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 354
Db 96 SerLeuGlnProGluAspPheAlaThrTyrCysGlnGlnGlyAsnThrLeuProPro 115
QY 355 ACTTTTGGCCAGGGGACCAAGCTGGAGATCAAAAGCAAGTCTGCTGCTGCTGCTGCTGCTGCT 414
Db 116 ThrPheGlyGlnGlyThrLysValGluLeuLysArgThrValAlaAlaProSerValPhe 135
QY 415 ATCTTCCCGCCATCTGATGAA 435
Db 136 IlePheProSerAspGlu 142

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RESULT 15

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US-08-704-744-80
; Sequence 80, Application US/08704744
; Patent No. 5705154
; GENERAL INFORMATION:
; APPLICANT: Dali, Barbara
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Tindall, Stephen
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5.3

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; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,744
; FILING DATE: 06-SEPT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208886
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: PCT/US/95/02400
; FILING DATE: 08-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: JB0429K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-2987
; TELEFAX: (908) 298-5388
; TELEX:
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-704-744-80

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Alignment Scores:
Pred. No.: 5,416-54 Length: 232
Score: 539.50 Matches: 108
Percent Similarity: 89.76% Conservative: 6
Best Local Similarity: 85.04% Mismatches: 12
Query Match: 68.20% Indels: 1
DB: 1 Gaps: 1

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US-08-728-463B-208 (1-439) x US-08-704-744-80 (1-232)

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QY 55 GGTGCCAGATGTGACATCCAGATGACCCAGCTCTCCATCTCTGCTGCTGCTGCTAGGA 114
Db 16 GlyValHisSerAspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGly 35
QY 115 GACAGAGTCCACATCCTTGTGGCGAGTCTGAGGTATTAGCAGCTGGTTAGCTGTGTAT 174
Db 36 AspArgValThrIleThrCysArgAlaSerGlnAsnIleTyrLysAsnLeuAlaTyr 55
QY 175 CAGCAGAAACCCAGAGAAAGCCCTTAAGTCCCTGATCTTCTGATCCATCCAGTTTGCAAGT 234
Db 56 GlnGlnLysProGlyLysAlaProLysLeuLeuIleTyrAsnAlaLysSerLeuGluThr 75
QY 235 GGGTCCCATCAAGGTTTCAGCGGAGTGGTCTGGGACAGATTTTCACTCTCCACCATCAGC 294
Db 76 GlyValProSerArgPheSerGlySerGlyThrAspPheThrLeuThrIleSer 95
QY 295 AGCTTCGAGCTGAAGATTTTGCACCTTATTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 354
Db 96 SerLeuGlnProGluAspPheAlaThrTyrCysGlnGlnTyrSer---GlyTyr 114
QY 355 ACTTTTGGCCAGGGGACCAAGCTGGAGATCAAAAGCAAGTCTGCTGCTGCTGCTGCTGCTGCT 414
Db 115 ThrPheGlyGlnGlyThrLysValGluLeuLysArgThrValAlaAlaProSerValPhe 134
QY 415 ATCTTCCCGCCATCTGATGAA 435
Db 135 IlePheProSerAspGlu 141

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Search completed: June 3, 2003, 09:47:31
Job time : 12.9924 secs

Result No.	Score	Query #		Length	DB	ID	Description
		Match	Length				
1	679	70.2	140	2	A49045		Ig heavy chain V r
2	639.5	66.1	140	2	S78052		Ig heavy chain pre
3	608	62.9	220	2	A49444		Ig gamma-1 heavy c
4	604	62.5	231	2	B23746		Ig Fab region IV-J
5	603	62.4	140	2	I37782		Ig variable region
6	593.5	61.4	126	2	S47010		Ig heavy chain V4.
7	590	61.0	147	2	S13519		Ig heavy chain V r
8	581.5	60.1	137	2	S31676		Ig heavy chain V r
9	581.5	60.1	139	2	S31586		Ig heavy chain V r
10	579	59.9	143	2	B49028		Ig heavy chain V-I
11	578	59.8	185	2	S34511		Ig heavy chain - h
12	576	59.6	155	2	S34512		Ig heavy chain - h
13	573	59.3	139	2	S31696		Ig heavy chain V r
14	572	59.2	146	1	G1HUH2		Ig heavy chain pre

Db 141 AlaLeuGlyCysLeuValLysAspTyrPheProGluPro 153

RESULT 4
B23746
Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C:Accession: B23746
R:Leonl, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin
A:Reference number: A23746; MUID:91131575; PMID:1993660
A:Accession: B23746
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-231 <LEO>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:140-209/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 1.71e-43 Length: 231
Score: 604.00 Matches: 118
Percent Similarity: 83.23% Conservative: 11
Best Local Similarity: 76.13% Mismatches: 20
Query Match: 62.46% Indels: 6
DB: 2 Gaps: 2

US-08-728-463B-219 (1-524) x B23746 (1-231)

QY 73 GTGCAGCTACAGAGTGGGGCGGAGGACTGTTGAAGCCTTCGGAGACCTGTCCTCACC 132
Db 1 ValGlnLeuGlnGlnTrpGlyAlaGlyLeuLeuLysProSerGluThrLeuSerLeuThr 20
QY 133 TGGCGTGTCTATGGTGGTTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCACCA 192
Db 21 GlyAlaValTyrGlyGlySerPheSerAspTyrTyrTrpSerTrpIleArgGlnProPro 40
QY 193 GGTAAAGGCTGGAGTGGATTTGGTGAATCAATCATAGTAGGAAAGCAACCACTACACCCG 252
Db 41 GlyLysGlyLeuGlnTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnPro 60
QY 253 TCTCTCAAGAGTCGAGTCACCATATCAGTAGACACCTCCCAAGAACCACTCTCTCGAA 312
Db 61 SerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeuLys 80
QY 313 CTGAGCTCTGTGACCGCTCGGACACGCTGTATTACTGTGCGAGAGTAATT----- 366
Db 81 LeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgProProHisAsp 100
QY 367 -----AATTGGTTCGACCCCTTGGGGCCAGGAAACCTGTGTCACCGTCTCTCAGCC 417
Db 101 ThrSerGlyHisTyrTrpAsnTyrTrpGlyGlnGlyThrLeuValThrValSerSerGly 120
QY 418 TCACCAAGGGCCATCGCTCTCCCGTGGCACCCTCTCCAGAGCACCTCTGGG--- 474
Db 121 SerAlaSerAlaProThrLeuPheProLeuValSerCysGluAsnSerProSerAspThr 140
QY 475 GGCACAGCGCCCTGGGCTGCTGCTGGTCAAGGACTACTTCCCGCAA 519
Db 141 SerSerValAlaValGlyCysLeuAlaGlnAspPheLeuProAsp 155

RESULT 5
I37782
Ig variable region (VDJ) (clone t23-9) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C:Accession: I37782; S25476
R:Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A:Title: Somatic diversification in the heavy chain variable region genes expressed by H
A:Reference number: A36876; MUID:94119917; PMID:8290556
A:Accession: I37782
A:Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-140 <RES>
A:Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:46-128/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 2.06e-43 Length: 140
Score: 603.00 Matches: 119
Percent Similarity: 87.86% Conservative: 4
Best Local Similarity: 85.00% Mismatches: 11
Query Match: 62.36% Indels: 6
DB: 2 Gaps: 2

US-08-728-463B-219 (1-524) x I37782 (1-140)

QY 13 ATGAACACCTGTGGTTCCTCAG 72
Db 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20
QY 73 GTGCAGCTACAGAGTGGGGCGGAGGACTGTTGAAGCCTTCGGAGACCTGTCCTCACC 132
Db 21 ValGlnLeuGlnGlnSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40
QY 133 TGGCGTGTCTATGGTGGTTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCACCA 192
Db 41 CysThrValSerGlyGlySerIleSerSerTyrTyrTrpSerTrpIleArgGlnProPro 60
QY 193 GGTAAAGGCTGTGGAGTGGATTTGGTGAATCAATCATAGTAGGAAAGCAACCACTACACCCG 252
Db 61 GlyLysGlyLeuGlnTrpIleGlyTyrIleTyrTyrSerGlySerThrAsnTyrAsnPro 80
QY 253 TCTCTCAAGAGTCGAGTCACCATATCAGTAGACACCTCCCAAGAACCACTCTCTCGAA 312
Db 81 SerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeuLys 100
QY 313 CTGAGCTCTGTGACCGCTCGGACACGCTGTATTACTGTGCGGAGA-----GTAATT 366
Db 101 LeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgHisAsnSerSer 120
QY 367 AATTGG-----TTCGACCCCTCGGGCCAGGAAACCTGTGTCACCGTCTCTCTCA 414
Db 121 SerTrpTyrGlyArgTyrPheAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 140

RESULT 6
S47010
Ig heavy chain V4.21-UniqueD-J5 region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S47010
R:Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.
submitted to the EMBL Data Library, July 1994
A:Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bi
A:Reference number: S47009
A:Accession: S47010
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-126 <MAH>
A:Cross-references: EMBL:235492; NID:g517254; PIDN:CAA84625.1; PID:g517255
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 1.32e-42 Length: 126
Score: 593.50 Matches: 113
Percent Similarity: 89.68% Conservative: 0
Best Local Similarity: 89.68% Mismatches: 2
Query Match: 61.38% Indels: 11
DB: 2 Gaps: 1

US-08-728-463B-219 (1-524) x S47010 (1-126)

```

QY 70 CAGGTGAGCTAGCAGAGTGGGCGCAGGAGCTGTGAAGCCTTCGAGACCCCTGCTCCCTC 129
Db 1 GlnValGlnLeuGlnGlnTrpGlyAlaGlyLeuLeuLysProSerGluThrLeuSerLeu 20
QY 130 ACCTGGCTCTCTATGGTGTCTCTCAGTGGTTACTACTGAGCTGGATCGGCCAGCCA 189
Db 21 ThrCysAlaValTrpGlySerPheSerGlyTyrTyrTrpSerTrpIleArgGlnPro 40
QY 190 CAGGTAAGGCTTGGAGTGGATTGGTGAATCAATCATAGTGAAGCAGCAACCTACAC 249
Db 41 ProGlyLysGlyLeuGluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsn 60
QY 250 CGCTCTCTCAGAGTGCAGCTACCATATCAGTAGACAGCTCCCAAGAACAGTTCTCTG 309
Db 61 ProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeu 80
QY 310 AAACCTGAGCTCTGTGACCCCTCGGACACGGCTGTATTACTGTGCGAGA----- 360
Db 81 LysLeuSerSerValThrAlaAlaAspThrAlaValTyrCysAlaArgGlyGlyGln 100
QY 361 -----GTAATTAAATGGTTTCGACCCCTTGGGGCCAGGGAACC 396
Db 101 CysProLysLysAlaSerCysTyrThrLysAsnTrpPheAspProTrpGlyGlnGlyThr 120
QY 397 CTGGTCACCGTCTCCCTCA 414
Db 121 LeuValThrValSerSer 126

RESULT 7
ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C>Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
R:Moxtari, F.; Ochse, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.
Nucleic Acids Res. 19, 673, 1991
A:Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked
A:Reference number: S13519; MUID:91187691; PMID:2011536
A:Accession: S13519
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-147 <MOR>
A:Cross-references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:41-125/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 2,62e-42 Length: 147
Score: 590.00 Matches: 116
Percent Similarity: 86.43% Conservative: 5
Best Local Similarity: 82.86% Mismatches: 13
Query Match: 61.01% Indels: 6
DB: 2 Gaps: 2

US-08-728-463B-219 (1-524) x S13519 (1-147)
QY 13 ATGAACACCTGTGGTTCTTCTCTCTCGTGGCAGCTCTAGATGGTCTGCTCTAG 72
Db 8 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 27
QY 73 GTCAGCTACAGAGTGGGCGCAGGACTGTTGAAGCCTTCGAGACCCCTGCTCCCTCACC 132
Db 28 LeuGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 47
QY 133 TGGCGTGTCTATGGTGGTCTCTTC-----AGTGGTTACTACTGGAGCTGGATCCGCAG 186
Db 48 CysThrValSerGlyGlySerIleSerSerSerSerTyrTyrTrpGlyTrpIleArgGln 67
QY 187 CCACCAAGGTAGGCTGAGTGGATTGTGAATCAATCATAGTGAAGCAGCAACCTAC 246
Db 68 ProProGlyLysGlyLeuGluTrpIleGlySerIleTyrTyrSerGlySerThrTyrTyr 87

ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)

```

```

QY 247 AACCCGTCTCTCAAGAGTCAGTCCATATCAGTAGACACGTCACAGAACCAAGTTCTCT 306
Db 88 AsnProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSer 107
QY 307 CTGAACCTGAGCTCTGTGACCGCTGGGACACGGCTGTATTACTGTGCGAGAGTAATT 366
Db 108 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrCysAlaArgProLeu 127
QY 367 AATTGG-----TTCGACCCCTTGGGCGCAGGAAACCCCTGGTCAACCGTCTCCCTCA 414
Db 128 LeuTrpPheGlyGluLeuPheAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 147

RESULT 8
ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31676
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-137 <CUI>
A:Cross-references: EMBL:Z14182; NID:g31031; PIDN:CAA78551.1; PID:g31032
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-116/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 1,38e-41 Length: 137
Score: 581.50 Matches: 114
Percent Similarity: 86.86% Conservative: 5
Best Local Similarity: 83.21% Mismatches: 15
Query Match: 60.13% Indels: 3
DB: 2 Gaps: 1

US-08-728-463B-219 (1-524) x S31676 (1-137)
QY 13 ATGAACACCTGTGGTTCTTCTCTCTCGTGGCAGCTCTAGATGGTCTGCTCTCAG 72
Db 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20
QY 73 GTCAGCTACAGCAGTGGGCGCAGGACTGTGAAGCCTTCGAGACCCCTGCTCCCTCACC 132
Db 21 ValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40
QY 133 TGGCGTGTCTATGGTGGTCTCTTCTAGTGGTTACTTCTGAGCTGGATCCGCCAGCCACCA 192
Db 41 CysThrValSerGlyGlySerIleSerSerTyrTyrTrpSerTrpIleArgGlnProAla 60
QY 193 GGTAAAGGCTCGGAGTGGATTGGTGAATCAATCATAGTGAAGCAGCAACCTACACCCG 252
Db 61 GlyLysGlyLeuGluTrpIleGlyArgIleTyrThrSerGlySerThrAsnTyrAsnPro 80
QY 253 TCTCTCAAGAGTCAGTCCATATCAGTAGACACGTCACAGACCCAGTCTCTCTGAAA 312
Db 81 SerLeuLysSerArgValThrMetSerValAspThrSerLysAsnGlnPheSerLeuLys 100
QY 313 CTGAGCTCTGTGACCGCTGGGACACGGCTGTATTACTGTGCGAGA-----GTA 363
Db 101 LeuSerSerValThrAlaAlaAspThrAlaValTyrCysAlaArgAspAlaProLeu 120
QY 364 ATTAATTGGTTCGACCCCTTGGGCGCAGGAAACCCCTGGTCAACCGTCTCCCTCA 414
Db 121 MetTyrGlyMetAspValTrpGlyGlnGlyThrValThrValSerSer 137

RESULT 9
ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)

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C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31586
R/Cuissinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31586
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-139 <UI>
A/Cross-references: EMBL:Z14196; NID:g30978; PIDN:CAA78565.1; PID:g30979
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:34-116/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 1,38e-41 Length: 139
Score: 581.50 Matches: 115
Percent Similarity: 85.61% Conservative: 4
Best Local Similarity: 82.73% Mismatches: 15
Query Match: 60.13% Indels: 5
DB: 2 Gaps: 1

US-08-728-463b-219 (1-524) x S31586 (1-139)
QY 13 ATGAACACCTGGTTCCTCTCTCGTGGCGAGCTCCTAGATGGGTCTGTCTCAG 72
Db 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20
QY 73 GTCACCTCAGCAGTGGGGCGCAGGACTGTTCAAGCCTTCGGAGACCTGTCCCTCACC 132
Db 21 ValGlnLeuGlnSerGlyProGlyLeuValProSerGlnThrLeuSerLeuThr 40
QY 133 TGGCGTCTGTATGGTGGTCTCTTCTCAGTGGTACTTACTGGAGCTGGATCCGCCAGCACCA 192
Db 41 CysThrValSerGlyGlySerIleSerSerTyTrpSerTrpIleArgGlnProAla 60
QY 193 GGTAAAGGCTGGAGTGGATGTGTAATCAATCATAGTGGAGACCACTACAACCCG 252
Db 61 GlyLysGlyLeuGlnTrpIleGlyArgIleTyThrSerGlySerThrAsnTyAsnPro 80
QY 253 TCTCTCAAGAGTGGAGTCCACCATATCAGTAGACACGTCCAAAGAACCACTCTCTCGAA 312
Db 81 SerLeuIleSerArgValThrMetSerValAspThrSerLysAsnGlnPheSerLeuLys 100
QY 313 CTGAGCTCTGTACCGCTGGGACACGGCTGTGTATTACTTGTCCGAGA----- 360
Db 101 LeuSerSerValThrAlaAlaAspThrAlaValTyTrpCysAlaArgGlyLeuGly 120
QY 361 ---GTAATTATGGTTCGACCTTGGGGCCAGGAAACCTGTCTACCGTCTCTCA 414
Db 121 IleArgArgGlyAlaPheAspIleTrpGlyGlnGlyThrMetValThrValSerSer 139

RESULT 10
B49028
Ig heavy chain V-IV region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
R/Timmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuur
Eur. J. Immunol. 21, 2355-2363, 1991
A/Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob
A/Reference number: A49028; MUID:92008140; PMID:1915549
A/Accession: B49028
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-143 <TIM>
A/Cross-references: GB:S64473; NID:g236906; PIDN:AAB20012.1; PID:g236907
A/Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines
A/Note: sequence extracted from NCBI backbone (NCBIN:64473, NCBI:P:64472)
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 2,26e-41 Length: 143
Score: 579.00 Matches: 114
Percent Similarity: 83.57% Conservative: 3
Best Local Similarity: 81.43% Mismatches: 9
Query Match: 59.88% Indels: 14
DB: 2 Gaps: 3

US-08-728-463b-219 (1-524) x B49028 (1-143)
QY 70 CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCTGTCTCCCTC 129
Db 1 GlnValGlnLeuGlnGlnTrpGlyAlaGlyLeuLysProSerGlnThrLeuSerLeu 20
QY 130 ACCTGCGCTGTATGGTGGTTCCTTCTCAGTGGTACTTACTGGAGCTGGATCCGCCAGCCA 189
Db 21 ThrCysAlaValTyArgGlySerPheSerGlyTyTrpSerTrpIleArgGlnPro 40
QY 190 CCAGGTAAAGGCTGGAGTGGATGTGTAATCAATCATAGTGGAGACCACTACAAC 249
Db 41 ProGlyLysGlyArgGlnTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyAsn 60
QY 250 CGGTCTCTCAAGAGTGGAGTCCACCATATCAGTAGACACGTCCAAAGAACCACTCTCTCTG 309
Db 61 ProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeu 80
QY 310 AAACCTCAGCTCTGTGACCGCTCGGACACGGCTGTGTATTACTTGTCCGAGA----- 360
Db 81 LysLeuSerSerValThrAlaAlaAspThrAlaValTyTrpCysAlaArgGlyProIle 100
QY 361 ---GTAATT-----AATTGG-----TTCGACCTTGGGGC 387
Db 101 ValValValProAlaAlaMetArgGlyArgGlyTrpAspTyArgIleMetAspValTrpGly 120
QY 388 CAGGGAACCTCGTGCACCGTCTCCTCAGCTCAACCAAGGGCCATCGGTCTTCCCTCC 447
Db 121 GlnGlyThrThrValThrValSerSerGlySerArgSerAlaProThrLeuPheProLeu 140

RESULT 11
S31511
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C/Accession: S31511
R/Chastagner, P.; Demaison, C.; These, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A/Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA au
A/Reference number: S31509
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-155 <CHA>
A/Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:47-129/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 2,75e-41 Length: 155
Score: 578.00 Matches: 112
Percent Similarity: 84.51% Conservative: 8
Best Local Similarity: 78.87% Mismatches: 14
Query Match: 59.77% Indels: 8
DB: 2 Gaps: 2

US-08-728-463b-219 (1-524) x S31511 (1-155)
QY 13 ATGAACACCTGGTGGTTCCTCTCTCCTCGTGGAGCTCCTAGATGGGTCTGTCTCAG 72
Db 14 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 33
QY 73 GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCTGTCTCCCTCACC 132

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Search completed: June 3, 2003, 09:07:59
Job time : 24.1646 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 9.9393 Seconds
(without alignments)
4373.264 Million cell updates/sec

Title: US-08-728-463B-219
Perfect score: 967
Sequence: 1 AGCTTGCCACCATGAACA.....GACTACTTCCCGAACCGGT 524

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 225784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-O=/cn2.1/USPTO_spool/US08728463/runat_03062003_085614_16804/app_query.fasta_1.3690
-DB=SwissProt 40 -OPMT=fastan -SUFFIX=rep -MINMATCH=0.1 -LOOPCI=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US08728463 @CGN 1.1.76 @runat_03062003_085614_16804 -NCPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LNGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	572	59.2	146	1 HV21_HUMAN	P06331 homo sapien
2	402	41.6	129	1 HV2F_HUMAN	P01824 homo sapien
3	396	41.0	117	1 HV2G_HUMAN	P01825 homo sapien
4	393.5	40.7	137	1 HV46_MOUSE	P01822 mus musculus
5	370	38.3	116	1 HV60_MOUSE	P18331 mus musculus
6	358	37.0	144	1 HV43_MOUSE	P01819 mus musculus
7	354	36.6	113	1 HV47_MOUSE	P01823 mus musculus
8	343	35.5	116	1 HV61_MOUSE	P18532 mus musculus
9	336	34.7	135	1 HV02_XENLA	P20957 xenopus lae
10	326.5	33.8	117	1 HV62_MOUSE	P18533 mus musculus
11	326.5	33.8	119	1 HV38_MOUSE	P01808 mus musculus
12	326	33.7	138	1 HV48_MOUSE	P03980 mus musculus
13	322.5	33.4	139	1 HV07_MOUSE	P01751 mus musculus
14	321	33.2	117	1 HV41_MOUSE	P01811 mus musculus
15	318.5	32.9	147	1 HV2H_HUMAN	P04438 homo sapien
16	317.5	32.8	119	1 HV37_MOUSE	P01807 mus musculus
17	316	32.7	115	1 HV44_MOUSE	P01820 mus musculus
18	314.5	32.5	119	1 HV40_MOUSE	P01810 mus musculus

19	311.5	32.2	136	1 HV01_XENLA	P20956 xenopus lae
20	311	32.2	142	1 HV01_RAT	P01805 rattus norv
21	308.5	31.9	137	1 HV11_MOUSE	P01755 mus musculu
22	308	31.9	118	1 HV39_MOUSE	P01809 mus musculu
23	305	31.5	117	1 HV12_MOUSE	P01756 mus musculu
24	304	31.4	116	1 HV45_MOUSE	P01821 mus musculu
25	303.5	31.4	120	1 HV50_MOUSE	P06329 mus musculu
26	300	31.0	117	1 HV13_MOUSE	P01757 mus musculu
27	298.5	30.9	114	1 HV3B_HUMAN	P01763 homo sapien
28	296.5	30.7	122	1 HV3G_HUMAN	P01768 homo sapien
29	294	30.4	121	1 HV01_MOUSE	P01745 mus musculu
30	293.5	30.4	118	1 HV51_MOUSE	P06330 mus musculu
31	290.5	30.0	117	1 HV04_MOUSE	P01748 mus musculu
32	288.5	29.8	120	1 HV2B_HUMAN	P01815 homo sapien
33	288	29.8	122	1 HV3A_HUMAN	P01762 homo sapien
34	288	29.8	117	1 HV42_MOUSE	P01812 mus musculu
35	288	29.8	123	1 HV25_MOUSE	P01794 mus musculu
36	287.5	29.7	116	1 HV36_MOUSE	P01806 mus musculu
37	287	29.7	115	1 HV3D_HUMAN	P01765 homo sapien
38	287	29.7	116	1 HV05_CARAU	P19181 carassius a
39	287	29.7	140	1 HV02_MOUSE	P01746 mus musculu
40	286	29.6	119	1 HV3I_HUMAN	P01770 homo sapien
41	285	29.5	121	1 HV3J_HUMAN	P01771 homo sapien
42	284	29.4	117	1 HV17_MOUSE	P01786 mus musculu
43	282.5	29.2	122	1 HV20_MOUSE	P01789 mus musculu
44	281.5	29.1	117	1 HV09_MOUSE	P01753 mus musculu
45	281.5	29.1	117	1 HV3C_HUMAN	P01764 homo sapien

ALIGNMENTS

RESULT 1
HV21_HUMAN
ID HV21_HUMAN STANDARD; PRT; 146 AA.
AC P06331;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region ARH-77 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85205332; PubMed=3922855;
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT "A cloned human immunoglobulin heavy chain gene with a novel direct-repeat sequence in 5' flanking region.";
RL Gene 33:181-189(1985).
DR PIR; A02101; GIHJH2.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 146 IG HEAVY CHAIN V-II REGION ARH-77.
FT DOMAIN 20 117 V SEGMENT.
FT DOMAIN 118 127 D SEGMENT.
FT DOMAIN 128 146 J SEGMENT.
FT DISULFID 42 115 BY SIMILARITY.
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;
Alignment Scores:
Pred. No.: 1.88e-41 Length: 146
Score: 572.00 Matches: 114
Percent Similarity: 81.51% Conservative: 5
Best Local Similarity: 78.08% Mismatches: 15
Query Match: 59.15% Indels: 13
DB: 1

SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

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FT STRAND 33 39
FT TURN 41 42
FT STRAND 46 51
FT TURN 53 54
FT STRAND 57 59
FT TURN 61 63
FT STRAND 64 66
FT TURN 67 72
FT STRAND 73 76
FT TURN 77 82
FT STRAND 87 89
FT TURN 91 98
FT STRAND 104 107
FT TURN 111 115
FT STRAND 117 117
SQ SEQUENCE 117 AA; 12790 MW; 2DA47B509562D237 CRC64;

Alignment Scores:
Pred. No.: 2,08e-26 Length: 117
Score: 396.00 Matches: 76
Percent Similarity: 81.20% Conservatives: 19
Best Local Similarity: 64.96% Mismatches: 20
Query Match: 40.95% Indels: 2
DB: 1 Gaps: 1

US-08-728-463b-219 (1-524) x HV2G_HUMAN (1-117)
QY 70 CAGGTGAGTCTGAGTGGCGGAGGAGTCTTGAAGCTTCGGAGACCCCTGTCCTC 129
Db 1 GlnValGlnLeuGlnSerGlyProGlyLeuValArgProSerGlnThrLeuSerLeu 20
QY 130 ACTGCGCTGCTATGCTGCTTCCTTCAGTGGTTACTACTGAGCTGGATCCGCCAGCCA 189
Db 21 ThrCysThrValSerGlySerThrPheSerAsnAspTyrTyrThrTrpValArgGlnPro 40
QY 190 CAGGTAAGGCTGCTGAGTGGTATTGTAATCAATCATAGTGTGAGACCACTACAAC 249
Db 41 ProGlyArgGlyLeuGlnTrpPileGlyTyrValPheTyrHisGlyThrSerAspThr 60
QY 250 CCGTCTCTCAAGAGTCCAGTCCACCATATCATGATAGACACGTCACCAAGACCATGTTCTCTCG 309
Db 61 ThrProLeuArgSerArgValThrMetLeuValAspThrSerIysGlnPheSerLeu 80
QY 310 AAATGAGTCTGTGACCGCTGCGGACACGGCTGTGTATTACTGTGCGAGA-----GTA 363
Db 81 ArgLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgAsnLeuLeu 100
QY 364 ATTAATGTTTCACCCCTGGGCGCCAGGACCCCTGTCACCGTCTCTCTCA 414
Db 101 AlaGlyCysIleAspValTrpGlyGlnGlySerLeuValThrValSerSer 117

RESULT 4
HV46 MOUSE STANDARD; PRT; 137 AA.
ID HV46 MOUSE
AC P01822;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig heavy chain V region MOPC 315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89238351; PubMed=2497341;
RA Rinfret A., Horne C., Dorrington K.J., Klein M.;
RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH
RT gene segment.";
RL Mol. Immunol. 26:431-434 (1989).
RN [2]
RP SEQUENCE OF 1-31.
RX MEDLINE=78094475; PubMed=414225;

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RA Jilka R.L., Pestka S.;
RT "Amino acid sequence of the precursor region of MOPC-315 mouse
RT immunoglobulin heavy chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696 (1977).
RN [3]
RP SEQUENCE OF 1-21.
RX MEDLINE=79148758; PubMed=428562;
RA Schechter I., Wolf O., Zemell R., Burstein Y.;
RT "Structure and function of immunoglobulin genes and precursors.";
RL Fed. Proc. 38:1839-1845 (1979).
RN [4]
RP SEQUENCE OF 19-136.
RX MEDLINE=74170779; PubMed=4524622;
RA Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.;
RT "Amino-acid sequence of the variable region of the heavy (alpha)
RT chain of a mouse myeloma protein with anti-hapten activity.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127 (1974).
RN [5]
RP REVISION TO 53.
RX MEDLINE=77244979; PubMed=268248;
RA Hood L., Margolies M.N., Givol D., Zakut R.;
RL Unpublished results, cited by:
RL Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
RL Cold Spring Harb. Symp. Quant. Biol. 41:627-637 (1977).
CC -!- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
CC -----
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CC -----
CC EMBL; M27638; AAA61337.1; -
CC EMBL; X07880; CAA30727.1; -
CC PIR; P0102; AVMS35.
CC HSP; P01825; 7FAB.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; ig_1.
CC SMART; SM00406; IGV; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 18
CC CHAIN 19 137 IG HEAVY CHAIN V REGION MOPC 315.
CC DOMAIN 19 48 FRAMEWORK-1.
CC DOMAIN 49 54 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 55 68 FRAMEWORK-2.
CC DOMAIN 69 84 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 85 116 FRAMEWORK-3.
CC DOMAIN 117 126 COMPLEMENTARITY-DETERMINING-3.
CC DOMAIN 127 137 FRAMEWORK-4.
CC DISULFID 40 114 BY SIMILARITY.
CC CONFLICT 15 15 G -> GG (IN REF. 1; CAA30727).
CC CONFLICT 15 15 G -> H (IN REF. 2).
CC CONFLICT 77 78 GY -> YG (IN REF. 4).
CC CONFLICT 102 102 N -> D (IN REF. 4).
CC CONFLICT 123 123 MISSING (IN REF. 4).
CC NON_TER 137 137
SQ SEQUENCE 137 AA; 15399 MW; FB3828304C2B81DC CRC64;

Alignment Scores:
Pred. No.: 3,44e-26 Length: 137
Score: 393.50 Matches: 82
Percent Similarity: 73.19% Conservatives: 19
Best Local Similarity: 59.42% Mismatches: 32
Query Match: 40.69% Indels: 5
DB: 1 Gaps: 3

US-08-728-463b-219 (1-524) x HV46_MOUSE (1-137)
QY 13 ATGAACACCTGTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCAG 72

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US-08-728-463B-219 (1-524) x HV60_MOUSE (1-116)

QY      13  ATGAACACCTGTGGTTCCTCCTCTGTGTGGCAGCTCTCTAGATGGGTCCTGTCTCAG 72
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1  MetLysValLeuSerLeuLeuTyLeuLeuThrAlaIlePro--GlyIleLeuSerAsp 19
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      73  GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTAGAGCCTTCGAGACCCCTGTCTCCCTACC 132
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      20  ValGlnLeuGlnGluSerGlyProGlyLeuValIleProSerGlnSerLeuSerLeuThr 39
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      133  TGCCTGTCTATGTGGTTCCTTC--AGTGGTTACTACTGGAGCTGGATCCGCCACGCCA 189
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      40  CysSerValThrGlyTySerIleThrSerGlyTyTyTrpAsnTrpIleArgGlnPhe 59
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      190  CCAGTAAGGCTCGGAGTCGATGGTGAATCAATCATAGTGGAGACCCAACTCAAC 249
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      60  ProGlyAsnLysLeuGluTrpMetGlyTyIleSerTyAspGlySerAsnAsnTyArgn 79
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      250  CCGTCTCTCAAGACTCGAGTCACCATCATAGTAGACACAGTCCAAGAACACAGTTCTCTCG 309
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      80  ProSerLeuLysAsnArgIleSerIleThrArgAspThrSerLysAsnGlnPhePheLeu 99
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      310  AAATGTAGCTCTGTGACCGCTCGGCACACGGCTGTGTATTACTGTGCGAGA 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      100  LysLeuAsnSerValThrGluAspThrAlaIleThrTyTyCysAlaArg 116
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 6
ID HV43 MOUSE
P01819; STANDARD; PRT; 144 AA.
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
IG heavy chain V region MOPC 141 precursor.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
MEDLINE=81012133; PubMed=6774258;
Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
"Two types of somatic recombination are necessary for the generation
of complete immunoglobulin heavy-chain genes.";
Nature 286:676-683(1980).
-!- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.

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or send an email to license@ebi.ac.uk.

Sequence	Length	Matches	Conservative
IG HEAVY CHAIN V REGION MOFC 141.	3.75e-23	358.00	74
8E47A7CB3706D30A CRC64;	15759 MW;	144 AA;	15759 MW;


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-Best Local Similarity: 51.39%  Mismatches: 38
Query Match: 37.02%  Indels: 10
DB: 1  Gaps: 1

US-08-728-463B-219 (1-524) x HV43_MOUSE (1-144)

Qy 13 ATGAACACACCTGTGGTCTTCTCTCTCTGGTGGCAGCTCTCTAGATGGGTCTGTCTCTAG 72
Db 1 MetAlaValLeuAlaLeuLeuPheCysLeuAlaThrPheProSerCysIleLeuSerGln 20
Qy 73 GTGCAGCTTACAGCAGCGGGGGCAGCACTGTTGAAGACCTTCGGAGACCTCTCCCTCAC 132
Db 21 ValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIleThr 40
Qy 133 TGCCTGTCTATGTGGTTCCTTCACTAGTGTACTACTGGAGCTGGATCCGCCAGCACCA 192
Db 41 CysThrValSerGlyPheSerLeuThrGlyTyGlyValAsnTrpValArgGlnProPro 60
Qy 193 GGTAAAGGCTCTGGAGTGGATTGGTCAATCAATCATATAGTGAAGACCAACTACAAACCG 252
Db 61 GlyLysGlyLeuGluTrpLeuGlyThrIleTrpGlyAsnGlySerThrAspTyrAsnSer 80
Qy 253 TCTCTCAAGAGTCGAGTCACCATATCAGTAGACAGCTCCAAGAACAGTTCCTCTCTGAA 312
Db 81 ThrLeuLysSerArgLeuThrIleThrLysAspAsnSerLysSerGlnValPheLeuLys 100
Qy 313 CTGAGCTCTGTGACCGCTCGGACACGGCTGTGTATTACTGTGCAGAGATTAATTATGG 372
Db 101 MetAsnSerLeuGlnThrAspAspThrAlaArgTyrTyrcysAlaSerValSerIleTy 120
Qy 373 TTC-----GACCCTTGGGGCCAGGAACCTGGTC 402
Db 121 TyrTyGlyArgSerAspLysTyrPheThrLeuAspTyrTrpGlyGlnGlyThrSerVal 140
Qy 403 ACCGTCCTCTCTCA 414
Db 141 ThrValSerSer 144

RESULT 7
HV47_MOUSE
ID HV47_MOUSE STANDARD; PRT; 113 AA.
AC P01823;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 36, Last annotation update)
DE Ig heavy chain v region 36-60.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=84024551; PubMed=6414509;
RA Juszczak E.C., Margolies M.N.;
RT "Amino acid sequence of the heavy chain variable region from the A/J
RT mouse anti-arsenate monoclonal antibody 36-60 bearing a minor
RT idioType.";
RL Biochemistry 22:4291-4296(1983).
CC -!- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM AN ANTIARSONATE
CC MONOCLONAL ANTIBODY OF THE IGG2A SUBCLASS. IT REPRESENTS A SECOND
CC IDIOTYPE FAMILY CHARACTERISTIC OF THE ANTIARSONATE RESPONSE OF
CC STRAIN A/J MICE.
CC PIR; A02098; G2MS60.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin v region; Antiarsenate antibody.
FT NON TER 113
SQ SEQUENCE 113 AA; 12734 MW; 38DC0E0E3F5075B7 CRC64;

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Alignment Scores:
Pred. No.: 8.1e-23 Length: 113
Score: 354.00 Matches: 70
Percent Similarity: 78.26% Conservative: 20
Best Local Similarity: 60.87% Mismatches: 23
Query Match: 36.61% Indels: 2
DB: 1 Gaps: 1

US-08-728-463B-219 (1-524) x HV47_MOUSE (1-113)

QY 70 CAGGTGCAGCTACAGCAGTGGCGGCGCAGGACTGTTGAAGACCTTTCGAGACCCCTGTCCCTC 129
DB 1 GluValGlnLeuGlnSerGlyProSerLeuVallyProSerGlnThrLeuSerLeu 20
QY 130 ACCTGCGCTGTACTATGTTGTTCTTCACTAGTGTACTACTGGAGTGGATCCGCAGCCA 189
DB 21 ThrCysSerValThrGlyAspSerIleThrSerAspTyrTrpAsnTrpIleArgLysPhe 40
QY 190 CCAGGTAAGGCTCGGAGTGGATTGGTCAATCAATCATAGTGGGAAGCACCACCACTACAAC 249
DB 41 ProGlyAsnLysLeuGluHiMetGlyTyrIleSerTyrSerGlySerThrTyrTyrAsn 60
QY 250 CCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGACAGTCAGTCACAGAACCCAGTTCTCTCTG 309
DB 61 ProSerLeuLysSerArgIleSerIleThrArgAspThrSerLysAsnGlnTyrTyrLeu 80
QY 310 AAACGTAGCTCTGTACCCGCTGCGGACACGGCTGTGTATTACTGTGCGAGAGTAATTAA 369
DB 81 GlnLeuAsnSerValThrSerGluAspThrAlaThrTyrTyrCysThrSerLeu----- 98
QY 370 TGGTTCGACCTTCGGGCGCAGGACCCCTGTGCACCGTCTCCTCA 414
DB 99 ArgPheAlaTyrTrpGlyGlnGlyThrLeuValThrValSerAla 113

RESULT 8
HV61_MOUSE
ID HV61_MOUSE STANDARD; PRT; 116 AA.
AC P18532;
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.
DR PIR: J070508; HVMS1B.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 116
FT DOMAIN 19 48
FT DOMAIN 49 53
FT DOMAIN 54 67
FT DOMAIN 68 84
FT DOMAIN 85 116
FT DISULFID 40 114
FT NON TER 116 116
SQ SEQUENCE 116 AA; 13158 MW; 1CB547253681EF74 CRC64;

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1 DISULFID 40 115 BY SIMILARITY.

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FT  NON TER      117      117
SQ  SEQUENCE     117 AA;  13223 MW;  1595517827P976BE CRC64;

Alignment Scores:
Pred. No.:      1.82e-20      Length:      117
Score:          326.50        Matches:      68
Percent Similarity: 70.34%    Conservative: 15
Best Local Similarity: 57.63%  Mismatches: 32
Query Match:     33.76%      Indels:      3
DB:              1          Gaps:      2

US-08-728-463B-219 (1-524) x HV62_MOUSE (1-117)
QY  13 ATGAACACCTGGTTCCTCCTCCTGGTGGCAGCTCCTAGATGGGTCTGTCTCAG 72
Db  1 MetLysMetPheThrLeuLeuTyrLeuLeuThrValValPro---GlyIleLeuSerAsp 19
QY  73 GTCAGCTACAGCAGTGGGGCGGAGGACTGTTGAAGCTTCGGAGACCCCTGTCCTCACC 132
Db  20 ValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGlnSerIleAlaLeuThr 39
QY  133 TGCCTGTCTATGGTGGTTCCTTTCAGT-----GGTTACTACTGGAGCTGGATCCGCCAG 186
Db  40 CysThrValThrGlyIleSerIleThrThrGlyAsnTyrArgTrpSerTrpIleArgGln 59
QY  187 CCACCACTAAGGCTCGAGTGGATGTGTAATCAATCATATAGTGAACCACTAC 246
Db  60 PheProGlyAsnLysLeuGluTrpIleGlyTyrIleTyrSerAlaIleThrSerTyr 79
QY  247 AACCCGTCTCTCAAGAGTCCAGTCCACCATATCATAGTACACGCTCCAGAACCACTCTCT 306
Db  80 AsnProSerProLysSerArgThrIleThrArgAspThrSerLysAsnGlnPhePhe 99
QY  307 CTGAACACTGAGCTCTGTGACCGCTGGCGACACGCTGTGTATTACTGTGCGAGA 360
Db  100 LeuGluMetAsnSerLeuThrAlaGluAspThrAlaThrTyrTyrCysAlaArg 117

RESULT 11
HV38_MOUSE
ID  HV38_MOUSE      STANDARD;      PRT;      119 AA.
AC  P01808;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig heavy chain V region T601.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=79223895; PubMed=111245;
RA  Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT  "Structural evidence for independent joining region gene in
RT  immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT  its potential role in generating diversity in
RT  complementarity-determining regions.";
RL  Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894 (1979).
CC  -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC  THAT BINDS GALACTAN.
DR  PIR; A02078; AWMST6.
DR  HSSP; P01810; 2FBJ.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; Ig_1.
DR  SMART; SM00406; IGV; 1.
KW  Immunoglobulin V region.
FT  NON TER      119
SQ  SEQUENCE     119 AA;  13169 MW;  BC38CC84E6EA00E8 CRC64;

Alignment Scores:
Pred. No.:      1.83e-20      Length:      119
Score:          326.50        Matches:      65

FT  NON TER      117      117
SQ  SEQUENCE     117 AA;  13223 MW;  1595517827P976BE CRC64;

Alignment Scores:
Pred. No.:      1.82e-20      Length:      119
Score:          326.50        Matches:      65

Percent Similarity: 69.49%    Conservative: 17
Best Local Similarity: 55.08%  Mismatches: 33
Query Match:     33.76%      Indels:      3
DB:              1          Gaps:      2

US-08-728-463B-219 (1-524) x HV38_MOUSE (1-119)
QY  70 CAGGTCCAGCTACAGCAGTGGGGCGGAGGACTGTTGAAGCTTCGGAGACCCCTGTCTCCTC 129
Db  1 GluValLysLeuGluSerGlyGlyLeuValGlnProGlyGlySerLeuLysLeu 20
QY  130 ACCTGGCGTGTCTATGGTGGTTCCTTTCAGTGGTGTACTTGGAGCTGGATCCGCCAGCCA 189
Db  21 SerCysAlaAlaSerGlyPheAspPheSerArgTyrTrpMetSerTrpValArgGlnAla 40
QY  190 CCAGGTAAGGGTCTGGAGTGGATTTGGTGAATCAATCATATAGTGAAGACACC---AACTAC 246
Db  41 ProGlyLysGlyLeuGluTrpIleGlyGluIleAsnProAspSerSerThrIleAsnTyr 60
QY  247 AACCCGTCTCTCAAGAGTCCAGTCCACCATATCATAGTACACGCTCCAGAACCACTCTCT 306
Db  61 ThrProSerLeuLysAspLysPheIleIleSerArgAspAsnAlaLysAsnThrLeuTyr 80
QY  307 CTGAACACTGAGCTCTGTGACCGCTGGCGACACGCTGTGTATTACTGTGCGAGATA--- 363
Db  81 LeuGlnMetSerLysValArgSerGluAspThrAlaLeuTyrTyrCysAlaArgLeuGly 100
QY  364 ---ATTAATTTGTTGACCCCTTGGGGCCAGGGAACCCCTGTGTACCCGTCTCTCTCA 414
Db  101 TyrTyrGlyTyrPheAspValTrpGlyAlaGlyThrThrValThrValSerSer 118

RESULT 12
HV48_MOUSE
ID  HV48_MOUSE      STANDARD;      PRT;      138 AA.
AC  P03980;
DT  23-OCT-1986 (Rel. 02, Created)
DT  23-OCT-1986 (Rel. 02, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig heavy chain V region TEPC 1017 precursor.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=84248078; PubMed=6429663;
RA  Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA  Tucker P.W.;
RT  "Illegitimate recombination generates a class switch from C mu to C
RT  delta in an Igd-secreting plasmacytoma.";
RL  Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168 (1984).
DR  HSSP; P01810; 2FBJ.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; Ig_1.
DR  SMART; SM00406; IGV; 1.
KW  Immunoglobulin V region; Signal.
FT  SIGNAL       1 20
FT  CHAIN        21 138      IG HEAVY CHAIN V REGION TEPC 1017.
FT  DOMAIN       21 49      FRAMEWORK-1.
FT  DOMAIN       50 54      COMPLEMENTARITY-DETERMINING-1.
FT  DOMAIN       55 68      FRAMEWORK-2.
FT  DOMAIN       69 85      COMPLEMENTARITY-DETERMINING-2.
FT  DOMAIN       86 117     FRAMEWORK-3.
FT  DOMAIN      118 127     COMPLEMENTARITY-DETERMINING-3.
FT  DOMAIN      128 138     FRAMEWORK-4.
FT  DISULFID     41 115     BY SIMILARITY.
FT  NON TER     138 138
SQ  SEQUENCE     138 AA;  15576 MW;  748157B4C6907B8E CRC64;

Alignment Scores:
Pred. No.:      2.04e-20      Length:      138

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Score: 326.00 Matches: 66
Percent Similarity: 67.16% Conservative: 24
Best Local Similarity: 49.25% Mismatches: 40
Query Match: 33.71% Indels: 4
DB: 1 Gaps: 2

US-08-728-463B-219 (1-524) x HV48_MOUSE (1-138)

QY 25 TGGTTCCTCTCCCTGCGGAGCTCCTAGATGGTCTCTCAGTGCAGCTACAG 84
Db 5 TyrilleleLeuPheLeuValAlaThrAlaThrAspValHisSerGlnValGlnLeuGln 24
QY 85 CAGTGGGCGCAGACGCTGTTGAAGCCTTCGAGACCTGTCCTCACCCTGCTGTCTAT 144
Db 25 GlnProGlyAlaGluLeuValValProGlyAlaSerValGlnLeuSerCysLysAlaSer 44
QY 145 GGTGGTTCCTTCAGTGGTCTACTGAGCTGCATCCGACCCAGCCAGGTAAGGCTG 204
Db 45 GlyHisThrPheThrAsnTyrTrpIleHisTrpValLysGlnArgProGlyGlnGlyLeu 64
QY 205 GAGTGGATGCTGAATCAAT---CATAGTGAAGCACCACCACTACAACCCGCTCTCTCAAG 261
Db 65 GluTrpIleGlyLeuLeuAsnProAsnAspGlyArgSerAsnTyrAsnGlnLysPheLys 84
QY 262 AGTCGAGTCACCATATACAGTACACGCTCCAGAACCCAGTCTCTCTGAACTGAGCTCT 321
Db 85 AsnLysAlaThrLeuThrValAspLysSerSerThrAlaTyrMetGlnLeuSerSer 104
QY 322 GTGACCGCTGGCGACACGCTGTGTATTACTGTGCGAGA-----GTAATTAATGG 372
Db 105 LeuThrProGluGluPheAlaValTyrCysAlaArgSerAspGlyTyrTyrAspTrp 124
QY 373 TTCGACCCCTGGGGCCAGGACCTGCTGCACCGCTCTCTCA 414
Db 125 PheValTyrTrpGlyGlnGlyThrLeuValThrPheSerAla 138

RESULT 13
HV07_MOUSE
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain v region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paekind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN mRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J00529; AAA38170.1;
CC PIR: A02034; MHMS18.
CC HSSP: P01810; 2PBJ.
CC InterPro: IPR003006; Ig_MHC.

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DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1...
DR SMART: SMO0406; IGv; 1:
KW Immunoglobulin V region; Signal.
FT CHAIN 1 19 IG HEAVY CHAIN V REGION B1-8/186-2.
FT DOMAIN 20 139 FRAMEWORK-1.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SO SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Alignment Scores:
Pred. No.: 4,06e-20 Length: 139
Score: 322.50 Matches: 65
Percent Similarity: 67.42% Conservative: 24
Best Local Similarity: 49.24% Mismatches: 38
Query Match: 33.35% Indels: 5
DB: 1 Gaps: 2

US-08-728-463B-219 (1-524) x HV07_MOUSE (1-139)

QY 34 CTCCTCTCTGTCGGAGCTCCTAGATGGTCTCTCAGTGCAGCTACAGCTGGGCG 93
Db 8 LeuPheLeuAlaThrAlaThrGlyValHisSerGlnValGlnLeuGlnProGly 27
QY 94 CGAGGACTGTTCAAGCCTTCGAGACCTGCTCCCTCACCCTGCTGTCTATGTTGGTTC 153
Db 28 AlaGluLeuValLysProGlyAlaSerValLysLeuSerCysLysAlaSerGlyTyrThr 47
QY 154 TTCAGTGTACTACTGGAGCTGGTCCGCGCAGCCAGCCAGCTAAGGCTCTGAGTGGATT 213
Db 48 PheThrSerTyrTrpMetHisTrpValLysGlnArgProGlyArgGlyLeuGlnTrpIle 67
QY 214 GGTGAATCAAT---CATAGTGAAGCACCACCACTACAACCCGCTCTCTCAAGTGCAGTC 270
Db 68 GlyArgLysAspProAsnSerGlyGlyThrLysTyrAsnGlnLysPheLysSerLysAla 87
QY 271 ACCATATCAGTAGACACGCTCCCAAGAACCCAGTCTCTCTGAAACTGAGCTCTGTGACCGCT 330
Db 88 ThrLeuThrValAspLysProSerSerThrAlaTyrMetGlnLeuSerSerLeuThrSer 107
QY 331 CGGACACCGCTGTATTACTGTGCGAGAGTA-----ATTAATTGTTTCGAC 378
Db 108 GluAspSerAlaValTyrTyrCysAlaArgTyrAspTyrTyrGlySerSerTyrPheAsp 127
QY 379 CTTTGGGGCCAGGAGAACCCCTGGTCCACCGCTCTCTCA 414
Db 128 TyrTrpGlyGlnGlyThrThrLeuThrValSerSer 139

RESULT 14
HV41_MOUSE
ID HV41_MOUSE STANDARD; PRT; 117 AA.
AC P01811;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig heavy chain v region UPC10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83021113; PubMed=6181731;
RA Aulicay C., Sikorav J.L., Ollio R., Rougeon F.;
RT "Correlation between D region structure and antigen-binding
RT specificity: evidences from the comparison of closely related

```

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RA	Takahashi N., Noma T., Honjo T.;
RT	"Rearranged immunoglobulin heavy chain variable region (VH)
RT	pseudogene that deletes the second complementarity-determining
RT	region.";
RL	Proc. Natl. Acad. Sci. U.S.A. 81:5194-5198(1984).
DR	PIR; A02090; G2HUCS.
DR	HSSP; F01825; 7FAB.
DR	InterPro; IPR003006; IG_MHC.
DR	InterPro; IPR003596; IG_V.
DR	Pfam; PF00047; Ig_1.
KW	SMART; SM00406; IGV; 1.
KW	Immunoglobulin V region; Signal.
FT	SIGNAL
FT	CHAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	NON_TER
SQ	SEQUENCE

Alignment Scores:

Pred. No.:	8.96e-20	Length:	147
Score:	318.50	Matches:	71
Percent Similarity:	62.41%	Conservative:	17
Best Local Similarity:	50.35%	Mismatches:	39
Query Match:	32.94%	Indels:	14
DB:	1	Gaps:	2

US-08-728-463B-219 (1-524) x HV2H_HUMAN (1-147)

QY	34	CTCTCTGTGGCAGCTTCTAGATGGTGCTCTCTCAGTCGAGCTACAGCAGG	
Db	8	LeuLeuLeuLeuThrValProSerGlyValLeuSerGlnValAsnLeuArgGlu	
QY	94	GCAGGACTGTGAAGCCTTCGGAGACCCTGTCCCTCACCTCGCGCTGTCTATGGT	
Db	28	ProAlaLeuValLysAlaThrHisThrLeuThrLeuThrCysThrPheSerGly	
QY	154	TTCAGT-----GGTTACTACTGGAGCTGGATCGGCCAGCCAGTAAAGG	
Db	48	ValAsnThrArgGlyMetSerValSerTrpIleArgGlnProProGlyLysAla	
QY	208	TGGATTGGTGAATCATCATATAGTGAAGCACAACTACAACCCGCTCTCTCAAAG	
Db	68	TrpLeuAlaArgIleAspTrpAspAspLysTyrtyrGlyThrSerLeuGlu	
QY	268	GTCACCATATCATGTAGACAGCTCCAGAACCAAGTCTCTCTGAAACTGACGCTCT	
Db	88	LeuThrIleSerLysAspThrSerLysAsnGlnValValLeuLysValThrAsn	
QY	328	GTCGGGACACGGCTGTGTATTACTGTGCGAGAGTA-----	
Db	108	ProAlaAspThrAlaThrTyrtyrCysAlaargMetGlnValThrMetValarg	
QY	364	-----ATTAAATGGTTTCACCCCTTGGGCCAGGGAACCTTGTCACCGTCTCT	
Db	128	MetIleThrSerAsnAlaPheAspIletpGlyGlnGlyThr-TrpSerProSer	
QY	415	G 415	
Db	147	n 147	

Search completed: June 3, 2003, 09:04:09
Job time : 11.9393 secs

Search completed: June 3, 2003, 09:04:09
Job time : 11.9393 secs

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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 46.5159 Seconds
(without alignments)
4642.224 Million cell updates/sec

Title: US-08-728-463B-219
Perfect score: 967
Sequence: 1 AGCTTGCCACCATGAACA.....GACTACTTCCCGAACCGGT 524

Scoring table:

	BLOSUM62
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1343160

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-Q/cgn2 1/USPTO spool/US08728463/runat_03062003 085614 16815/app query.fasta_1.3690
-DB=SPTRMBL 21 -OPMT=fastan -SURF=rspt -MINMATCH=0 1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US08728463 @CGN 1 1 380 @runat_03062003 085614 16815 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

SPTRMBL 21:
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archesp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	716.5	74.1	588	4	Q8WUX4	Q8wux4 homo sapien

ID	Q8WUX4	PRELIMINARY;	PRT;	588 AA.
2	716.5	74.1	597	4
3	716.5	74.1	618	4
4	710.5	73.5	597	4
5	655.5	67.8	473	4
6	641	66.3	613	4
7	590	61.0	496	4
8	583.5	60.3	150	4
9	504.5	52.2	471	4
10	496	51.3	479	11
11	491	50.8	119	4
12	449	46.4	278	11
13	441.5	45.7	473	11
14	421	43.5	468	11
15	420	43.4	168	11
16	419.5	43.4	463	11
17	416	43.0	482	11
18	412	42.6	613	11
19	407.5	42.1	147	4
20	399.5	41.3	473	11
21	399.5	41.3	473	11
22	398	41.2	469	11
23	394	40.7	613	4
24	387.5	40.1	437	11
25	380.5	39.3	597	4
26	380	39.3	494	4
27	378	39.1	474	11
28	372.5	38.5	497	4
29	371	38.4	488	11
30	367.5	38.0	489	11
31	363.5	37.6	122	4
32	363	37.5	487	11
33	363	37.5	573	4
34	359.5	37.2	480	11
35	358	37.0	481	11
36	355.5	36.8	484	11
37	355.5	36.8	486	11
38	355.5	36.8	614	4
39	354.5	36.7	481	11
40	353.5	36.6	298	11
41	351	36.3	140	11
42	351	36.3	496	4
43	350.5	36.2	479	11
44	343.5	35.5	484	11
45	342.5	35.4	481	11

ALIGNMENTS

RESULT 1

ID	Q8WUX4	PRELIMINARY;	PRT;	588 AA.
AC	Q8WUX4;			
DT	01-MAR-2002 (TrEMBLrel. 20, Created)			
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)			
DE	Hypothetical 64.4 kDa protein.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LYMPH;			
RA	Strausberg R.;			
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC019235; AAH19235.1; -			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR003597; IG.c1.			
DR	InterPro; IPR003006; IG.MHC.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; PF00047; ig_5.			
DR	SMART; SM00409; IG; 2.			
DR	SMART; SM00407; IGc1; 4.			

RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC016369; AAH16369.1; --
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;

Alignment Scores:
 Pred. No.: 2,496-50 Length: 496
 Score: 590.00 Matches: 120
 Percent Similarity: 74.16% Conservative: 12
 Best Local Similarity: 67.42% Mismatches: 36
 Query Match: 61.01% Indels: 10
 DB: 4 Gaps: 3

US-08-728-463B-219 (1-524) x Q96KX8 (1-496)

QY 13 ATGAACACCTGGTTCCTCTCTCTGGTGGAGCTCTAGATGGGTCTCTCTCAG 72
 DB 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20
 QY 73 GTCAGCTACAGAGTGGGGCGCAGACTGTTGAAGCTTTCGAGACCTCTGCTCCAC 132
 DB 21 LeuGlnLeuGlnSerGlyProGlyLeuValLysSerSerGluThrLeuSerLeuThr 40
 QY 133 TGGCGTCTCTATCGTGGTCTCTC-----AGTGGTCTCTCTGAGCTGGATCCGCCAG 186
 DB 41 CysThrValSerGlySerLeuSerSerSerSerSerTrpTrpGlyTrpLeuArgGln 60
 QY 187 CCACAGGTAAGGCTCTGAGTGGATGGTGAATCAATCATAGTGAAGCACTAC 246
 DB 61 ProProGlyLysGlyLeuGluTrpLeuAlaAsnThrTrpTyrSerGlyLeuThrTyr 80
 QY 247 AACCGTCTCTCAAGAGTGGAGTACATATCATAGTAGACACAGTCCAAAGACCTCTCT 306
 DB 81 AsnProSerLeuLysSerArgValThrLeuSerValAspThrSerLysAsnGlnLeuSer 100
 QY 307 CTGAACACTGAGCTCTGACCGTGGGACACGGCTGTGTATTACTGTGGAGA----- 360
 DB 101 LeuLysValArgSerValThrAlaAlaAspThrAlaValTyrPheCysAlaArgGly 120
 QY 361 -----GTAATTAATTGTTCCGACCTTGGGGCCAGGAACTCTGTCACC 405
 DB 121 TyrSerArgSerGlyArgThrGlyAlaAlaAspTyrTrpGlyGlnGlyThrLeuValThr 140
 QY 406 GTCTCTCAGCTCAACCAAGGCGCCATCGGTCTTCCCGCTGGCACCTCTCTCCAAAGAGC 465
 DB 141 ValSerSerAlaSerProThrSerProLysValPheProLeuSerLeuLysSer---Thr 159
 QY 466 ACCTCTGGGGGACAGCGGCCCTGGCTGCTGGTCAAGGACTACTTCCCGAA 519
 DB 160 GlnProAspGlyAsnValValIleAlaCysLeuValGlnGlyPhePheProGln 177

RESULT 8

O95973 PRELIMINARY; PRT; 150 AA.
 ID O95973;
 AC O95973;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE VH4 heavy chain variable region precursor (Fragment).
 GN IGM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Sun C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
 RA

RT "Clonal proliferation of IgM secreting B cell in the synovium of
 Behcet's patient with arthritis.";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF103795; AAC79084.1; --
 DR HSP; P01825; 7FAB.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 >150 VH4 HEAVY CHAIN VARIABLE REGION.
 FT NON_TER 150 150
 SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Alignment Scores:

Pred. No.: 8,286-50 Length: 150
 Score: 583.50 Matches: 115
 Percent Similarity: 84.21% Conservative: 13
 Best Local Similarity: 75.66% Mismatches: 19
 Query Match: 60.34% Indels: 5
 DB: 4 Gaps: 3

US-08-728-463B-219 (1-524) x O95973 (1-150)

QY 13 ATGAACACCTGGTTCCTCTCTCTGGTGGAGCTCTAGATGGGTCTCTCTCAG 72
 DB 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20
 QY 73 GTCAGCTACAGAGTGGGGCGCAGACTGTTGAAGCTTTCGAGACCTCTGCTCCAC 132
 DB 21 LeuGlnLeuGlnSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuSer 40
 QY 133 TGGCGTCTCTATGGTGGTTCCTCTCAGT-----GGTTACTCTGGAGCTGGATCCGCCAG 186
 DB 41 CysThrValSerGlySerLeuSerSerSerSerTrpAsnTyrTrpGlyTrpLeuArgGln 60
 QY 187 CCACAGGTAAGGCTCTGAGTGGATGGTGAATCAATCATAGTGAAGCACTAC 246
 DB 61 ProProGlyLysGlyLeuGluTrpLeuGlySerLeuHisAsnSerGlySerAspTyr 80
 QY 247 AACCGTCTCTCAAGAGTGGAGTCCACCATATCATAGTAGACACAGTCCAAAGACCTCTCT 306
 DB 81 AsnProSerLeuLysSerArgValThrLeuSerValAspThrSerLysAsnGlnPheSer 100
 QY 307 CTGAACACTGAGCTCTGACCGTGGGACACGGCTGTGTATTACTGTGGAGAGTA--- 363
 DB 101 LeuArgLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgLeuGly 120
 QY 364 ATTAATTGGTTCGACCTTGGGGCCAGGAACTCTGGTCCACCTCTCTCTCAGCTCAAC 423
 DB 121 MetGlyAlaPheAspPheTrpGlyHisGlyThrMetValThrValSerSerGlySerAla 140
 QY 424 AAGGGCCCATCGGTCTTCCCTCTGGCACCTCTCTCC 459
 DB 141 SerAlaProThrLeuPhePro-----ProSerSer 150

RESULT 9

O8TC77 PRELIMINARY; PRT; 471 AA.
 ID O8TC77;
 AC O8TC77;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical 51.8 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SPLEEN;
 RA Strausberg R.;

RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035041; AAD56277.1; -;
 DR HSSP; P01825; 7FAB.

DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 119
 FT NON_TER 119
 SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EAOBE CRC64;

Alignment Scores:
 Pred. No.: 1.4e-40 Length: 119
 Score: 491.00 Matches: 95
 Percent Similarity: 85.71% Conservative: 7
 Best Local Similarity: 79.83% Mismatches: 13
 Query Match: 50.78% Indels: 4
 DB: 4 Gaps: 1

US-08-728-463B-219 (1-524) x Q9UL73 (1-119)

QY 70 CAGTCCACAGCAGTGGGGCGGCGAGCTGTTCAAGCTTCGAGACCTTCCTC 129
 Db 1 GlnValGlnLeuGlnSerGlyProGlyLeuValLysProSerGlnThrLeuSerLeu 20
 QY 130 ACTGCGCTGTATGCTGCTCTTCACTGAGTGGTACTGAGCTGGAGTCCGCCAGCCA 189
 Db 21 ThrCysThrValSerGlyGlySerIleCysSerTyrTyrSerTrpIleArgGlnPro 40
 QY 190 CAGGTAAGGCTGCTGAGTGGATGTGTAATCAATCATAGTGGAGACCAACTACAAC 249
 Db 41 ProGlyLysGlyLeuGlnTrpIleGlyTyrIleTyrTyrSerGlySerThrAsnTyrThr 60
 QY 250 CCGTCTCTCAAGAGTCGAGTCCACCATATCAGTAGACACGCTCCAGAACCTCTCTCTG 309
 Db 61 ProSerLeuLysSerArgValThrIleSerValAspArgSerLysAsnGlnPheSerLeu 80
 QY 310 AAAGTCAAGCTCTGACCGCTGGGACACGGCTGTATTACTGTCCGAGAGTAATAAT 369
 Db 81 LysLeuThrSerLeuThrAlaAlaAspThrAlaValTyrPheCysAlaArgLeuSerAsn 100
 QY 370 TGG-----TTCACACCTTGGGCGCAGGGAACCTGTCTACCGTCTCTCTCA 414
 Db 101 TrpGlyProTyrTyrPheAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 119

RESULT 12

Q9DBL4 PRELIMINARY; PRT; 473 AA.
 AC Q9DBL4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE 1810060009Rik protein.
 GN IGH-1 OR 1810060009RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCB_TaxId=10090;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fietcher C., Fujita M., Gariboldi M.,
 RA Gustingich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL; AK007918; BAB25349.1; -;
 DR HSSP; P01842; 7FAB.
 DR MGD; MGI:96443; Igh-1.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00406; IGV; 1.
 DR SMART; SM00410; IG_Like; 1.
 DR SMART; SM00410; IG_Like; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 SQ SEQUENCE 473 AA; 51699 MW; 9DE57A514475FBB CRC64;

Alignment Scores:
 Pred. No.: 3.14e-36 Length: 473
 Score: 449.00 Matches: 87
 Percent Similarity: 67.82% Conservative: 31
 Best Local Similarity: 50.00% Mismatches: 52
 Query Match: 46.43% Indels: 4
 DB: 11 Gaps: 2

US-08-728-463B-219 (1-524) x Q9DBL4 (1-473)

QY 13 ATGAACACCTGTGTCAG 72
 Db 1 MetGluTrpSerTrpValPheLeuPheLeuLeuSerValThrAlaGlyValHisCysGln 20
 QY 73 GTGAGCTACACAGTGGGGCGGCGAGCTGTTGAAGCTTCGGAGACCTCTCTCTCTCTCACC 132
 Db 21 ValGlnLeuLysGlnSerGlyAlaGluLeuValLysProGlyAlaSerValLysIleSer 40
 QY 133 TCGCGCTGTATGCTGCT 192
 Db 41 CysLysAlaSerGlyTyrThrPheThrAspTyrTyrIleAsnTrpValLysGlnArgPro 60
 QY 193 GGTAAAGGCTCTGGAGTGGATTGGTGAATCAAT---CATAGTGAAGACCACTACAAC 249
 Db 61 GlyGlnGlyLeuGluTrpIleGlyLysIleGlyProGlySerGlySerThrTyrTyrAsn 80
 QY 250 CCGTCTCTCAAGAGTCGAGTCCATATCAGTAGACACGCTCCAAAGAACCGTCTCTCTG 309
 Db 81 GluLysPheLysGlyLysAlaThrLeuThrAlaAspLysSerSerSerThrAlaTyrMet 100
 QY 310 AAAGTCAAGCTCTGTGACCGCTGGGACACGGCTGTATTACTGTCTCTCTCTCTCTCTCTCT 363
 Db 101 GlnLeuSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgSerGlyTyr 120
 QY 364 ---ATTAATTGGTTCACCGCTTGGGCGCAGGGAACCTCTCTCTCTCTCTCTCTCTCTCA 420
 Db 121 AspTyrAspTrpPheAlaTyrTrpGlyGlnGlyThrLeuValThrValSerAlaLys 140
 QY 421 ACCAAGGGCCCATCGGTCTTCCCTCTGGCACCGCTCTCTCTCAAGAGCACCTCTCTGGGGCACA 480
 Db 141 ThrThrAlaProSerValTyrProLeuAlaProValCysGlyGlyThrThrGlySerSer 160
 QY 481 CGGGCCCTGGTCTGTCT 522
 Db 161 ValThrLeuGlyCysLeuValLysGlyTyrPheProGluPro 174

RESULT 13

Q921K1 ID Q921K1 PRELIMINARY; PRT; 278 AA.
 AC Q921K1;
 DT 01-DEC-2001 (T-EMBLrel. 19, Created)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
 DE Unknown (protein for MGC:189777).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC012207; AAH12207.1;
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 2
 SQ SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;

Alignment Scores:

Pred. No.: 1,55e-35 Length: 278
 Score: 441.50 Matches: 88
 Percent Similarity: 67.26% Conservative: 25
 Best Local Similarity: 52.38% Mismatches: 50
 Query Match: 45.68% Indels: 5
 DB: 11 Gaps: 2

US-08-728-463B-219 (1-524) x Q921K1 (1-278)

QY 34 CTCCTCTGGTGGAGCTCCTAGATGGCTCTGCTCAGGTGACGTACAGCAGTGGGC 93
 DB |||||
 QY 8 LeuPheLeuValAlaThrAlaThrGlyValHisSerGlnValGlnLeuGlnGlnProGly 27
 DB |||||
 QY 94 GCAGGAGTGTGAAGCTTCGGAGACCTGCTCCCTCAGCTGCTGCTATGGTGGTTC 153
 DB |||||
 QY 28 AlaGluLeuValValProGlyAlaSerValLysLeuSerCysLysAlaSerGlyTyrThr 47
 DB |||||
 QY 154 TTCAGTGGTTACTAGGAGCTGATCGCCAGCCACAGTAAAGTCTCGAGTGGATT 213
 DB |||||
 QY 48 PheThrSerTyrTrpMetHisTrpValLysGlnArgGlyGlnGlyLeuGluTrpIle 67
 DB |||||
 QY 214 GGTGAATCAAT---CATAGTGAAGCAGCACTACACCGCTCTCTCAAGATCGATC 270
 DB |||||
 QY 68 GlyAsnIleAsnProAsnSerGlyGlyThrAsnTyrAsnGlnLysPheLysAsnLysAla 87
 DB |||||
 QY 271 ACCATATCAGTACAGCTCCAGAACACAGTTCTCTGAACTGAGCTCTGTGACCGCT 330
 DB |||||
 QY 88 ThrLeuAlaValAspLysSerSerThrValTyrMetGlnLeuSerSerLeuThrSer 107
 DB |||||
 QY 331 CGGACACAGCTGTATTACTGTGCGAGAGTAAAT---TGGTTTCGAC 378
 DB |||||
 QY 108 GluAspSerAlaValTyrCysThrArgGlyTyrGlyTyrAspValTyrPheAsp 127
 DB |||||
 QY 379 CTTTGGGGCAGGAACTTCCTGTCACCGCTCTCTCAGCTCAACCAAGGCGCCATCGTC 438
 DB |||||
 QY 128 ValTrpGlyAlaGlyThrValThrValLysSerAlaLysThrAlaProSerVal 147
 DB |||||
 QY 439 TTCCCTCGACACCTCTCAAGAGCAGCTCTGGGGGACAGCGCCCTGGGCTGCTG 498
 DB |||||
 QY 148 TyrProLeuAlaProValCysGlyThrThrGlySerSerValThrLeuGlyCysLeu 167
 DB |||||
 QY 499 GTCAAGGACTTCTCCCGCAACCG 522
 DB |||||
 QY 168 ValLysGlyTyrPheProGluPro 175
 DB |||||

RESULT 14

Q99L31 ID Q99L31 PRELIMINARY; PRT; 468 AA.
 AC Q99L31;
 DT 01-JUN-2001 (T-EMBLrel. 17, Created)

DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
 DE Similar to RIKEN CDNA i810060009 gene.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC003878; AAH03878.1;
 DR HSP; P01842; 7FAB.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003600; Ig_like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR SMART; SM00410; IG_like; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Alignment Scores:

Pred. No.: 1,98e-33 Length: 468
 Score: 421.00 Matches: 84
 Percent Similarity: 63.22% Conservative: 26
 Best Local Similarity: 48.28% Mismatches: 60
 Query Match: 43.54% Indels: 4
 DB: 11 Gaps: 2

US-08-728-463B-219 (1-524) x Q99L31 (1-468)

QY 13 ATGAACACCTGTGTGTTCTCTCTCTGGTGGAGCTCTAGATGGTCTGTCTCAG 72
 DB |||||
 QY 1 MetLysCysSerTrpValIlePhePheLeuMetAlaValIleGlyValAsnSerGlu 20
 DB |||||
 QY 73 GTGACGTACAGCTGGGGCGCAGGACTGTGAAGCTTCGGAGACCTGTCTCTCACC 132
 DB |||||
 QY 21 ValGlnLeuGlnGlnSerGlyAlaGluLeuValArgProGlyAlaSerValLysLeuSer 40
 DB |||||
 QY 133 TCGCTGTCTATGTGTGTCTCTCTCTGTTACTTCTGAGCTGGATCGCCAGCCACCA 192
 DB |||||
 QY 41 CysThrAlaSerGlyPheAsnIleLysAspSerLeuMetHisTrpValLysGlnArgPro 60
 DB |||||
 QY 193 GGTAGGCTCTGAGTGGATTGGTGAATCAAT---CATAGTGAAGCAGCCAACTACAAC 249
 DB |||||
 QY 61 GluGlnGlyLeuGluTrpIleGlyTrpIleAspProGluAspGlyGluThrLysTyrAla 80
 DB |||||
 QY 250 CCGTCTCTCAAGAGTCAGATCACCATATCAGTACAGACGTCACAGACCACTCTCTG 309
 DB |||||
 QY 81 ProlLysPheGlnAspLysAlaThrIleThrAlaAspThrSerSerAsnThrAlaTyrLeu 100
 DB |||||
 QY 310 AAATGAGCTCTGTGACCGCTGGCAGACCGCTGTGTATTACTGTCTGAGAGTAAT--- 366
 DB |||||
 QY 101 GlnLeuSerSerLeuThrSerGluAspThrAlaIleTyrCysAlaArgAsnLeuLeu 120
 DB |||||
 QY 367 -----AATGGTTCGACCTTGGGGCCAGGACCTGTGTACCGTCTCTCAGCTCA 420
 DB |||||
 QY 121 TyrGlyGlyTyrTyrAspTyrTrpGlyGlnGlyThrThrIleThrValSerSerAlaLys 140
 DB |||||
 QY 421 ACCAAGGCCCATCGGTCTTCCCTGGCACCTCTCTCAAGAGCAGCTCTGGGGGCACA 480
 DB |||||
 QY 141 ThrThrAlaProSerValTyrProLeuAlaProValCysGlyAspThrThrGlySerSer 160
 DB |||||
 QY 481 CGGCCCTGGCTGCTGTCAGGACTACTTCCCGCAACCG 522
 DB |||||
 QY 161 ValThrLeuGlyCysLeuValLysGlyTyrPheProGluPro 174
 DB |||||

RESULT 15

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model
Run on: June 3, 2003, 08:56:21 ; Search time 33.893 Seconds
(without alignments)
4120.219 Million cell updates/sec

Title: US-08-728-463B-219
Perfect score: 967
Sequence: 1 AAGCTTGCCACATGAACA.....GACTTACTTCCCGAACCGGT 524

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 1816940

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2 1/USPTO spool/US08728463/runat 03062003 085613 16797/app query.fasta_1.3690
-DB=A Genesec 101002 -QFMT=fastan -SUFFIX=rag -MTNMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US08728463 @CGN 1 1 353 @runat 03062003 085613 16797 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Genesec_101002.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	812	84.0	462	21	AAB26884	Human immunoglobulin
2	784.5	81.1	193	23	ABP43199	Human ovarian anti
3	783	81.0	472	17	AAR93166	Anti-rhesus D reco
4	766.5	79.3	473	22	AAB36206	Human immune syste
5	739	76.4	476	18	AAW01822	Primate anti-hu
6	739	76.4	476	19	AAW63765	Macaque primatized
7	739	76.4	476	23	AAU11646	Protein sequence o
8	729	75.4	470	21	AAU44721	Human immune syste
9	722	74.7	476	18	AAW01818	Primate anti-hu
10	722	74.7	476	19	AAW63761	Macaque primatized
11	714.5	73.9	476	23	AAU11539	Protein sequence o
12	706.5	73.1	537	21	AAU96290	Human IGPAM-2 immu
13	706.5	73.1	537	21	AAU96290	Human IGPAM-2 immu
14	700	72.4	467	18	AAW14927	Human gamma-4PE he
15	700	72.4	467	18	AAW14925	Human gamma-4PE he
16	700	72.4	467	18	AAW14926	Human gamma-4PE he
17	699	72.3	528	15	AAU52952	Human anti-IgE MAb
18	680.5	70.4	139	21	AAU99556	Human LH1238 mono
19	622	64.3	116	16	AAU66324	Human immunoglobul
20	615	63.6	487	22	ABN90607	Human secreted pro
21	615	63.6	487	23	ABG65445	Human albumin fusi
22	609.5	63.0	229	21	AAU30593	Variable and first
23	609.5	63.0	256	23	ABG35335	Thrombopoietin ago
24	608	62.9	155	21	AAU64727	Human 5' EST relat
25	607.5	62.8	832	17	AAW04302	Antibody/beta gluc
26	605	62.6	507	21	AAU96304	Human IGPAM-16 imm
27	603	62.4	470	13	AAU22757	Reshaped CAMPATH-1
28	602.5	62.3	266	23	ABG35336	Thrombopoietin ago
29	600.5	62.1	467	13	ABP43199	Reshaped CD4 antib
30	597.5	61.8	249	23	ABP45310	Human BLYS binding
31	597.5	61.8	467	13	ABP22758	Reshaped CD4 antib
32	593.5	61.4	524	23	AAE21618	Human gene 2 encod
33	592.5	61.3	133	23	ABG35331	Thrombopoietin ago
34	590.5	61.1	139	21	AAU92628	Human PTHrP monocl
35	585.5	60.5	172	21	AAU93173	The heavy chain of
36	580.5	60.0	581	22	AAU81972	Ganglioside GD2 sp
37	578	59.8	123	17	AAU03757	Anti-rhesus D mono
38	576.5	59.6	475	22	AAU63640	Amino acid sequenc
39	576	59.6	205	20	AAU34299	IGM antibody CEM 1
40	574.5	59.4	244	20	AAU21883	Amino acid sequenc
41	572	59.2	241	22	AAU46061	Human TF anti-idio
42	565	58.4	142	14	AAU41285	F105 rearranged va
43	564.5	58.4	139	21	AAU64676	Human 5' EST relat
44	564.5	58.4	273	17	AAU05827	Humanised 1D10 ant
45	564.5	58.4	446	17	AAU05829	Humanised 1D10 ant

ALIGNMENTS

RESULT 1
AAB26884
ID AAB26884 standard; Protein; 462 AA.
XX
AC AAB26884;
XX
DT 01-FEB-2001 (first entry)
XX
DE Human immunoglobulin heavy chain amino acid sequence.
KW Monoclonal antibody; immunoglobulin heavy chain; human.
XX Homo sapiens.
OS
XX WO200058499-A1.
XX
PD 05-OCT-2000.
XX
PF 30-MAR-2000; 2000WO-JP02022.

QY 334 GACACGGCTGTGTTACTGTGCGAGAGTAATT-----AAT 369
 |||||
 Db 108 AspThrAlaValTyrCysAlaArgAlaProGluTyrLysTrpLysTyrHisGlyAsp 127
 |||||
 QY 370 TGGTTGACCCCTTGGGGCCAGGAGACCTTGGTCACCGTCTCTCAGCCTCAACCAAGGCG 429
 |||||
 Db 128 TrpPheAspProTrpGlyGlnGlyThrValThrValSerSerAlaSerThrLysGly 147
 |||||
 QY 430 CCATCGTCTTCCCCCTGCACCCCTCTCCAGAGCACCTCTGGGGGCACAGCGGCCCTG 489
 |||||
 Db 148 ProSerValPheProLeuAlaProSerSerLysSerThrSerGlyThrAlaAlaLeu 167
 |||||
 QY 490 GCGTGGCTGCAAGGACTACTTCCCGAACCG 522
 |||||
 Db 168 GlyCysLeuValTyrAspTyrPheProGluPro 178
 |||||

RESULT 4

AAB36206
 ID AAB36206 standard; protein; 473 AA.
 AC AAB36206;
 XX
 XX 15-FEB-2001 (first entry)
 DT
 XX Human immune system associated protein HISAP-4.
 DE
 XX Human; immune system associated protein; HISAP-4; immune disorder;
 KW infection; autoimmune disease; cancer.
 XX
 OS Homo sapiens.
 XX
 XX US6135941-A.
 XX
 XX 24-OCT-2000.
 XX
 XX 27-MAR-1998; 98US-0049672.
 XX
 XX 27-MAR-1998; 98US-0049672.
 XX (INCY-) INCYTE PHARM INC.
 XX
 XX Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;
 PI Hillman JL, Au-Young J;
 XX
 XX WPI; 2001-030926/04.
 DR N-PSDB; AAC66522.

XX New human immune system associated proteins (HISAP) and polynucleotides
 PT encoding the HISAP, useful for diagnosing, treating or preventing
 PT immune or cell proliferative disorders or infections
 XX
 PS Claim 1; Column 53-56; 54pp; English.
 XX
 XX The present invention provides the coding and protein sequences for a
 CC number of human immune system associated proteins (HISAPs). These can be
 CC used in the diagnosis and treatment of various autoimmune disorders,
 CC infections and cell proliferation diseases. The diseases include AIDS,
 CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
 CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
 CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
 CC erythematosus, arteriosclerosis, cirrhosis and cancer.

XX Sequence 473 AA;

Alignment Scores:
 Pred. No.: 2,49e-61 Length: 473
 Score: 766.50 Matches: 154
 Percent Similarity: 88.83% Conservative: 5
 Best Local Similarity: 86.03% Mismatches: 11
 Query Match: 79.27% Indels: 9
 DB: 22 Gaps: 3

US-08-728-463B-219 (1-524) x AAB36206 (1-473)
 QY 13 ATGAACACCTGTGGTTCCTCTCTCTGTCGAGCTCTCTAGATGGTCTGTCTCAG 72
 |||||
 Db 1 MetLysHisLeuTyrPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20
 |||||
 QY 73 GTGAGCTACAGCAGTGGGGCGCAGGACTTGAAGCTTCGGAGACCTGTCCCTCACC 132
 |||||
 Db 21 ValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40
 |||||
 QY 133 TGGCTGTCTATGGTGGTTCCTTCAGT-----GGTTACTGTGAGCTGGATCCGCCAG 186
 |||||
 Db 41 CysAlaValSerGlyGlySerIleThrSerGlyGlyTyrTyrTrpSerTrpIleArgGln 60
 |||||
 QY 187 CCACGAGTAAGGCTCTGAGTGGATTGGTGAATCAATCATAGTGAAGCACCAACTAC 246
 |||||
 Db 61 ProProGlyLysGlyLeuGluTrpIleGlyTyrIleTyrTyrSerGlySerThrLeuTyr 80
 |||||
 QY 247 AACCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAAGACCACTCTCT 306
 |||||
 Db 81 AsnProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSer 100
 |||||
 QY 307 CTGAACCTGAGCTCTGTGACCGCTCGCGACACGCGTGTGTATTACTGTCCGAGACTAAT 366
 |||||
 Db 101 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgAsp 120
 |||||
 QY 367 -----AATTGG-----TTCGACCCCTTGGGGCCAGGGAACCTGTGTCACC 405
 |||||
 Db 121 ValGlyLeuArgGlyGlyAsnTyrGlyMetAspValTrpGlyGlnGlyThrLeuValThr 140
 |||||
 QY 406 GTCTCTCAGCTCAACCAAGGGCCCATCGGTCTTCCCTCGGACACCTCTCCAGAGC 465
 |||||
 Db 141 ValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSer 160
 |||||
 QY 466 ACCTCTGGGGCACAGCGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGAACCG 522
 |||||
 Db 161 ThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro 179
 |||||
 RESULT 5
 AAW01822
 ID AAW01822 standard; Protein; 476 AA.
 XX
 AC AAW01822;
 XX
 XX 25-MAY-1997 (first entry)
 DT
 XX Primatised anti-human B7.1 antigen antibody 16C10 heavy chain.
 DE
 XX Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
 KW primatised antibody; B7 antigen; CD28; immunosuppressive;
 KW autoimmune disease; idiopathic thrombocytopenia purpura;
 KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
 KW type 1 diabetes mellitus; graft versus host disease;
 KW hetero-hybridoma; transfectoma.
 XX
 XX Chimeric Macaca cynomolgus;
 OS Chimeric Homo sapiens.
 OS
 PN WO9640878-A1.
 XX
 PD 19-DEC-1996.
 XX
 XX 06-JUN-1996; 96WO-US10053.
 XX
 XX 07-JUN-1995; 95US-0487550.
 XX (IDEC-) IDEC PHARM CORP.
 PA
 XX Anderson DR, Brams P, Hanna N, Shestowsky WS;
 PI
 XX WPI: 1997-108638/10.
 DR N-PSDB; AAT62513.
 XX

34	CTCTCTCTGGTGGCAGCTCTCTAGATGGGTCTGTCTCAGGTGCAGCTACAGCAGTGGGGC	93
QY		
Db		
8	LeuPheLeuValAlaThrAlaThrGlyValHisSerGlnValGlnLeuGlnGlnTrpGly	27
QY		
94	GCAGCACTGTTTGAAGCCCTTCGGAGACCCCTGTCCTCACCCTCCGCTGCTCTATGGTGGTTC	153
Db		
28	AlaGlyLeuLeuLeuProSerGluThrLeuSerLeuThrCysThrValTyGlyGlySer	47
QY		
154	TTCACTGGTTCCTACTGGAGCTGGATCGCCAGCCACCAGGTAAAGGCTCTGGAGTGGATT	213
Db		
48	PheSerGlyTyrTyTrpSerTrpIleArgGlnProProGlyLeuGlyLeuGluTrpIle	67
QY		
214	GGTGAATCAATCATAGTGGAAAGCACCACCACTACAAACCGCTCTCAAGAGTCGAGTCACC	273
Db		
68	GlyGluIleAenHisSerGlySerThrAsnTyRasnProSerLeuIysSerArgValThr	87
QY		
274	ATACAGTACAGACGTCCAGAACCACTTCTCTCTGAAACTGAGCTCTGTGACCCGTGCG	333
Db		
88	IleSerValAspThrSerLysAsnGlnPheSerLeuLysLeuAenSerValTrpAlaLeu	107

Db 21 ValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40
 QY 133 TCGCTGTCTATGGTGTCTTCACTGAGTGGAGTGGATCGCCAGCA 189
 Db 41 CysAlaValSerGlyGlySerIleSerGlyGlyTyrGlyTyrPileArgGlnPro 60
 QY 190 CCAGGTAAGGCTCTGAGTGGATTGGTGAATC---AATCATAGTGAAGCACCACCTAC 246
 Db 61 ProGlyLysGlyLeuGluTrpIleGlySerPheTyrSerSerGlyAsnThrTyrTyr 80
 QY 247 AACCCGCTCTCAAGAGTCGAGTCCACCATATCAGTACAGTCCACGATCCAGAACCTCTCT 306
 Db 81 AsnProSerLeuLysSerGlnValThrIleSerThrAspThrSerLysAsnGlnPheSer 100
 QY 307 CTGAAGTACGCTCTGACCGCTCGGACAGCGCTGTGTATTACTGTGCGAGA----- 360
 Db 101 LeuLysLeuAsnSerMetThrAlaAlaAspThrAlaValTyrCysValArgAspArg 120
 QY 361 -----GTAAAT-----AATTGGTTCGACCTTGGGGCCAGGAAAC 396
 Db 121 LeuPheSerValValGlyMetValTyrAsnAsnTrpPheAspValTrpGlyProGlyVal 140
 QY 397 CTGGTCAACCGTCTCTCAGCTCAACCAAGGCGCCATCGGCTTCCCGCTGGCACCTCC 456
 Db 141 LeuValThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSer 160
 QY 457 TCCAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGGCTGGTCAAGGACTACTTCCCC 516
 Db 161 SerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPhePro 180
 QY 517 GAACCG 522
 Db 181 GluPro 182

RESULT 7

AAU11646
 ID AAU11646 standard; Protein; 476 AA.

AC AAU11646;
 XX

DT 12-MAR-2002 (first entry)
 XX

DE Protein sequence of primatised form of the heavy chain of 16C10 antibody.
 XX

KW Human; macaque monkey; light chain; primatised antibody; 16C10 antibody;
 KW neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
 KW B7_1 antigen; CD80; B7_2 antigen; CD86; B cell cancer; metastasis;
 KW tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
 KW graft-vs-host disease; immunosuppression; organ rejection;
 KW interleukin-2; IL-2; mutant; mutein.
 XX

OS Chimeric - Homo sapiens.
 OS

OS Chimeric - Macaca sp.
 OS

OS Synthetic.
 OS

PN WO200189567-A1.
 XX

PD 29-NOV-2001.
 XX

PF 22-MAY-2001; 2001WO-US16364.
 XX

PR 22-MAY-2000; 2000US-0576424.
 XX

PA (IDEC-) IDEC PHARM CORP.
 XX

PI Anderson DR, Hanna N, Brans P;
 XX

XX WPI; 2002-089895/12.
 DR

DR N-PSDB; AAS17247.
 XX

XX Use of monoclonal antibody which specifically binds to B7.1 antigen
 PT CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
 PT treating cancer, graft-vs-host disease and autoimmune disease such as

PT allergy -

XX Example 8; Fig 5b; 89pp; English.

CC The present invention relates to a new use of a monoclonal antibody
 CC which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
 CC (CD86) for inducing the apoptosis of B7+ cells. The invention is
 CC useful for treating diseases such as B cell cancer, lymphoma, a
 CC cancer where B cells promote the growth and/or metastasis of tumours,
 CC B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
 CC idiopathic thrombocytopenia purpura, systemic lupus, erythematous,
 CC type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
 CC anaemia, inflammatory bile disease, allergy, multiple sclerosis
 CC or graft-vs-host disease. The antibody is useful for immunosuppression
 CC in a human or animal and for treating or preventing resistance to or
 CC rejection of transplanted organ or tissue for treating proliferative
 CC and hyperproliferative diseases, for treating reversible obstructive
 CC always disease, intestinal inflammations and allergies e.g. Crohn's
 CC disease and ulcerative colitis, food-related allergies e.g. migraine,
 CC rhinitis and eczema, and other types of allergies. The present protein
 CC sequence represents the heavy chain of 16C10, a primatised antibody
 CC used in the invention to induce apoptosis and inhibit production of
 CC interleukin-2 (IL-2).

XX Sequence 476 AA;

Alignment Scores:

Pred. No.: 7,85e-59 Length: 476
 Score: 739.00 Matches: 147
 Percent Similarity: 85.16% Conservative: 8
 Best Local Similarity: 80.77% Mismatches: 15
 Query Match: 76.42% Indels: 12
 DB: 23 Gaps: 4

US-08-728-463B-219 (1-524) x AAU11646 (1-476)

QY 13 ATGAACACCTGTGTGTTCTTCTCTCTCTGTGGCAGCTCTAGATGGTCTGTCTCAG 72
 Db 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20
 QY 73 GTGCAGCTACAGCAGTGGGGCGCAGGAGTGTGAAGCCTTCGGAGACCTGTCCCTCAC 132
 Db 21 ValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40
 QY 133 TCGCGTGTCTATGGTGTCTTCTTCACTGAGTGGAGTGGATCGGACCTCCGCGAGCA 189
 Db 41 CysAlaValSerGlyGlySerIleSerGlyGlyTyrGlyTrpGlyTrpIleArgGlnPro 60
 QY 190 CCAGTAAAGGCTCTGGAGTGGATTGGTGAATC---AATCATAGTGAAGCACCACCTAC 246
 Db 61 ProGlyLysGlyLeuGluTrpIleGlySerPheTyrSerSerGlyAsnThrTyrTyr 80
 QY 247 AACCCGCTCTCAAGAGTCGAGTCCACCATATCAGTACAGTCCAGGACCAAGCTTCTCT 306
 Db 81 AsnProSerLeuLysSerGlnValThrIleSerThrAspThrSerLysAsnGlnPheSer 100
 QY 307 CTGAAGTACGCTCTGTGACCGCTCGGACAGCGCTGTGTATTACTGTGCGAGA----- 360
 Db 101 LeuLysLeuAsnSerMetThrAlaAlaAspThrAlaValTyrCysValArgAspArg 120
 QY 361 -----GTAAAT-----AATTGGTTCGACCTTGGGGCCAGGAAAC 396
 Db 121 LeuPheSerValValGlyMetValTyrAsnAsnTrpPheAspValTrpGlyProGlyVal 140
 QY 397 CTGGTCAACCGTCTCTCAGCTCAACCAAGGCGCCATCGGCTTCCCGCTGGCACCTCC 456
 Db 141 LeuValThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSer 160
 QY 457 TCCAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGGCTGGTCAAGGACTACTTCCCC 516
 Db 161 SerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPhePro 180
 QY 517 GAACCG 522

QY 475 GGCACAGCGCCCTGGCTGCTGGTCAAGGACTACTTCCCGAACCG 522
 Db 161 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro 176

RESULT 9

ID AAW01818 standard; Protein; 476 AA.

AC AAW01818;
 XX 25-MAY-1997 (first entry)
 XX

XX Primatised anti-human B7.1 antigen antibody 7C10 heavy chain.

XX Monoclonal antibody; cynomolgus monkey; macaque; 7C10;
 KW primatised antibody; B7 antigen; CD28; immunosuppressive;
 KW autoimmune disease; idiopathic thrombocytopenia purpura;
 KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
 KW type 1 diabetes mellitus; graft versus host disease;
 KW hetero-hybridoma; transfectoma.

XX Chimeric Macaca cynomolgus;
 OS Chimeric Homo sapiens.

XX WO9640878-A1.

XX 19-DEC-1996.

XX 06-JUN-1996; 96WO-US10053.

XX 07-JUN-1995; 95US-0487550.

XX (IDEC-) IDEC PHARM CORP.

XX Anderson DR, Brams P, Hanna N, Shestowsky WS;

XX WPI; 1997-108638/10.

XX N-PSDB; AAT62510.

XX Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
 PT useful for treating autoimmune disease or graft-versus-host disease

XX Claim 6; Fig 8B; 81pp; English.

XX 2 Polypeptides (AAW01817 and AAW01818) respectively comprise primatised
 CC forms of the light and heavy chains of cynomolgus monkey anti-human
 CC B7.1 antigen monoclonal antibody 7C10. Cloned 7C10 light and heavy
 CC variable genes (see also AAT62509 and AAT62510) are inserted into
 CC an expression vector (pref. NEOSPLA) which contains human light and
 CC heavy chain constant region genes to allow prodn. of the primatised
 CC antibody in e.g. CHO cells. Primatised 7B6 and 16C10 anti-B7.1
 CC antibodies have also been produced (see also AAW01819-22). The
 CC primatised antibodies inhibit the B7:CD28 pathway, making them
 CC useful immunosuppressants for the treatment of autoimmune disorders
 CC and graft-versus-host disease.

XX Sequence 476 AA;

Alignment Scores:

Pred. No.:	2,75e-57	Length:	476
Score:	722.00	Matches:	143
Percent Similarity:	82.42%	Conservative:	7
Best Local Similarity:	78.57%	Mismatches:	20
Query Match:	74.66%	Indels:	12
DB:	18	Gaps:	3

US-08-728-463B-219 (1-524) x AAW01818 (1-476)

QY '13 ATGAACACCTGGTGTCTTCCTCCTCGTGGCAGCTCCTAGATGGGTCTGTCTCAG 72
 Db 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20

QY 73 GTGACGTACACGACTGGGGCCAGCAGCTGTGAAGCCTTCGGAGACCTGTCCCTCACC 132
 Db 21 ValLysLeuGlnGlnTrpGlyLeuGluGlnProSerGluThrLeuSerArgThr 40
 QY 133 TCGCGTCTCTATGGTGGTTCCTTCAGTGT---TACTACTGAGCTGGATCCGCCAGCCA 189
 Db 41 CysValValSerGlyGlySerIleSerGlyTyrTyrTrpTrpThrTrpIleArgGlnThr 60
 QY 190 CCAGGTAAAGGTCTCGAGTGGATTGGTGAATCAATCATAGTGA---AGCACCAACTAC 246
 Db 61 ProGlyArgGlyLeuGluTrpIleGlyHisIleTyrGlyAsnGlyAlaThrThrAsnTyr 80
 QY 247 ACCCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCACAGAACCAAGTCTCT 306
 Db 81 AsnProSerLeuLysSerArgValThrIleSerLysAspThrSerLysAsnGlnPhePhe 100
 QY 307 CTGAAACTGAGCTCTGTGACCTCGCGACACGGCTGTATTACTGTGCGAGA----- 360
 Db 101 LeuAsnLeuAsnSerValThrAspAlaAspThrAlaValTyrTyrCysAlaArgGlyPro 120
 QY 361 -----GTAATTAATGGTTCGACCTTGGCCCTTGGGGCCAGGGAACC 396
 Db 121 ArgProAspCysThrThrIleCysTyrGlyGlyTyrValAspValTrpGlyProGlyAsp 140
 QY 397 CTGGTCACCGTCTCTCAGCCTCAACCAAGGGCCCATCGGTCTTCCCTCGGCACCTCC 456
 Db 141 LeuValThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSer 160
 QY 457 TCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTTCCCC 516
 Db 161 SerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPhePro 180
 QY 517 GAACCG 522
 Db 181 GluPro 182
 RESULT 10
 AAW63761
 ID AAW63761 standard; Protein; 476 AA.
 XX
 AC AAW63761;
 XX 29-SEP-1998 (first entry)
 DT
 XX Macaque primatized 7C10 heavy chain DNA.
 XX Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
 KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
 KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
 KW immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
 KW T cell proliferation; ss.
 XX Macaca fascicularis.
 XX WO9819706-A1.
 XX 14-MAY-1998.
 XX 29-OCT-1997; 97WO-US19906.
 XX 08-NOV-1996; 96US-0746361.
 XX (IDEC-) IDEC PHARM CORP.
 XX Anderson DR, Brams P, Hanna N;
 XX WPI; 1998-286601/25.
 XX N-PSDB; AAV35485.
 XX New monoclonal antibodies specific for B7.1 or B7.2 antigens and
 PT inhibiting binding to CD28 - useful as specific immunosuppressants
 PT for treating diseases that involve interactions between T and B
 PT cells, e.g. graft rejection or tumours

Bd		181 Glupro 182	
	RESULT 8		
ID	AAY44721		
AC	AAI44721 standard; Protein; 470 AA.		
XX	AAY44721;		
XX			
DT	25-APR-2000 (first entry)		
XX			
DE	Human immune system molecule, ISMO-2.		
XX			
KW	Human; immune system molecule; ISMO-2; Incyte clone 2849752; diagnosis;		
KW	treatment; prevention; cell proliferation; immune system disorder.		
XX			
OS	Homo sapiens.		
XX			
FH	Key Location/Qualifiers		
FT	Peptide 1..19	/label= Signal_peptide	
FT	Protein 20..470	/label= Mature_ISMO-2	
FT	Modified-site 120	/note= "N-glycosylated"	
FT	Modified-site 320	/note= "N-glycosylated"	
FT	Modified-site 105	/note= "Casein kinase II phosphorylation site"	
FT	Modified-site 232	/note= "Casein kinase II phosphorylation site"	
FT	Modified-site 290	/note= "Casein kinase II phosphorylation site"	
FT	Modified-site 377	/note= "Casein kinase II phosphorylation site"	
FT	Modified-site 47	/note= "Protein kinase C phosphorylation site"	
FT	Modified-site 81	/note= "Protein kinase C phosphorylation site"	
FT	Modified-site 92	/note= "Protein kinase C phosphorylation site"	
FT	Modified-site 98	/note= "Protein kinase C phosphorylation site"	
FT	Modified-site 142	/note= "Protein kinase C phosphorylation site"	
FT	Modified-site 154	/note= "Protein kinase C phosphorylation site"	
FT	Modified-site 322	/note= "Protein kinase C phosphorylation site"	
FT	Modified-site 347	/note= "Protein kinase C phosphorylation site"	
FT	Modified-site 460	/note= "Protein kinase C phosphorylation site"	
FT	Modified-site 69	/note= "Tyrosine kinase phosphorylation site"	
FT	Modified-site 319	/note= "Tyrosine kinase phosphorylation site"	
Region	387..409	/note= "conserved Ig/MHC protein block"	
Region	446..463	/note= "conserved Ig/MHC protein block"	
Domain	34..116	/notes "shows similarity to Ig superfamily protein domain"	
Domain	160..225	/note= "shows similarity to Ig superfamily protein domain"	
Domain	383..450	/note= "shows similarity to Ig superfamily protein domain"	
PX	WC0200000608-A2.		
XX			

XX

PS Example 7; Fig 3b; 87pp; English.

XX

This sequence represents a primatized form of the antibody 7C10 heavy chain from macaque. This sequence is used in a method which studies new monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such Mab's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoimmune disease, specifically idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple sclerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. Mab's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleukin-2 (IL-2), T cell proliferation and antigen-specific immunoglobulin G (IgG) responses.

XX

SQ Sequence 476 AA;

Alignment Scores:

Pred. No.:	2,75e-57	Length:	476
Score:	722.00	Matches:	143
Percent Similarity:	82.42%	Conservative:	7
Best Local Similarity:	78.57%	Mismatches:	20
Query Match:	74.66%	Indels:	12
DB:	19	Gaps:	3

US-08-728-463B-219 (1-524) x AAW63761 (1-476)

QY	13	ATGAACACCTGGTGGTCTTCCTCCCTGGTGGCAGCTCCTAGATGGTCTGTCTCAG	72
DB	1	MetLysHisLeuTrpPheLeuLeuLeuValAlaAlaProArgTrpValLeuSerGln	20
QY	73	GTGACACTACAGCAGTGGGGCGCAGCACTGTTGAACCTTCGGAGACCTGTCCCTCACC	132
DB	21	ValLysLeuGlnGlnTrpGlyGluGlyLeuLeuGlnProSerGlnThrLeuSerArgThr	40
QY	133	TCGCCTGTCTATGGTGGTCTTCCTCAGTGGT---	189
DB	41	CysValValSerGlyGlySerIleSerGlyTyrTyrTrpTrpTrpIleArgGlnThr	60
QY	190	CCAGGTAAGGCTGAGTGGATTGGTGAATCAATCATAGTGA---AGCACCACTAC	246
DB	61	ProGlyArgGlyLeuGlnTrpIleGlyHisIleTyrGlyAsnGlyAlaThrThrAsnTyr	80
QY	247	AACCCCTCTCTCAAGAGTCGAGTCACCATATCATAGTACACAGTCACCAAGAACCACTTCTCT	306
DB	81	AsnProSerLeuLysSerArgValThrIleSerLysAspThrSerLysAsnGlnPhePhe	100
QY	307	CTGAACACTGAGCTCTGACCGCTGGGACACGGCTGTGTATTACTGTGGAGA-----	360
DB	101	LeuAsnLeuAsnSerValThrAspAlaAspThrAlaValTyrCysAlaArgGlyPro	120
QY	361	-----GTAATTAATGGTTCGACCTTCACCTGGGCCAGGCAACC	396
DB	121	ArgProAspCysThrThrIleCysTyrGlyGlyTrpValAspValTrpGlyProGlyAsp	140
QY	397	CTGGTCACCGCTCTCCCTCAGCCTCAACCAAGGGGCCATCGCTCTTCCCTGGCACCTCC	456
DB	141	LeuValThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSer	160
QY	457	TCAAGAGCACCTCTCGGGGGCAAGCGGCCCTGGCTGGCTGTGCTCAAGCACTACTTCCC	516
DB	161	SerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPhePro	180
QY	517	GAACCG	522
DB	181	GluPro	182

RESULT 11

AAU11539

ID AAU11539 standard; Protein; 476 AA.

AC AAU11539;

XX

DT 12-MAR-2002 (first entry)

XX

DE Protein sequence of primatized form of the heavy chain of 7C10 antibody.

XX

Human; macaque monkey; light chain; primatized antibody; 7C10 antibody; neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist; B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis; tumour; B cell lymphoma; B cell leukaemia; autoimmune disease; graft-vs-host disease; immunosuppression; organ rejection; interleukin-2; IL-2; mutant; mutein.

XX

OS Chimeric - Homo sapiens.

OS

OS Chimeric - Macaca sp.

OS

OS Synthetic.

XX

PN WO200189567-A1.

XX

PD 29-NOV-2001.

XX

PF 22-MAY-2001; 2001WO-US16364.

XX

PR 22-MAY-2000; 2000US-0576424.

XX

PA (IDEC-) IDEC PHARM CORP.

XX

PI Anderson DR, Hanna N, Brams P;

XX

WPI: 2002-089895/12.

DR

N-PSDB; AAS17243.

XX

Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as allergy

PT

PS Example 8; Fig 3b; 89pp; English.

XX

The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen (CD86) for inducing the apoptosis of B7+ cells. The invention is useful for treating diseases such as B cell cancer, lymphoma, a

CC

cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell leukaemia, and autoimmune diseases such as

CC

idiopathic thrombocytopenia purpura, systemic lupus, erythematosus, type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic

CC

anaemia, inflammatory bile disease, allergy, multiple sclerosis or graft-vs-host disease. The antibody is useful for immunosuppression

CC

in a human or animal and for treating or preventing resistance to or rejection of transplanted organ or tissue for treating proliferative

CC

and hyperproliferative diseases, for treating reversible obstructive airways disease, intestinal inflammations and allergies e.g. Crohn's

CC

disease and ulcerative colitis, food-related allergies e.g. migraine, rhinitis and eczema, and other types of allergies. The present protein

CC

sequence represents the heavy chain of 7C10, a primatized antibody used in the invention to induce apoptosis and inhibit production of

CC

XX Sequence 476 AA;

SQ

Alignment Scores:

Pred. No.:	2,75e-57	Length:	476
Score:	722.00	Matches:	143
Percent Similarity:	82.42%	Conservative:	7
Best Local Similarity:	78.57%	Mismatches:	20
Query Match:	74.66%	Indels:	12
DB:	23	Gaps:	3

ID AAY96290 standard; protein; 537 AA.

/note= "site of L236E mutation"

FT XX
 PN W09709351-A1.
 PD 13-MAR-1997.
 PP 05-SEP-1996; 96WO-US14324.
 PP 06-SEP-1995; 95US-0523894.
 PR (IDEC-) IDEC PHARM CORP.
 PA Hanna N, Newman RA, Reff ME;
 XX WPI; 1997-201913/18.
 XX N-PSDB; AAT62870.
 DR Chimeric antibody comprising monkey variable domains and human
 PT constant domains - affects CD4-mediated immune functions, esp.
 PT useful for treatment of autoimmune disease, e.g. rheumatoid
 PT arthritis
 XX
 PS Claim 6; Page 91-93; 155pp; English.
 XX
 CC 3 Polypeptides (AAW14925-27) respectively comprise the heavy chain
 CC regions of human gamma-4, gamma-4E carrying an L236E mutation in
 CC the hinge region, and gamma-4PE carrying L236E and S229P mutations.
 CC They can be incorporated into novel monoclonal and chimeric
 CC antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4PE, in
 CC which the human IGG4 Fc binding domain framework is combined with
 CC the antigen binding domains (see also AAW14922-23) of macaque anti-
 CC human CD4 monoclonal antibody E9.1. These antibodies show high
 CC affinity to human CD4, have little or no immunogenicity in humans
 CC and show reduced or absence of effector function. The gamma-4E and
 CC -4PE mutations confer activity enhanced stability and eliminate
 CC depleting activity. The antibodies can be used to treat autoimmune
 CC diseases such as rheumatoid arthritis.
 XX
 SQ Sequence 467 AA;

Alignment Scores:
 Pred. No.: 2,73e-55 Length: 467
 Score: 700.00 Matches: 139
 Percent Similarity: 84.66% Conservative: 10
 Best Local Similarity: 78.98% Mismatches: 21
 Query Match: 72.39% Indels: 6
 DB: 18 Gaps: 3

US-08-728-463B-219 (1-524) x AAW14927 (1-467)

QY 13 ATGAACACCTGTGGTTCCTCTCTCGTGGCAGCTCCTAGATGGGTCTCTCTCAG 72
 Db 1 MethyHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20
 QY 73 GTGCAGCTACAGAGTGGCGGAGGACTGTTCAAGCCTTCGAGACCTGCTCCCTCACC 132
 Db 21 ValGlnLeuGlnSerGlyProGlyLeuValProSerGlyThrLeuSerLeuThr 40
 QY 133 TGCCTGTCTATGTGGTTCCTCTCTCAGTGGT---TACTACTGGAGCTGGATCCGCCAGCCA 189
 Db 41 CysSerValSerGlyGlySerIleSerGlyAspTyTrpTrpPheTrpIleArgGlnSer 60
 QY 190 CCAGGTAAAGGCTGGAGTGGATGGTGAATCAATCATAGT---GGAAGCCCAACTAC 246
 Db 61 ProGlyLysGlyLeuGluTrpIleGlyTyTrpIleTyTrpGlySerGlyGlyThrAsnTy 80
 QY 247 AACCCGTCTCTCAAGAGTCAGTCACATATAGTACACAGCTCCAAAGAACCACTCTCT 306
 Db 81 AsnProSerLeuAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer 100
 QY 307 CTGAATCTAGCTGTGTGACCGCTGGGACACGGCTGTGTATTACTGTGCG----- 357
 Db 101 LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyTrpCysAlaSerAsnIle 120

QY 358 ---AGAGTAATTAATTGGTTCCACCTTGGGGCCAGGNAACCTGGTCAACCTCTCTCTCA 414
 Db 121 LeuLysLeuHisTrpLeuLeuTyTrpGlyGlnGlyValLeuValTrpValSerSer 140
 QY 415 GCCTCAACCAAGGGCCCATCGGTCTTCCCTCGGACCTCTCTCAAGAGCACCTCTGGG 474
 Db 141 AlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGlu 160
 QY 475 GGCACAGCGCCCTGGGTGCTGCTCAAGGACTACTTCCCGCAACCG 522
 Db 161 SerThrAlaAlaLeuGlyCysLeuValLysAspTyTrpPheProGluPro 176

RESULT 15

AAW14925
 ID AAW14925 standard; Protein; 467 AA.
 XX
 AC AAW14925;
 XX
 DT 18-OCT-1997 (first entry)
 XX
 DE Human gamma-4 heavy chain.
 XX
 KW CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
 KW cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
 KW leukaemia; lymphoma; graft-versus-host disease; asthma;
 KW transplant rejection; HIV; therapy; CE9 gamma 4.
 XX
 OS Homo sapiens.
 XX
 PN W09709351-A1.
 XX
 PD 13-MAR-1997.
 PP 05-SEP-1996; 96WO-US14324.
 PP 06-SEP-1995; 95US-0523894.
 XX
 XX (IDEC-) IDEC PHARM CORP.
 XX
 PI Hanna N, Newman RA, Reff ME;
 XX
 DR WPI; 1997-201913/18.
 DR N-PSDB; AAT62868.
 XX
 PT Chimeric antibody comprising monkey variable domains and human
 PT constant domains - affects CD4-mediated immune functions, esp.
 PT useful for treatment of autoimmune disease, e.g. rheumatoid
 PT arthritis
 XX
 PS Claim 6; Page 82-84; 155pp; English.

3 Polypeptides (AAW14925-27) respectively comprise the heavy chain
 regions of human gamma-4, gamma-4E carrying an L236E mutation in
 the hinge region, and gamma-4PE carrying L236E and S229P mutations.
 They can be incorporated into novel monoclonal and chimeric
 antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4PE, in
 which the human IGG4 Fc binding domain framework is combined with
 the antigen binding domains (see also AAW14922-23) of macaque anti-
 human CD4 monoclonal antibody E9.1. These antibodies show high
 affinity to human CD4, have little or no immunogenicity in humans
 and show reduced or absence of effector function. They can be used
 to treat autoimmune diseases such as rheumatoid arthritis.

SQ Sequence 467 AA;

Alignment Scores:

Pred. No.: 2,73e-55 Length: 467
 Score: 700.00 Matches: 139
 Percent Similarity: 84.66% Conservative: 10
 Best Local Similarity: 78.98% Mismatches: 21
 Query Match: 72.39% Indels: 6
 DB: 18 Gaps: 3

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73	GTCCAGCTACAGCAGTGGGGCGCAGGAGCTGTGAAGCTTCGAGAGCCCTGTCCTCAC	132
QY		
21	ValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr	40
Db		
133	TGCGCTGCTATGGTGGTTCCTTCAGTGGT---TACTACTGGAGCTGGATCGCCAGCCA	189
QY		
41	CysSerValSerGlyGlySerIleSerGlyAspTyrTrpPheTrpIleArgGlnSer	60
Db		
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QY		
61	ProGlyLysGlyLeuGluTrpIleGlyTyrIleTyrGlySerGlyGlyThrAsnTyr	90
Db		
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QY		
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Db		
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QY		
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QY		
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QY		
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Db		

Search completed: June 3, 2003, 09:02:28
Job time : 39.0597 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 09:04:15 ; Search time 22.264 Seconds

(without alignments)
4764.744 Million cell updates/sec

Title: US-08-728-463B-219

Perfect score: 967

Sequence: 1 AAGCTTGCCACCATGAACA.....GACTACTTCCCGAACCGGT 524

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 767038

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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Database :

Published Applications AA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
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2	739	76.4	476	9 US-09-948-429B-12
3	722	74.7	476	9 US-10-124-905-4
4	722	74.7	476	9 US-09-948-429B-4

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9	615	63.6	487	10	US-09-800-729-145																																																																																												
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24	552	57.1	451	10	US-09-920-171-16																																																																																												
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ALIGNMENTS

RESULT 1
US-10-124-905-12
; Sequence 12, Application US/10124905
; Patent No. US20020166136A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRINATIZED FORMS THEREOF."
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"
; TITLE OF INVENTION: 12
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,905
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:


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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1321

Alignment Scores:
Pred. No.: 6,56e-43 Length: 249
Score: 597.50 Matches: 121
Percent Similarity: 71.75% Conservative: 6
Best Local Similarity: 68.36% Mismatches: 16
Query Match: 61.79% Indels: 34
DB: 9 Gaps: 3

US-08-728-463B-219 (1-524) x US-09-880-748-1321 (1-249)
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QY 130 ACCTGCGCTGTATGTTGTTCTCTCAGTGGTTACTTGGAGCTGGATCCGCCAGCCA 189
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QY 190 CCAGTAAAGGCTGGAGTGGATGTTGTAATCAATCATAGTGGAGCCCACTACAAC 249
Db 41 ProGlyLysGlyLeuGluTrpIleGlyGluIleAenHisSerGlySerThrAsnTyrAsn 60
QY 250 CCGTCTCTCAAGAGTCCAGTCACCATATCAGTAGACACGTCCTCAAGAACCACTGCTCTG 309
Db 61 ProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeu 80
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Db 81 LysLeuSerSerValThrAlaAlaAspThrAlaValTyrCysAlaArgGlyProArg 100
QY 361 -----GTAAATTAATGTTGCTGACCTTCACCTTGGGCGCCAGGAACC 396
Db 101 TyrTyrAspIleLeuThrGlyTyrArgTyrAsnTrpPheAspProTrpGlyArgGlyThr 120
QY 397 CTGCTACCGCTCTCTCCAGCCTCA----- 420
Db 121 LeuValThrValSerSerGlyGlyGlyGlyGlySerGlyGlyGlyGlyGlyGly 140
QY 421 -----ACCAAGGCGCCATCGGTCTTCCCTCCCTGGCAGCCTCTCCCAAGAGC 465
Db 141 SerAspIleValMetThrGlnSerProSerThrLeuSerAlaSerValGlyAspArgVal 160
QY 466 ACC-----TCTGGGGCACAGCGCCCTGGCTGGCTGG 499
Db 161 ThrIleThrCysArgAlaSerGlnGlyIleSerSer-TripLeuAlaTrp 176

RESULT 12
US-10-153-382-21
; Sequence 21, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/233042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-382-21

Alignment Scores:
Pred. No.: 6,71e-42 Length: 172
Score: 585.50 Matches: 118
Percent Similarity: 82.19% Conservative: 2

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1321

Alignment Scores:
Pred. No.: 1,14e-40 Length: 152
Score: 571.00 Matches: 118
Percent Similarity: 82.19% Conservative: 2
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Best Local Similarity: 80.82% Mismatches: 20
Query Match: 59.05% Indels: 7
DB: 9 Gaps: 1

US-08-728-463B-219 (1-524) x US-09-187-693-68 (1-152)

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QY 226 CATAGTGAAGACCAACCACTACACCCGCTCTCTCAAGAGTCAGTCCACCATATCAGTAGAC 285
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QY 286 ACCTCCAAAGAACAGATTCTCTGAAACTGAGCTCTGTGACCGCTCGGACACGGCTGG 345
DB 61 ThrSerLysAsnGlnPheSerLeuLysLeuSerValThrAlaAlaAspThrAlaVal 80
QY 346 TATTACTGTGCGAGA-----GTAATTAATTGGTTCCGACCCCTTCGGGC 387
DB 81 TyrTyrCysAlaArgGlyProGlyGlySerTyrTyrTyrGlyMetAspValTrpGly 100
QY 388 CAGGGAACCTGTGCTACCGTCTCTCAGCTCAACCAAGGCCCATCGGTCTTCCCGCTG 447
DB 101 GlnGlyThrThrValThrValSerAlaSerThrLysGlyProSerValPheProLeu 120
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QY 507 CTACTTCCCCGAAACCGGT 524
DB 141 LeuLeuProArgThrGly 146

RESULT 14
US-09-910-059-93
; Sequence 93, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 93
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HuVh1-HuIgG1 Fd heavy chain
US-09-910-059-93

Alignment Scores:
Pred. No.: 1,02e-39 Length: 260
Score: 560.00 Matches: 114
Percent Similarity: 75.14% Conservative: 16

Best Local Similarity: 65.90% Mismatches: 37
Query Match: 57.91% Indels: 6
DB: 10 Gaps: 3

US-08-728-463B-219 (1-524) x US-09-910-059-93 (1-260)

QY 22 CTGTGGTTC--TTCTCTCTCTGGTGGCAGCTCTAGATGGTCTGTCTCAGGTGCAG 78
DB 3 LeuTrpLeuAsnTrpIlePheLeuValThrLeuLeuAsnGlyIleGlnCysGluValGln 22
QY 79 CTACAGCAGTGGGGCGGAGACTGTGAAGCCCTTCGGAGACCTGTCCCTCAGCTCCGCT 138
DB 23 LeuGlnGlnSerGlyProGlyLeuValArgProSerGlnThrLeuSerLeuThrCysThr 42
QY 139 GTCTATGTGGTTCCTCTCAGTGGTTACTACTCGAGCTGGATCCGCCAGCCACAGTAAG 198
DB 43 AlaSerGlyPheAsnIleLysAspAsnTyrMetHisTrpValArgGlnProProGlyArg 62
QY 199 GGTCTGGAGTGGATTGGTGAATCAAT---CATAGTGGAGGACCACTACACCGTCTCT 255
DB 63 GlyLeuGluTrpIleGlyTrpIleAspProGluAsnGlyAspThrGluTyrAlaProLys 82
QY 256 CTCGAAGTCCGAGTCCACATATCAGTAGACAGTCCCAAGAACCCAGTTCTCTGAAACTG 315
DB 83 PheArgGlyArgValThrMetLeuAlaAspThrSerLysAsnGlnPheSerLeuArgLeu 102
QY 316 AGCTCTGTGACCGCTCGGACACGGCTGTGTATTACTGTGCGAGAGTAATAAT----- 369
DB 103 SerSerValThrAlaAlaAspThrAlaValTyrTyrCysHisValLeuIleTyrAlaGly 122
QY 370 -----TGGTTGACCCCTTGGGGCCAGGAAACCTGGTCCAGCTCTCCTCAGCTCAACC 423
DB 123 TyrLeuAlaMetAspTyrTrpGlyGlnGlyThrLeuValThrValSerAlaSerThr 142
QY 424 AAGGGCCCATCGTCTTCTCCCTGGCAGCCCTCTCCAGAGCACCTCTCGGGGCACAGCG 483
DB 143 LysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThrAla 162
QY 484 GCCCTGGGCTGCTGCTCAAGGACTACTTCCCGGAAACCG 522
DB 163 AlaLeuGlyCysLeuValLysAspTyrPheProGluPro 175

RESULT 15
US-09-880-748-957
; Sequence 957, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 957
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-957

Alignment Scores:
Pred. No.: 1.24e-39 Length: 249
Score: 559.00 Matches: 113

Percent Similarity: 74.07% Conservative: 7
Best Local Similarity: 69.75% Mismatches: 22
Query Match: 57.81% Indels: 20
DB: 9 Gaps: 2

US-08-728-463B-219 (1-524) x US-09-880-748-957 (1-249)

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QY 130 ACCTGGCTGTCTATGCTGCTTCCTTCAGTGTACTACTGGAGCTGGATCCGCCAGCCA 189
Db 21 ThrCysAlaValTyrGlySerPheSerAsnTyrTyrTrpSerTrpIleArgGlnPro 40
QY 190 CCAGTAAAGGCTCTGGAGTGGATTGCTGAATCAATCATAGTGAAGCACCACCACTACAAC 249
Db 41 ProGlyLysGlyLeuGlnTrpValGlyGluLeuHisSerGlySerThrAsnTyrAsn 60
QY 250 CCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGACAGTCCAAAGAACCACTTCTCTCTG 309
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QY 310 AAACGTGACTCTGTACCGCTGCGGACACGGCTGTGTATTAATCTGCGAGAGTAATTAAT 369
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QY 370 TGGTTC-----GACCCCTGGGCGCAGGGAACC 396
Db 101 TyrTyrAspIleLeuThrGlyTyrTyrProSerGlyMetAspValTrpGlyLysGlyThr 120
QY 397 CTGGTCACCGTCTCTCA-----GCCTCAACCAAGGGC 429
Db 121 LeuValThrValSerSerGlyGlyGlySerGlyGlySerGlyGlyGly 140
QY 430 CCATCGGTCTTCCCTGGCACCCCTCTCCAGAGCACCTCTGGGGGACAGGGCCCTG 489
Db 141 SerSerGluLeuThrGlnAspProAlaValSerValAlaLeuGlyGlnThrValArgile 160
QY 490 GGCTGC 495
Db 161 ThrCys 162
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Search completed: June 3, 2003, 09:51:24
Job time : 26.264 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 09:02:35 ; Search time 11.9272 Seconds
(without alignments)
2585.294 Million cell updates/sec

Title: US-08-728-463B-219
Perfect score: 967
Sequence: 1 AGCTTGCCACCATGAACA.....GACTACTTCCCGACCGGT 524

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 525148

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=BITS -START=1 -END=1 -MATRIX=btosum62 -TRANS=human0.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	780	80.7	472	4	US-08-793-450-8
2	766.5	79.3	473	4	US-09-049-672A-4
3	739	76.4	476	3	US-08-487-550-12
4	722	74.7	476	3	US-08-487-550-4
5	700	72.4	467	4	US-08-523-894-8
6	700	72.4	467	4	US-08-523-894-10
7	700	72.4	467	4	US-08-523-894-12
8	622	64.3	116	3	US-08-545-809A-118
9	607.5	62.8	832	3	US-08-630-820-7
10	607	62.8	219	4	US-09-460-384-37
11	578	59.8	123	4	US-08-793-450-4
12	565	58.4	142	2	US-08-480-774A-2

13	564.5	58.4	273	3	US-08-397-411-6	Sequence 6, Appli
14	564.5	58.4	446	3	US-08-397-411-7	Sequence 7, Appli
15	560	57.9	260	4	US-09-171-945-93	Sequence 93, Appl
16	552	57.1	229	2	US-08-887-352B-20	Sequence 20, Appl
17	552	57.1	229	4	US-09-109-207C-20	Sequence 20, Appl
18	552	57.1	229	4	US-09-296-005-20	Sequence 20, Appl
19	552	57.1	233	2	US-08-887-352B-25	Sequence 25, Appl
20	552	57.1	233	4	US-09-109-207C-25	Sequence 25, Appl
21	552	57.1	233	4	US-09-296-005-25	Sequence 25, Appl
22	552	57.1	306	4	US-09-171-945-95	Sequence 95, Appl
23	552	57.1	451	2	US-08-887-352B-14	Sequence 14, Appl
24	552	57.1	451	2	US-08-887-352B-16	Sequence 14, Appl
25	552	57.1	451	3	US-08-466-151-65	Sequence 65, Appl
26	552	57.1	451	4	US-09-109-207C-14	Sequence 14, Appl
27	552	57.1	451	4	US-09-109-207C-16	Sequence 14, Appl
28	552	57.1	451	4	US-09-296-005-14	Sequence 14, Appl
29	552	57.1	451	4	US-09-296-005-16	Sequence 16, Appl
30	552	57.1	613	4	US-09-171-945-113	Sequence 113, App
31	550	56.9	116	3	US-08-545-809A-140	Sequence 140, App
32	546.5	56.5	716	4	US-09-171-945-125	Sequence 125, App
33	546	56.5	229	2	US-08-887-352B-21	Sequence 21, Appl
34	546	56.5	229	4	US-09-109-207C-21	Sequence 21, Appl
35	546	56.5	229	4	US-09-296-005-21	Sequence 21, Appl
36	546	56.5	233	2	US-08-887-352B-26	Sequence 26, Appl
37	546	56.5	233	4	US-09-109-207C-26	Sequence 26, Appl
38	546	56.5	233	4	US-09-296-005-26	Sequence 18, Appl
39	546	56.5	451	2	US-08-887-352B-18	Sequence 18, Appl
40	546	56.5	451	4	US-09-109-207C-18	Sequence 18, Appl
41	546	56.5	451	4	US-09-282-505-2	Sequence 2, Appli
42	546	56.5	451	4	US-09-054-255-2	Sequence 2, Appli
43	546	56.5	451	4	US-09-296-005-18	Sequence 18, Appl
44	539	55.7	118	3	US-08-545-809A-142	Sequence 142, App
45	538	55.6	116	3	US-08-545-809A-92	Sequence 92, Appl

ALIGNMENTS

RESULT 1
US-08-793-450-8
; Sequence 8, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CHRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHAABITHI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,450
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/10566
; FILING DATE: 02-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000
 TELEFAX: 703-413-2220
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 472 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-793-450-8

Alignment Scores:

Pred. No.: 6,2e-69 Length: 472
 Score: 780.00 Matches: 150
 Percent Similarity: 89.47% Conservative: 3
 Best Local Similarity: 87.72% Mismatches: 10
 Query Match: 80.66% Indels: 8
 DB: 4 Gaps: 1

US-08-728-463B-219 (1-524) x US-08-793-450-8 (1-472)

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QY 34 CTCCTCTGGTGGCAGCTCTAGATGGGTCTCTCAGGTGCAGCTACAGCAGTGGGGC 93
Db      |||||
QY 8 LeuPheLeuValAlaThrGlyValHisSerGlnValGlnLeuGlnLutrpGly 27
Db      |||||
QY 94 GCAGGCTGTTCAAGCCTTCGAGACCTGTCCCTCACCTCGCTGTCTATGTTGGTTC 153
Db      |||||
QY 28 AlaGlyLeuLeuPheProSerGluThrLeuSerLeuThrCysThrValTyrGlySer 47
Db      |||||
QY 154 TTCAGTGGTTACTCTGAGCTGGATCCGCCAGCCAGCAGTAAGGCTCTGGAGTGA 213
Db      |||||
QY 48 PheSerGlyTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeuGluTrpIle 67
Db      |||||
QY 214 GGTGAATCAATCATAGTGGAGCAGCACTACCAACCGCTCTCTCAAGAGTCGAGTCACC 273
Db      |||||
QY 68 GlyGluLeuAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr 87
Db      |||||
QY 274 ATATCAGTAGACACCTCAAGAACAGTCTCTCTGAACTGAGCTCTGTGACCGTGGC 333
Db      |||||
QY 88 IleSerValAspThrSerLysAsnGlnPheSerLeuLysLeuAsnSerValThrAlaA 107
Db      |||||
QY 334 GACACGGCTGTGTTACTGTGCGAGAGTAAT-----AAT 369
Db      |||||
QY 108 AspThrAlaValTyrTyrCysAlaArgAlaProGluTyrLysTrpLysTyrHisGlyAsp 127
Db      |||||
QY 370 TGGTTCGACCTTCGGCCAGGACCTCTGTCACCGTCTCTCAGCTCTCAACCAAGGCG 429
Db      |||||
QY 128 TrpPheAspProTrpGlyGlnGlyThrValThrValSerSerAlaSerThrLysGly 147
Db      |||||
QY 430 CCATCGCTCTCCCTCGCACCTCTCTCAAGAGCAGCCTCTGGGGCAGCGGCCCTG 489
Db      |||||
QY 148 ProSerValPheProLeuAlaProSerSerLysSerThrSerGlyThrAlaAlaLeu 167
Db      |||||
QY 490 GGCTGCTGCTCAGGACTACTTCCCGAACC 522
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QY 168 GlyCysLeuValLysAspTyrPheProGluPro 178
  
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RESULT 2

US-09-049-672A-4

Sequence 4, Application US/09049672A

Patent No. 6135941

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Lal, Preeti

APPLICANT: Tang, Y. Tom

APPLICANT: Yue, Henry

APPLICANT: Au-Young, Janice

APPLICANT: Corley, Neil C.

APPLICANT: Guegler, Karl J.

APPLICANT: Baughn, Marian R.

TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/049,672A
 FILING DATE: HERewith
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Cerrone, Michael C
 REGISTRATION NUMBER: 39,132
 REFERENCE/DOCKET NUMBER: PF-0497 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 473 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: PANCTUT01
 CLONE: 1513264
 US-09-049-672A-4

Alignment Scores:
 Pred. No.: 1.33e-67 Length: 473
 Score: 766.50 Matches: 154
 Percent Similarity: 88.83% Conservative: 5
 Best Local Similarity: 86.03% Mismatches: 11
 Query Match: 79.27% Indels: 9
 DB: 4 Gaps: 3

US-08-728-463B-219 (1-524) x US-09-049-672A-4 (1-473)

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QY 13 ATGAACACCTGTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 72
Db      |||||
QY 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20
Db      |||||
QY 73 GTGCAGCTACAGCAGTGGGCGCAGGACTGTTCAAGCCTTCGAGACCTCTGCTCCCTCACC 132
Db      |||||
QY 21 ValGlnLeuGlnLutrpGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40
Db      |||||
QY 133 TGCCTCTCTATGTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 186
Db      |||||
QY 41 CysAlaValSerGlyGlySerIleThrSerGlyTyrTyrTrpSerTrpIleArgGln 60
Db      |||||
QY 187 CCACCGTAAGGCTCTGGAGTGGATGGTGAATCAATCATAGTGGAGACCACTAC 246
Db      |||||
QY 61 ProProGlyLysGlyLeuGluTrpIleGlyTyrIleTyrSerGlySerThrLeuTyr 80
Db      |||||
QY 247 AACCCGCTCTCAAGAGTGCAGTCCACATATCAGTAGACACCTGCCAAGAACCACTCTCT 306
Db      |||||
QY 81 AsnProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSer 100
Db      |||||
QY 307 CTGAATCTGAGCTCTGACCCCTGCGGACACGGCTGTGTATTACTGTGCGAGATAATT 366
Db      |||||
QY 101 LeuLeuSerSerValThrAlaAlaAspThrAlaValTyrCysAlaArgAsp 120
Db      |||||
QY 367 -----AATTGG-----TTCGACCTCTGGGCGCAGGAACTCTGCTCACC 405
Db      |||||
  
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Score: 722.00 Matches: 143
Percent Similarity: 82.42% Conservative: 7
Best Local Similarity: 78.57% Mismatches: 20
Query Match: 74.66% Indels: 12
DB: 3 Gaps: 3

US-08-728-463B-219 (1-524) x US-08-487-550-4 (1-476)

QY 13 ATGAACACCTGCTGGTTCCTCTCCTGGTGGCAGCTCCTAGATGGGTCTGTCTCAG 72
Db 1 MetLysHisLeuTrpPheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20

QY 73 GTCACGCTACAGCAGTGGGGCGCAGCAGCTTGAAGCCTCGAGACCCCTGCTCCAC 132
Db 21 ValLysLeuGlnTrpGlyGluGlyLeuLeuGlnProSerGluThrLeuSerArgThr 40

QY 133 TGGCGTGTCTATGCTGCTCTTCAGTGGT---TACTACTGGAGCTGGATCCGCCAGCCA 189
Db 41 CysValValSerGlyGlySerIleSerGlyTyTrpTrpTrpTrpIleArgGlnThr 60

QY 190 CCAGGTAAGGGTCTGAGTGGATTGGTGAATCAATCATAGTGA---AGCACCAACTAC 246
Db 61 ProGlyArgGlyLeuGluTrpIleGlyHisIleTyGlyAsnGlyAlaThrThrAsnTyr 80

QY 247 AACCGTCTCTCAAGAGTCAGTCACCATATCAGTAGACACAGCTCCAGAACGAGTCTCT 306
Db 81 AsnProSerLeuLysSerArgValThrIleSerLysAspThrSerLysAsnGlnPhe 100

QY 307 CTGAACAGTACGCTGTGACCGCTGGCGACACGGCTGTGTATTACTGTGGAGA----- 360
Db 101 LeuAsnLeuAsnSerValThrAspAlaAspThrAlaValTyTrpCysAlaArgGlyPro 120

QY 361 -----GTAATTAAATGGTTCGACCTTGGCCCGCCAGGGAACC 396
Db 121 ArgProAspCysThrThrIleCysTyTrpGlyTrpValAspValTrpGlyProGlyAsp 140

QY 397 CTGGTACCGCTCTCCTCAGCCTCAACCAAGGGCCCATCGGTCTTCCCGCTGGCACCTCC 456
Db 141 LeuValThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSer 160

QY 457 TCCAAGAGCACCTCTGGGGCCACAGCGCCCTGGGCTGCTGCTCAAGGAGTACTTCCCC 516
Db 161 SerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyTrpPhePro 180

QY 517 GAACCG 522
Db 181 GluPro 182

RESULT 5
US-08-523-894-8
; Sequence 8, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DONNE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523.894

FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-523-894-8

Alignment Scores:
Pred. No.: 4,748-61 Length: 467
Score: 700.00 Matches: 139
Percent Similarity: 84.66% Conservative: 10
Best Local Similarity: 78.98% Mismatches: 21
Query Match: 72.39% Indels: 6
DB: 4 Gaps: 3

US-08-728-463B-219 (1-524) x US-08-523-894-8 (1-467)

QY 13 ATGAACACCTGCTGGTTCCTCTCCTGGTGGCAGCTCCTAGATGGGTCTGTCTCAG 72
Db 1 MetLysHisLeuTrpPheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20

QY 73 GTCACGCTACAGCAGTGGGGCGCAGCAGCTTGAAGCCTCGAGACCCCTGCTCCAC 132
Db 21 ValGlnLeuGlnSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40

QY 133 TGGCGTGTCTATGCTGCTCTTCAGTGGT---TACTACTGGAGCTGGATCCGCCAGCCA 189
Db 41 CysSerValSerGlyGlySerIleSerGlyAspTyTrpTrpTrpTrpIleArgGlnSer 60

QY 190 CCAGGTAAGGGTCTGAGTGGATTGGTGAATCAATCATAGT---GGAAGCACCAACTAC 246
Db 61 ProGlyLysGlyLeuGluTrpIleGlyTyTrpIleTyGlySerGlyGlyThrAsnTyr 80

QY 247 AACCGTCTCTCAAGAGTCAGTCACCATATCAGTAGACACAGCTCCAGAACGAGTCTCT 306
Db 81 AsnProSerLeuAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer 100

QY 307 CTGAACAGTACGCTGTGACCGCTGGCGACACGGCTGTGTATTACTGTGGG----- 357
Db 101 LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyTrpCysAlaSerAsnIle 120

QY 358 ---AGAGTAATTAATGGTTCGACCCCTGGGGCCAGGAAACCTGTGCTCCCGTCTCTCA 414
Db 121 LeuLysTyLeuHisTrpLeuLeuTyTrpGlyGlnGlyValLeuValThrValSerSer 140

QY 415 GCCTCAACCAAGGGCCCATCGGTCTTCCCGCTGGCACCCCTCTCCAGAGACACCTCTGG 474
Db 141 AlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGlu 160

QY 475 GGCACAGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCGAACCG 522
Db 161 SerThrAlaAlaLeuGlyCysLeuValLysAspTyTrpPheProGluPro 176

RESULT 6
US-08-523-894-10
; Sequence 10, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy

130	CCAGTAAAGGCTCTCGAGTGGATTGGTGAATC-----AATCATAGTGGAGACCAACATAC	246
61	ProGlyLysGlyLeuGluTirpIleGlySerPheTyrSerSerGlyAsnThrTyrTyr	80
247	AACCCGTCCTCAAGAGTCGAGTCACCATATACAGTAGACACGTCCAAGAACACAGTTCTCT	306
81	AsnProSerLeuLysSerGlnValThrIleSerThrAspThrSerLysAsnGlnPheSer	100
307	CTGAAACTGAGCTCTGTGACCGCTCGGCACACGGCTGTGTATTACTGTGCGGAGA-----	360
101	LeuLysLeuAsnSerMetThrAlaAlaAspThrAlaValTyrTyrCysValArgAspArg	120
361	-----GTAATT-----AATGGTTTCACCTTGGGGCCAGGGAACC	396
121	LeuPheSerValValGlyMetValTyrAsnAsnTrpPheAspValTirpGlyProGlyVal	140
397	CTGGTCACCGTCTCTCAGCCTCAACNAGGGCCCATCGGTCTTCCCGCTGGCACCCCTCC	456
141	LeuValThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSer	160
457	TCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC	516
161	SerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPhePro	180
517	GAACCG	522
181	GluPro	182

RESULT 4
US-08-487-550-4
; Sequence 4, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"

```

CORRESPONDENCE ADDRESS :
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

```

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1 SOFTWARE: PatentIn Release #1.0, Version #1.30
2
3 CURRENT APPLICATION DATA:
4
5 APPLICATION NUMBER: US/08/487,550
6
7 FILING DATE: 07-JUN-1995
8
9 CLASSIFICATION: 435
10
11 ATTORNEY/AGENT INFORMATION:
12
13 NAME: Teskin, Robin L.
14
15 REGISTRATION NUMBER: 35,030
16
17 REFERENCE/DOCKET NUMBER: 012712-131
18
19 TELECOMMUNICATION INFORMATION:
20

```

```

; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-487-550-4
;
; Alignment Scores:
; Pred. No.: 3 23e-63
; Length: 476

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	247	AACCGCTCTCAAGAGTCGAGTGCACCATATCAGTAGACACGTCCCAAGAACCAAGTTCTCT	306
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Db	81	AsnProSerLeuAsnAsnArgValSerIleSerIleAspThrSerLyAsnLeuPheSer	100
		:::::	
Qy	307	CTGAACACTGAGCTCTGTGACCGCTCGCGACACGGCTGTATTACTGTGGC-----	357
		:::::	
Db	101	LeuLySLeuArgSerValThrAlaAlaAspThrAlaValTyTrCysAlaSerAsnIle	120
		:::::	
Qy	359	---AGAGTAATTAAATGGTTTCGACCCCTTGCGGCCAGGGAAACCTGTGCACCGTCTCCTCA	414
		:::::	
Db	121	LeuLyTyTrLeuHisTrpLeuLeuTyTrTpGlyGlnGlyValLeuValThrValSerSer	140
		:::::	
Qy	415	GCTCAACAAGGGCCCATCGTCTCCCCCTGCACCCTCTCCCAAGAGCACCTCTGGG	474
		:::::	
Db	141	AlaSerThrLySGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGlu	160
		:::::	
Qy	475	GGCACAGCGGCGCTGGGTGCTGGTCAAGACTACTTCCCAGAACCG	522
		:::::	
Db	161	SerThrAlaAlaLeuGlyCySLeuValTyAspTyRpheProGluPro	176

RESULT

US-08-545-809A-118
; Sequence 118, Application US/08545809A

Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:

```

ADDRESSSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0

```

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070

```

```

;
; TELEFAX: 617-542-8906
;
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 118:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 116 amino acids
;
; TYPE: amino acid
;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-545-809A-118
;
; Alignment Scores:
;
; Pred. No.: 1,55A-53
; Score: 622.00
; Percent Similarity: 100.00%
; Best Local Similarity: 100.00%
; Query Match: 64.32%
; DB: 3
;
; Length: 116
; Matches: 116
; Conservative: 0
; Mismatches: 0
; Indels: 0
; Gaps: 0

```

US-08-728-463B-219 (1-524) x US-08-545-809A-118 (1-116)

Qy	13	ATGAAACACCTGTGGTTCTCTCTCTGTGGAGCTCTAGATGGGTCTCTGTCTAG	72
Db	1	MetLysHisLeuTrpPhePheLeuLeuLeuValAlaProArgTrpValLeuSerGln	20
Qy	73	GTGCAGCTACAGCTGGGGCGCAGGACTGTGAAGCCTTCGGAGACCTCTCCCTCACC	132
Db	21	ValGlnLeuGlnGlnTrpGlyAlaGlyLeuLeuLysProSerGluThrLeuSerLeuThr	40
Qy	133	TGCGCTGTCTATGTGTGTTCTTCCTCAGTCGGTTACTCTGAGCTGGATCGGCACGCCACCA	192
Db	41	CysAlaValTyrGlyGlySerPheSerGlyTyrTrpSerTrpIleArgGlnProPro	60
Qy	193	GGTAAGGGTCTGGAGTGGATTGGTCAAAATCAATCATAGTGAAGCACCAACTACAACCG	252
Db	61	GlyLysGlyLeuGluTrpIleGlyGluLeuAsnHisSerGlySerThrAsnTyrAsnPro	80
Qy	253	TCTCTCAAGAGTCGAGTCACCATATCAGTAGACAGCTCCAAAGAACCAAGTTCTCTCTGAAA	312
Db	81	SerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeuLys	100
Qy	313	CTGAGCTCTGTGACCGCTCGGACACGCGTGTGTATTACTGTGGCAGA	360
Db	101	LeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaAsnArg	116

RESULT 9

RESOL 3
US-08-630-820-7
; Sequence 7, Application US/08630820

Patent No. 6008023
GENERAL INFORMATION:
APPLICANT: OPFER, Martin
APPLICANT: BOSSLET, Klaus
APPLICANT: CZECH, Joerg
TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES
TITLE OF INVENTION: IN E. COLI

```

1  TITLE OF INVENTION:  IN E. COLI
2
3  NUMBER OF SEQUENCES:  7
4
5  CORRESPONDENCE ADDRESS:
6  ADDRESSEE:  Foley & Lardner
7  STREET:  3000 K Street, N.W., Suite 500
8  CITY:  Washington
9  STATE:  D.C.
10 COUNTRY:  USA
11 ZIP:  20007-5109
12
13 COMPUTER READABLE FORM:
14
15 MEDIUM TYPE:  Floppy disk
16
17 COMPUTER:  IBM PC compatible
18 OPERATING SYSTEM:  PC-DOS/MS-DOS
19 SOFTWARE:  Patent In Release #1.0.
20
21 Version #1.30

```

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0808
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19
FILING DATE: 11-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: GRANAPOS, Patricia
REGISTRATION NUMBER: 33.6
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

```

```

; INDEX: 504138
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 832 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-630-820-7

Alignment Scores:
Pred. No.: 7,316-52
Length: 832

```

Score: 607.50 Matches: 121
Percent Similarity: 85.44% Conservative: 14
Best Local Similarity: 76.58% Mismatches: 16
Query Match: 62.82% Indels: 7
DB: 3 Gaps: 4

US-08-728-463B-219 (1-524) x US-08-630-820-7 (1-832)

QY 70 CAGGTGACAGTACAGAGTGGGGCGGAGGACTGTGAAGCTTCGAGACCCCTGCTCCCTC 129
Db 2 GluValGlnLeuGlnGlnSerGlyProGlyLeuValArgProSerGlnThrLeuSerLeu 21
QY 130 ACCTGCGCTCTATGCTGCTTCTCTTC---AGTGGTTACTACTGGAGCTGGATCCGCCAG 186
Db 22 ThrCysThrValSerGlyPheThrIleSerSerGlyTyrSerTrpHisTrpValArgGln 41
QY 187 CCACAGGTGAAGGCTGAGGTGGATGGTGAATCAATCATAGTGGAAAGCACTAC 246
Db 42 ProProGlyArgGlyLeuGlnTrpIleGlyTyrIleGlnTyrSerGlyIleThrAsnTyr 61
QY 247 AACCGTCTCTCAAGAGTGGAGTACCATATCATAGTGGTGGTGGTGGTGGTGGTGGT 306
Db 62 AsnProSerLeuLysSerArgValThrMetLeuValAspThrSerLysAsnGlnPheSer 81
QY 307 CTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 363
Db 82 LeuArgLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgGluAsp 101
QY 364 -----ATTAATGG---TTGACACCTTGGGGCGGAGGAAACCTG-----GTCACCGTC 408
Db 102 TyrAspTyrHisTrpTyrPheAspValTrpGlyGlnGlySerLeuValThrValThrVal 121
QY 409 TCTCAGCTCAACCAAGGCCCATCGTCTTCCCTGCGACCCCTCCTCCCAAGACACC 468
Db 122 SerSerAlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThr 141
QY 469 TCTGGGGGACACGCGCCCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 522
Db 142 SerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro 159

RESULT 10
US-08-728-463B-219 (1-524) x US-08-630-820-7 (1-832)
; Sequence 37, Application US/09460384
; Patent No. 6337316
; GENERAL INFORMATION:
; APPLICANT: EL TAYAR, Nabil
; BLECHNER, Steven
; JAMESON, Brad
; TEPPER, Mark
; TITLE OF INVENTION: CD28/CTLA-4 INHIBITING PEPTIDOMIMETICS,
; PHARMACEUTICAL COMPOSITIONS THEREOF, AND METHOD OF USING
; SAME
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 624 Ninth Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/460,384
; FILING DATE: 13-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/12312
; FILING DATE: 11-JUN-1998
; APPLICATION NUMBER: US 60/049,470

FILING DATE: 12-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: EL TAYAR=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-460-384-37

Alignment Scores:
Pred. No.: 5,6e-52 Length: 219
Score: 607.00 Matches: 121
Percent Similarity: 86.99% Conservative: 6
Best Local Similarity: 82.88% Mismatches: 17
Query Match: 62.77% Indels: 2
DB: 4 Gaps: 1

US-08-728-463B-219 (1-524) x US-09-460-384-37 (1-219)

QY 91 GCGCGAGGAGCTGTGAAGCTTCGAGACCTGTCCTCCCTCAGCTGGCTCTCTATGGTGGT 150
Db 2 GlyProGlyLeuValLysProSerGluAlaLeuSerLeuThrCysThrValSerGlyAsp 21
QY 151 TCCTTCACTAGTGT-----TACTACTGGAGCTGGATCCGCCAGCCACAGGTAAAGGTCTG 204
Db 22 SerIleAsnThrIleLeuTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu 41
QY 205 GAGTGGATTGGTGAATCAATCATAGTGGAAAGCACTACACCCGCTCTCTCAAGAGT 264
Db 42 GluTrpIleGlyTyrIleTyrSerGlySerThrTyrGlyAsnProSerLeuLysSer 61
QY 265 CGAGTCACCATATCATAGTACACACGCTCCCAAGAACCACTCTCTCTGAAACTGAGCTCTGTG 324
Db 62 ArgValThrIleSerValAsnThrSerLysAsnGlnPheTyrSerLysLeuSerVal 81
QY 325 ACCGCTGGGACACCGCTGTGTATTACTGTGCGAGAGTAAATTAATGGTTCGACCCCTGG 384
Db 82 ThrAlaAlaAspThrAlaValTyrTyrCysAlaAaGValProLeuValValAsnProTrp 101
QY 385 GCGCAGGAGACCTGGTCACTCCCTCTCTCAGCTCAACCAAGGGCCCATCGCTCTTCCCC 444
Db 102 GlyGlnGlyThrLeuValThrValSerSerAlaSerThrLysGlyProSerValPhePro 121
QY 445 CTGGCACCTCTCTCAAGAGACCTCTGGGGGCACAGCGCCCTGGGCTGGCTGGTCAAG 504
Db 122 LeuAlaProSerSerLysSerThrSerGlyThrAlaAlaLeuGlyCysLeuValLys 141
QY 505 GACTACTTCCCGGAACCG 522
Db 142 AspTyrPheProGlnPro 147

RESULT 11
US-08-793-450-4
; Sequence 4, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CHRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHAABIHI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:

ADDRESS: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994

ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT

TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220

SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid

MOLECULE TYPE: protein
US-08-793-450-4

Alignment Scores:
Pred. No.: 3,43e-49 Length: 123

Score: 578.00 Matches: 109

Percent Similarity: 90.24% Conservative: 2

Best Local Similarity: 88.62% Mismatches: 4

Query Match: 59.77% Indels: 8

DB: 4 Gaps: 1

US-08-728-463B-219 (1-524) x US-08-793-450-4 (1-123)

Qy 70 CAGGTGAGTACAGCAGTGGGCGCAGGACTGTGAAGCTTCGGAGACCCGTGCTC 129

Db 1 GlnValGlnLeuGlnTrpGlyAlaGlyLeuLeuLysProSerGluThrLeuSerLeu 20

Qy 130 ACCTGCGCTCTATGTTGGTTCCTTCAGTGGTACTACTGGAGCTGGATCCCGACCA 189

Db 21 ThrCysThrValTyrGlyGlySerPheSerGlyTyrTrpSerTrpIleArgGlnPro 40

Qy 190 CCAGGTAAAGGCTCTGAGTGGATTGGTGAATCAATCATAGTGAAGCACTACAC 249

Db 41 ProGlyLysGlyLeuGluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsn 60

Qy 250 CCGTCTCTAAGAGTGGAGTCACATATCAGTACACAGTCCAGAACCCAGTTCTCTG 309

Db 61 ProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeu 80

Qy 310 AAAGTGGCTCTGAGCCTGGGCGGACCGCTGTATATCTACTGTCGAGAGTAAT 366

Db 81 LysLeuAsnSerValThrAlaAlaAspThrAlaValTyrCysAlaArgAlaProGlu 100

Qy 367 -----AATGTTCCAGCCCTTGGGCGCAGGAAACCCCTGGTCACC 405

Db 101 TyrLysTrpLysTyrHisGlyAspTrpPheAspProTrpGlyGlnGlyThrValThr 120

Qy 406 GTCTCTCA 414

Db 121 ValSerSer 123

RESULT 12

US-08-480-774A-2

Sequence 2, Application US/08480774A

Patent No. 5852186

GENERAL INFORMATION:

APPLICANT: MARASCO, Wayne A.

APPLICANT: SODOSKI, Joseph G.

APPLICANT: HAZELTINE, William A.

APPLICANT: POSNER, Marshall R.

TITLE OF INVENTION: REACTIVE NEUTRALIZING HUMAN

TITLE OF INVENTION: ANTI-9P 120 RECOMBINANT ANTIBODY, DNA CODING THE SAME

TITLE OF INVENTION: AND USE THEREOF

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/480,774A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/400,674

FILING DATE: 08-MAR-1995

APPLICATION NUMBER: 07/804,652

FILING DATE: 10-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Resnick, David S

REGISTRATION NUMBER: 34,235

REFERENCE/DOCKET NUMBER: 41450-FWC-DIV

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 142 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-08-480-774A-2

Alignment Scores:

Pred. No.: 6,83e-48 Length: 142

Score: 565.00 Matches: 110

Percent Similarity: 85.92% Conservative: 12

Best Local Similarity: 77.46% Mismatches: 12

Query Match: 58.43% Indels: 8

DB: 2 Gaps: 2

US-08-728-463B-219 (1-524) x US-08-480-774A-2 (1-142)

Qy 13 ATGAACACCTGTGTGTTCTTCTCTCTCTGTCGAGCTCTAGATGGTCTGTCTCAG 72

Db 1 MetGluHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20

Qy 73 GTGACGTACAGCAGTGGGCGCAGGACTGTGAAGCTTCGGAGACCTCTCCCTCACC 132

Db 21 ValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40

Qy 133 TGCCTGTCTATGTTGGTTCCTTTCAGTGGTGTACTTGGAGCTGATCCGACGCCACCA 192

Db 41 CysThrValSerGlyGlySerIleSerHisIleSerHisIleSerHisIleArgGlnSerPro 60

QY 193 GCTAGGCTCGAGTGGATTGGTGAATCAATCATAGTGGAGACCACTACACCG 252
Db 61 GlyLysGlyLeuGlnTrpLeuGlyTrpLeuGlySerGlySerThrAsnTyrSerPro 80
QY 253 TCTCTCAAGAGTCGAGTCACCATATCAGTAGACACAGTCCAAAGAACAGTTCTCTGAAA 312
Db 81 SerLeuLysSerArgValThrLeuSerValGluThrSerLysAsnGlnPheSerLeuLys 100
QY 313 CTGAGCTCTGTGACCGCTCGGACACAGCGTGTGTATTACTGTGCGAGA----- 360
Db 101 LeuThrSerMetThrAlaAlaAspThrAlaValTyrTyrCysAlaArgGlyProValPro 120
QY 361 GTAATTAATGG-----TTTCGACCCCTTGGGGCCAGGACCGTGTGTCACCGNC 408
Db 121 AlaValPheTyrGlyAspTyrArgLeuAspProTrpGlyGlnGlyThrLeuValThrVal 140
QY 409 TCTCA 414
Db 141 SerSer 142

RESULT 13
US-08-397-411-6
; Sequence 6, Application US/08397411
; Patent No. 6129914
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Gingrich, Roger
; APPLICANT: Link, Brian
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Bispecific Antibody Effective to Treat
; TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/397,411
; FILING DATE: 01-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/859,583
; FILING DATE: 27-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-004901
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2420
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-397-411-6

Alignment Scores:
Pred. No.: 9.21e-48 Length: 273
Score: 564.50 Matches: 115
Percent Similarity: 81.58% Conservative: 9
Best Local Similarity: 75.66% Mismatches: 27
Query Match: 58.38% Indels: 1

DB: 3 Gaps: 1
US-08-728-463B-219 (1-524) x US-08-397-411-6 (1-273)
QY 70 CAGGTGACAGCTACAGCAGTGGGGCCAGGACTGTGTGAAGCCTTCGGAGACCCCTGTCCCTC 129
Db 1.GlnValGlnLeuGlnGlnSerGlyProGlyLeuValLysProSerGluThrLeuSerLeu 20
QY 130 ACCTCGCTGTCTATGTGGTTCCTTCACTAGTGGTTACTACTGGAGCTGGATCCGCCAGCCA 189
Db 21 ThrCysThrValSerGlyPheSerLeuThrAsnTyrGlyValHisTrpValArgGlnSer 40
QY 190 CCAGTAAGGCTCGAGTGGATTGGTGAATCAATCATAGTGGAGACCACTACAC 249
Db 41 ProGlyLysGlyLeuGlnTrpLeuGlyValLysTrpSerGlyGlySerThrGluTyrAsn 60
QY 250 CCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGACACAGTCCAAAGAACAGTTCTCTCG 309
Db 61 AlaAlaPheLeuSerArgLeuThrLeuSerLysAspThrSerLysAsnGlnValSerLeu 80
QY 310 AAATGAGCTGTGACCGCTCGGACACAGCGTGTGTATTACTGTGCGAGAGTAAATAAT 369
Db 81 LysLeuAsnSerLeuThrAlaAlaAspThrAlaValTyrTyrCysAlaAlaArgAsnAspArg 100
QY 370 TGG---TTTCGACCCCTTGGGGCCAGGACCGTGTGTTACTCTCTCAGCTCAACCCANG 426
Db 101 TyrAlaMetAspTyrTrpGlyGlnGlyThrLeuValThrValSerSerAlaSerThrLys 120
QY 427 GSCCATCGTCTTCCCTCGCACCCCTCTCCAAGAGCACCTCTGGGGGCGACAGCGCC 486
Db 121 GlyProSerValPheProLeuAlaProSerSerLysSerThrSerGlyThrAlaAla 140
QY 487 CTGGGCTGCTGTGTCAGGACTACTTCCCGAACCG 522
Db 141 LeuGlyCysLeuValLysAspTyrPheProGluPro 152

RESULT 14
US-08-397-411-7
; Sequence 7, Application US/08397411
; Patent No. 6129914
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Gingrich, Roger
; APPLICANT: Link, Brian
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Bispecific Antibody Effective to Treat
; TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/397,411
; FILING DATE: 01-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/859,583
; FILING DATE: 27-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-004901
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2420
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-397-411-6

TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 446 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-397-411-7

Alignment Scores:
Pred. No.: 1.06e-47 Length: 446
Score: 564.50 Matches: 115
Percent Similarity: 81.58% Conservative: 9
Best Local Similarity: 75.66% Mismatches: 27
Query Match: 58.38% Indels: 1
DB: 3 Gaps: 1

US-08-728-463B-219 (1-524) x US-08-397-411-7 (1-446)

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QY 70 CAGGTGACGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCCTGTCCTC 129
      |||||.....|||
Db 1 GlnValGlnLeuGlnSerGlyProGlyLeuVallyProSerGluThrLeuSerLeu 20

QY 130 ACTGCGCTGCTATAGTGTGCTTCCTTCAGCTGGTTACTACTGGAGCTGGATCCGCCAGCCA 189
      |||||.....|||
Db 21 ThrCysThrValSerGlyPheSerLeuThrAsnTyrGlyValHisTrpValA:GlnSer 40

QY 190 CCAGTAAGGCTGGAGTGGATGGTGAATCAATCATAGTGGAGCACAACACTACAAC 249
      |||||.....|||
Db 41 ProGlyLysGlyLeuGluTrpIleGlyVallySerGlyGlySerThrGluTyrAsn 60

QY 250 CCGTCTCTCAAGAGTCCAGTCACCATATCAGTAGACACAGCTCCAGAACCACTGCTCTCTG 309
      |||||.....|||
Db 61 AlaAlaPheIleSerArgLeuThrIleSerLysAspThrSerLysAsnGlnValSerLeu 80

QY 310 AAAGTACGCTGTGACCGCTGGCGACACCGCTGTGTATTACTGTGCGAGAGTAATTAAT 369
      |||||.....|||
Db 81 LysLeuAsnSerLeuThrAlaAlaAspThrAlaValTyrCysAlaA:GlnAspArg 100

QY 370 TGG---TTCCACCTTCGGGCGCAGGAAACCTGGTCAACCTCTCCAGCTCAACCAAG 426
      |||||.....|||
Db 101 TyrAlaMetAspTyrTrpGlyGlnGlyThrLeuValThrValSerAlaSerThrLys 120

QY 427 GGCCCATCGCTTCTCCCTCGCACCTCTCCCAAGAGACCTCTCGGGGCACAGCGGCC 486
      |||||.....|||
Db 121 GlyProSerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThrAlaAla 140

QY 487 CTGGGCTGCTGTCAAGGACTACTTCCCGAACC 522
      |||||.....|||
Db 141 LeuGlyCysLeuVallyAspTyrPheProGluPro 152
```

RESULT 15

US-09-171-945-93

Sequence 93, Application US/09171945
Patent No. 6277599
GENERAL INFORMATION:
APPLICANT: Emery, Stephen
APPLICANT: Copley, Clive Graham
APPLICANT: Edge, Michael Derek
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
FILE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
FILE REFERENCE: Monoclonal Antibody to CEA
CURRENT APPLICATION NUMBER: US/09171,945
CURRENT FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: GB9703103.3
PRIOR FILING DATE: 1997-02-14
PRIOR APPLICATION NUMBER: GB9609405.7
PRIOR FILING DATE: 1996-05-04
PRIOR APPLICATION NUMBER: PCT/GB97/01165
PRIOR FILING DATE: 1997-04-29
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 93
LENGTH: 260
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-93

Alignment Scores:
Pred. No.: 2.52e-47 Length: 260
Score: 560.00 Matches: 114
Percent Similarity: 75.14% Conservative: 16
Best Local Similarity: 65.90% Mismatches: 37
Query Match: 57.91% Indels: 6
DB: 4 Gaps: 3

US-08-728-463B-219 (1-524) x US-09-171-945-93 (1-260)

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QY 22 CTGTGCTTC---TTCCTCTCTGTGGCAGCTCTCTAGATGGTCTCTCAGGTGCAG 78
      |||||.....|||
Db 3 LeuTrpLeuAsnTrpIlePheLeuValThrLeuLeuAsnGlyIleGlnCysGluValGln 22

QY 79 CTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCCTGCTCCCTCAGCTCGCT 138
      |||||.....|||
Db 23 LeuGlnGlnSerGlyProGlyLeuValArgProSerGlnThrLeuSerLeuThrCysThr 42

QY 139 GTCTATGGTGGTTCCTTCAGTGGTTACTACTCGAGCTGGATCCGCCAGCACCAGGTAAG 198
      |||||.....|||
Db 43 AlaSerGlyPheAsnIleLysAspAsnTyrMetHisTrpValArgGlnProProGlyA:G 62

QY 199 GGTCTGAGTGGATTGGTGAATCAAT---CATAGTGGAGCACCACCACTACACCCGTCT 255
      |||||.....|||
Db 63 GlyLeuGluTrpIleGlyTrpIleAspProGluAsnGlyAspThrGluTyrAlaProLys 82

QY 256 CTCACAGCTCGAGTCACCATATCAGTAGACACAGCTCCAGAACCACTCTCTGAAACTG 315
      |||||.....|||
Db 83 PheArgGlyArgValThrMetLeuAlaAspThrSerLysAsnGlnPheSerLeuArgLeu 102

QY 316 AGCTCTGTGACCGCTCGGCACACCGCTGTGTATTACTGTGCGAGAGTAATTAAT----- 369
      |||||.....|||
Db 103 SerSerValThrAlaAlaAspThrAlaValTyrCysHisValLeuIleTyrAlaGly 122

QY 370 -----TGTTTCGACCTTTGGGGCGCAGGAAACCTGGTCCACCGTCTCTCAGCCTCAAC 423
      |||||.....|||
Db 123 TyrLeuAlaMetAspTyrTrpGlyGlnGlyThrLeuValThrValSerSerAlaSerThr 142

QY 424 AAGGGCCCATCGCTCTCCCTCGCACCTCTCCCAAGAGCACCCTCTCGGGGCACAGCG 483
      |||||.....|||
Db 143 LysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThrAla 162

QY 484 GCCCTGGGCTGCTGCTCAAGGACTACTTCCCGAACC 522
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Db 163 AlaLeuGlyCysLeuVallyAspTyrPheProGluPro 175
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Search completed: June 3, 2003, 09:47:34

Job time : 14.9272 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 17.7656 Seconds
(without alignments)
4545.477 Million cell updates/sec

Title: US-08-728-463B-220
Perfect score: 761
Sequence: 1 AGCTTGCCACCATGATGTT.....TGCTGCACCATCTGCTTC 420

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283224 seqs, 9613422 residues

Total number of hits satisfying chosen parameters: 566448

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-Q=/cgn2 1/USPTO.spool/US08728463/runat_03062003_085615_16827/app.query.fasta_1.3690
-DB=PIR 73 -QMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCI=0 -LOOPEXT=0
-UNITS=bits START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 73:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	621	81.6	130	2	S40368
2	592	77.8	141	2	A49134
3	590	77.5	125	2	S40333
4	587	77.1	125	2	S40316
5	586	77.0	132	2	S40334
6	581	76.3	127	2	S40367
7	580	76.2	117	2	S21527
8	574	75.4	117	2	S46376
9	571	75.0	131	2	S40352
10	570	74.9	129	2	S40369
11	564	74.1	125	2	S40349
12	562	73.9	123	2	S40331
13	562	73.9	128	2	S46372
14	558.5	73.4	124	2	S40336
					Ig kappa chain - h
					Ig kappa chain V-I
					Ig kappa chain V-J
					Ig kappa chain - h
					Ig kappa chain - h
					Ig kappa chain V-J
					Ig kappa chain pre
					Ig kappa chain V-J
					Ig kappa chain V-J
					Ig kappa chain - h
					Ig kappa chain - h
					Ig kappa chain V-J
					Ig kappa chain - h
					Ig kappa chain var
					Ig kappa chain V-J

15	557	73.2	132	2	S38646	Ig kappa chain V r
16	556	73.1	127	2	S11240	Ig kappa chain V r
17	553	72.7	129	2	S52793	Ig kappa chain V r
18	550	72.3	125	2	S40353	Ig kappa chain V-J
19	550	72.3	126	2	S40335	Ig kappa chain V-J
20	549	72.1	129	1	K1HUKK	Ig kappa chain pre
21	548	72.0	124	2	S40318	Ig kappa chain V r
22	546	71.7	129	2	S40317	Ig kappa chain - h
23	546	71.7	139	2	S40365	Ig kappa chain - h
24	545	71.6	129	2	S52789	Ig kappa chain V r
25	540.5	71.0	129	2	S40332	Ig kappa chain - h
26	537	70.6	123	2	S40313	Ig kappa chain V-J
27	535	70.3	129	2	S52792	Ig kappa chain V r
28	533.5	70.1	125	2	S40315	Ig kappa chain - h
29	533.5	70.1	135	2	S24320	Ig kappa chain pre
30	531	69.9	117	2	S46371	Ig kappa chain V-J
31	531	69.8	117	1	K1HU12	Ig kappa chain pre
32	528	69.4	117	2	B21056	Ig kappa chain pre
33	526.5	69.2	120	2	S46374	Ig kappa chain V-J
34	526	69.1	117	2	S24206	Ig kappa chain V r
35	523	68.7	117	1	K1HU11	Ig kappa chain pre
36	522	68.6	117	2	S11700	Ig kappa chain pre
37	521	68.5	117	2	S41809	Ig kappa chain V r
38	521	68.5	122	2	S40314	Ig kappa chain - h
39	520	68.3	117	2	C21056	Ig kappa chain pre
40	520	68.3	122	2	S40370	Ig kappa chain - h
41	517.5	68.0	122	2	S40351	Ig kappa chain V-J
42	516	67.8	120	2	S46370	Ig kappa chain V-J
43	514	67.5	117	2	S41810	Ig kappa chain V r
44	513	67.4	116	2	A27594	Ig kappa chain pre
45	509	66.9	125	2	S40350	Ig kappa chain - h

ALIGNMENTS

RESULT 1

S40368
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40368
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40368
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-130 <KLE>
A;Cross-references: EMBL:X72478; NID:G441424; PIDN:CAA51146.1; PID:G441425
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 1.28e-46 Length: 130
Score: 621.00 Matches: 118
Percent Similarity: 94.62% Conservative: 5
Best Local Similarity: 90.77% Mismatches: 7
Query Match: 81.60% Indels: 0
DB: 2 Gaps: 0

US-08-728-463B-220 (1-420) x S40368 (1-130)

Qy	22	CCAGCTCAGCTCCTCGGTCCTCGTCTGGTCCAGGTTCCAGATCCGACATCCAG	81
Db	1	ProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpPheProGlySerArgCysAspIleGln	20
Qy	82	ATGACCCAGCTCTCCATCTTCCGTCGTCTGTCATCTGTAGGAGACAGAGTCACCATCTGT	141
Db	21	MetThrGlnSerProSerValSerAlaSerValGlyAspArgValIleThrCys	40
Qy	142	CGGGCGAGTCAGGATATTAGCAGCTGGTGTAGCTGTATGATGATTAACACGAGTAAAGCA	201

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Db 41 ArgAlaSerGlnAspValAlaGlyTrpLeuAlaTrpTyrGlnGlnLysProGlyAlaAla 60
QY 202 CCTAAGCTCCTGATCTATGTCGATCCAGTTTGCAGAGTGTGTCCTCCATCAAGGTTCCAGC 261
Db 61 ProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGluValProProArgPheSer 80
QY 262 GGAAGTGGATCTGGACAGATTTTCACTCTCCATCAGCAGCCCTGCAGCCTGAAGATTTT 321
Db 81 GlySerGlySerGlyThrAspPheSerLeuThrIleSerArgLeuGlnProGluAspPhe 100
QY 322 GCAACTTACTATTGTCACAGGCTAATAGTTTCCGTACACTTTTGGTCAGGGAACCAAG 381
Db 101 AlaThrTyrTyrCysGlnGlnAlaAsnSerPheProItrPheGlyGlnGlyThrLys 120
QY 382 CTGGAGATCAACAGCACTGTGGTCACCA 411
Db 121 ValGluIleLysAcsGThrValAlaAlaPro 130

RESULT 2
A: kapp chain V-I region (ISE) - human (fragment)
C: Species: Homo sapiens (man)
C: Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C: Accession: A49134; S25115
R: Rocca, A.; Khammichi, A.A.; Aucouturier, P.; Noel, L.H.; Denoroy, L.; Preud'homme, J.I.
Clin. Exp. Immunol. 91, 506-509, 1993
A: Title: Primary structure of a variable region of the V kappa I subgroup (ISE) in light
A: Reference number: A49134; MUID: 93185310; PMID: 7680298
A: Accession: A49134
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-141 <ROC>
A: Cross-references: EMBL:X67322; NID:933268; PIDN:CAA47736.1; PID:933269
A: Note: sequence extracted from NCBI backbone (NCBIP:127088)
C: Superfamily: immunoglobulin V region; immunoglobulin homology
C: Keywords: heterotetramer; immunoglobulin
F: 38-112/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 4,46-44 Length: 141
Score: 592.00 Matches: 111
Percent Similarity: 91.18% Conservative: 13
Best Local Similarity: 81.62% Mismatches: 12
Query Match: 77.79% Indels: 0
DB: 2 Gaps: 0

US-08-728-463B-220 (1-420) x A49134 (1-141)
QY 13 ATGATGTCCTCAGCTCCTCGGTCCTCTGCTGCTCTGTTCCAGGTTCCAGATGC 72
Db 3 MetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuProGlyAlaLysCys 22
QY 73 GACATCCAGATGACCCAGTCTCCATCTTCCTGCTGCTCATCTGTAGGACAGAGTCACC 132
Db 23 AspIleGlnMetThrGlnSerProSerThrLeuSerAlaSerValGlyAspArgValThr 42
QY 133 ATCACTTGTGGGAGTCAGGATATTAGCAGCTGGTGTAGCTGTATCAGCATAACCA 192
Db 43 IleThrCysArgAlaSerLeuGlyIleAsnIleTrpLeuAlaTrpTyrGlnGlnLysPro 62
QY 193 GGTAAAGCACCTAAGCTCCTGATCTATGTCGATCCAGTTTGCAGGTTGTCCTATCA 252
Db 63 GlyLysAlaProAsnLeuLeuIleTyrLysAlaThrAsnLeuGlnSerGlyValProSer 82
QY 253 AGGTTACGGGAAGTGGATCTGGACAGATTTTCACTCTCCATCAGCAGCCTGCAGCCT 312
Db 83 ArgPheSerAlaSerGlySerGlyThrGluPheThrLeuThrIleSerGlyLeuGlnPro 102
QY 313 GAGATTTTCCAACTTACTATTGTCACAGGCTAATAGTTTCCGTCACATTTTGGTGTG 372
Db 103 AspAspPheAlaThrTyrTyrCysHisGlnTyrAspSerTyrProItrPheGlyGln 122
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QY 373 GGAACCAAGCTGAGATCAACGAACTGTGGCTGCACCATCTCTCTTC 420
Db 123 GlyThrLysValGluIleLysArgThrValAlaAlaProSerValPhe 138

RESULT 3
S40333
Ig kappa chain V-J region - human
C: Species: Homo sapiens (man)
C: Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C: Accession: S40333
R: Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A: Title: Expressed human immunoglobulin chi genes and their hypermutation.
A: Reference number: S40312; MUID: 94080891; PMID: 8258341
A: Accession: S40333
A: Status: preliminary; translation not shown
A: Molecule type: mRNA
A: Residues: 1-125 <KLE>
A: Cross-references: EMBL:X72443; NID:9441354; PIDN:CAA51111.1; PID:9441355
C: Superfamily: immunoglobulin V region; immunoglobulin homology
C: Keywords: heterotetramer; immunoglobulin
F: 34-108/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 6,71e-44 Length: 125
Score: 590.00 Matches: 110
Percent Similarity: 96.00% Conservative: 10
Best Local Similarity: 88.00% Mismatches: 5
Query Match: 77.53% Indels: 0
DB: 2 Gaps: 0

US-08-728-463B-220 (1-420) x S40333 (1-125)
QY 19 GTCCAGCTCAGCTCCTCGGTCCTCTGCTGCTCTGTTCCAGGTTCCAGATCCGACATC 78
Db 1 ValProAlaGlnLeuLeuGlyLeuLeuLeuLeuLeuLeuTrpLeuProGlyAlaLysCysAspIle 20
QY 79 CAGATGACCCAGTCTCCATCTTCCGTCCTGTCATCTGTAGGACAGAGTCACCATCAT 138
Db 21 GlnMetThrGlnSerProSerThrLeuSerAlaSerValGlyAspArgValThrIleThr 40
QY 139 TGTGGGCGGAGTCAGGATATTAGCAGCTGTGTAGCTGTATCAGCATAAACCGATAA 198
Db 41 CysArgAlaSerGlnSerIleSerIleSerIleTrpLeuAlaTrpTyrGlnGlnLysProGlyLys 60
QY 199 GCACCTAAGCTCCTGATCTATGTCATCTGTCATCTGTCAGTTTGCAGAGTGTGTC 258
Db 61 AlaProLysLeuLeuIleTyrLysAlaSerSerLeuGluSerGlyValProSerArgPhe 80
QY 259 ACGGNAAGTGGATCTGGACAGATTTCTCTCAGCATCAGCAGCTGCAGCTGAAGAT 318
Db 81 SerGlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeuGlnProAspAsp 100
QY 319 TTTCGAACCTACTATTGTCAACAGGCTAATAGTTTCCGTCACATTTTGGTCAGGNAAC 378
Db 101 PheAlaThrTyrTyrCysGlnGlnTyrAsnSerTyrProItrPheGlyGlnGlyThr 120
QY 379 AAGCTGGAGATCAAA 393
Db 121 LysValGluIleLys 125

RESULT 4
S40316
Ig kappa chain - human
C: Species: Homo sapiens (man)
C: Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C: Accession: S40316
R: Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A: Title: Expressed human immunoglobulin chi genes and their hypermutation.
A: Reference number: S40312; MUID: 94080891; PMID: 8258341
A: Accession: S40316
A: Status: preliminary; translation not shown
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Qy	13	ATGATGTCCTCAGCTCCTCGGTCCTCTCGTCTCTGTCGTCTCTGTTCCCGAGTTCCAGATGC	72
Db			
Db	2	MetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpLeuProGlyAlaArgCys	21
Qy	73	GACATCCAGATGACCCAGTCTCCATCTCCGTGTCGTGATCTGTAGGACAGAGTCACC	132
Db			
Db	22	AspIleGlnLeuThrGlnSerProSerPheLeuSerAlaSerIleGlyAspArgValThr	41
Qy	133	ATCACTTGTTCGGCGAGTCAGGATATTAGCAGCTGGTTAGCTCGTGTATCAGCATAAACCA	192
Db			
Db	42	IleThrCysArgAlaSerGlnGlyIleAsnSerTyrLeuAlaTrpTyrGlnGlnLysPro	61
Qy	193	GGTAAAGCACCTAAGTCCTCATCTATGCTGTCATCCAGTTTGCCAAAGTGGTGTCCCATCA	252
Db			
Db	62	GlyLysAlaProLysLeuLeuIleTyrValAlaSerThrLeuGlnSerGlyValProSer	81
Qy	253	AGTTCACGCGAAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT	312
Db			
Db	82	ArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeuGlnPro	101
Qy	313	GAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTTCAG	372
Db			
Db	102	GluAspPheAlaSerTyrTyrCysGlnGlnPheAsnSerTyrProPheThrPheGlyGly	121
Qy	373	GGAACCAAGCTGGAGATCAAAACGAACTGTGGCT	405
Db			
Db	122	GlyThrLysValGluIleArgArgThrValAla	132

RESULT 6

S40367

Ig kappa chain V-J-C region - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40367

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8259341

A:Accession: S40367

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-127 <KLE>

A:Cross-references: EMBL:X72477

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:33-107/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	4,11e-43	Length:	127
Score:	581.00	Matches:	112
Percent Similarity:	94.49%	Conservative:	8
Best Local Similarity:	88.19%	Mismatches:	7
Query Match:	76.35%	Indels:	0
DB:	2	Gaps:	0

US-08-728-463B-220 (1-420) x S40367 (1-127)

Qy	22	CCAGCTCAGCTCTCGGTCCTCGTCTCTGTCGTTCAGGTTCCAGATGCGACATCCAG	81
Db			
Db	1	ProAlaGlnLeuLeuGlyLeuLeuLeuTrpLeuArgGlyAlaArgCysAspIleGln	20
Qy	82	ATGACCCAGTCTCCATCTTCGTCCTGCATCTGTAGGACAGAGTACCACATCTGT	141
Db			
Db	21	MetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThrCys	40
Qy	142	CGGCGAGTCAGGATATTAGCAGCTGGTTAGCTCGTATCAGCATAAACCCAGTAAAGCA	201
Db			
Db	41	ArgAlaSerGlnSerIleSerAsnTyrLeuAsnTrpTyrGlnArgLysProGlyLysAla	60
Qy	202	CCTAAGCTCTGCATCTATGCTGCATCCAGTTTGCCAAAGTGGTGTCCCATCAAGTTTCAG	261
Db			
Db	61	ProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgPheSer	80

[illegible]

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US-08-728-463B-220 (1-420) x S40369 (1-129)

QY   13 ATGATGTCTCCAGCTCAGTTCCTCGGTCTCTGCTGCTCTGGTTGCCAGGTTCCAGATGC 72
Db    ||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      2 MetArgValLeuAlaGlnLeuLeuGlyLeuLeuLeuCysPheProGlyAlaAtrgCys 21
QY   73 GACATCCAGATGACCAGTCTCCATCTTCGGTGCTCATCTCTGATCTCTGATGAGACAGAGTCACC 133
Db    ||| |||| | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | |
      22 AspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThr 41
QY   133 ATCACTTTGTCGGCGAGTCAGGATATTAGCAGCTGGTTAGCTGCTGATCAGCATAAACCA 199
Db    ||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      42 IleThrCysArgAlaSerHisValIleSerAsnHisLeuValTrpPheGlnGlnLysPro 61
QY   193 GGTAAGCACCTAAAGCTCCGATCATCTGCTGCTGATCCAGTTGGAAGAGTGGTGTCCCCATCA 255
Db    ||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      62 GlyLysAlaProLysSerLeuLeuTyAlaAlaSerSerLeuGlnSerGlyValProSer 81
QY   253 AGGTTACGGGAAGTAGGATCGGACAGATTTACTCTCACCATCAGCAGCTGCAGCCT 311
Db    ::| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      82 LysPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 100
QY   313 GAAGATTGTCACCTACTATTGTCACACAGCTAATAGTTTCCCGTACACTTTTGGTCAG 373
Db    ||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      102 GluaspHealathrtyrtyrCysGlnGlnTyraasnserityrProtyrThrpheglyGln 129
QY   373 GGAACCAAGCTGGAGATCAAACA 396
Db    ||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      122 GlyThrlysLeuGlulleLysArg 129

RESULT 11
S40349
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
R:Accession: S40349
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40349
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLE>
A:Cross-references: EMBL:X72459; NID:g441386; PIDN:CAA51127.1; PID:g441387
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:33-107/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:          1,27e-41           Length:       125
Score:              564.00             Matches:     109
Percent Similarity: 92.80%             Conservative: 7
Best Local Similarity: 87.20%           Mismatches: 9
Query Match:        74.11%             Indels:      0
DB:                 2                  Gaps:        0

US-08-728-463B-220 (1-420) x S40349 (1-125)

QY   22 CCAGTCAGTCTCGGTCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 81
Db    ||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      1 ProalaGlnLeuLeuGlyLeuLeuLeuTrpLeuProGlyAlaAtrgCysAlaileGln 20
QY   82 ATGACCCAGTCTCCATCTTCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 141
Db    ::| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      21 LeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIlethrCys 40
QY   142 CGGCGAGTCAGGATATTAGCAGCTGGTTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 203
Db    ||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      41 ArgAlaSerGlnGlylleSerSerAlaLeuAlatrpyrGlnGlnLysProGlyLysAla 60
QY   202 CCTAAGTCTCTGATCTATGCTGATCCAGTTGCAAGTGGTGTCCCATCAGGTTCCAG 261

```

A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-131 <KLE>
A:Cross-references: EMBL:X72462; NID:g441392; PIDN:CAA51130.1; PID:g441393
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Pred. No.:	3,08e-42	Length:	131
Score:	571.00	Matches:	110
Percent Similarity:	92.31%	Conservative:	10
Best Local Similarity:	84.62%	Mismatches:	10
Indels:	0	Gaps:	0
DB:	2		

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US-08-728-463B-220 (1-420) x S40352 (1-131)

QY   13 ATGATGTCTCCAGCTCAGTTCCTCGGTCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 72
Db    ||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      1 MetArgValProalaGlnLeuLeuGlyLeuLeuLeuTrpLeuProaspThrLysCys 20
QY   73 GACATCCAGATGACCAGTCTCCATCTTCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 132
Db    ||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      21 AspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAsnArgValThr 40
QY   133 ATCACTTTGTCGGCGAGTCAGGATATTAGCAGCTGGTTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 192
Db    ||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      41 IleThrCysArgAlaSerGlnGlylleSerAsnTyrlauAlatrpyrGlnGlnLysPro 60
QY   193 GGTAAGCACCTAAAGCTCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 252
Db    ||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      61 GlyLysValProLysLeuLeuLeuTyAlaAlaSerThrLeuGlnSerGlyValProSer 80
QY   253 AGGTTACGGGAAGTAGGATCGGACAGATTTACTCTCACCATCAGCAGCTGCAGCCT 312
Db    ::| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      81 ArgPheSerGlySerGlySerGlyThrAspPheSerLeuThrIleSerSerLeuGlnPro 100
QY   313 GAAGATTGTCACCTACTATTGTCACACAGCTAATAGTTTCCCGTACACTTTTGGTCAG 372
Db    ||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      101 GluaspValAlatrtyrtyrCysGlnLysTyraasnserValproargThrphedGln 120
QY   373 GGAACCAAGCTGGAGATCAAACAAGTGTG 402
Db    ||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      121 GlyThrlysValGlulleLysArgThrVal 130

RESULT 10
S40369
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
R:Accession: S40369
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40369
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-129 <KLE>
A:Cross-references: EMBL:X72479; NID:g441426; PIDN:CAA51147.1; PID:g441427
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:          3,77e-42           Length:       129
Score:              570.00             Matches:     112
Percent Similarity: 92.19%             Conservative: 6
Best Local Similarity: 87.50%           Mismatches: 10
Query Match:        74.90%             Indels:      0
DB:                 2                  Gaps:        0

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75 GACATCCAGATGACCCAGTCTCCATCTTCGGTGTCGTCATCTGTAGGAGACAGAGTCACC 132

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 7.96662 Seconds
(without alignments)
4373.264 Million cell updates/sec

Title: US-08-728-463B-220
Perfect score: 761
Sequence: 1 AGCTTGCCACCATGATGTT.....TGCTGCACCATCTGCTTTC 420

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 225784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+n2p.model -DEV=xlp
-Q=/cgn2.1/USPTO.spool/US08728463/runat_03062003_085614_16804/app_query.fasta_1.3690
-DB=SwissProt_40 -OPWT=fastan -SUFFIX=rsp -MINMATCH=0.1 -LOOPCT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08728463 @CGN 1.1 76 @runat_03062003_085614_16804 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	549	72.1	129	1 KV1W HUMAN	P04431 homo sapien
2	531	69.8	117	1 KV1J HUMAN	P01602 homo sapien
3	523	68.7	117	1 KV1I HUMAN	P01601 homo sapien
4	508	66.8	129	1 KV1X HUMAN	P04432 homo sapien
5	484	63.6	108	1 KV1S HUMAN	P01611 homo sapien
6	478	62.1	128	1 KV5E MOUSE	P01637 mus musculus
7	472.5	62.1	107	1 KV1D HUMAN	P01596 homo sapien
8	472	62.0	108	1 KV1H HUMAN	P01600 homo sapien
9	471	61.9	108	1 KV1V HUMAN	P04430 homo sapien
10	470	61.8	108	1 KV1L HUMAN	P01604 homo sapien
11	464	61.0	108	1 KV1F HUMAN	P01598 homo sapien
12	464	61.0	108	1 KV1O HUMAN	P01607 homo sapien
13	463	60.8	108	1 KV1R HUMAN	P01610 homo sapien
14	462	60.7	108	1 KV1G HUMAN	P01599 homo sapien
15	458	60.2	108	1 KV1B HUMAN	P01594 homo sapien
16	457	60.1	108	1 KV1N HUMAN	P01606 homo sapien
17	453.5	59.6	129	1 KV3M HUMAN	P18136 homo sapien
18	452.5	59.5	129	1 KV3L HUMAN	P18135 homo sapien

SUMMARIES

19	451	59.3	108	1 KV1E HUMAN	P01597 homo sapien
20	451	59.3	108	1 KV1M HUMAN	P01605 homo sapien
21	450	59.1	108	1 KV1P HUMAN	P01608 homo sapien
22	445	58.5	108	1 KV1C HUMAN	P01595 homo sapien
23	445	58.5	108	1 KV1Y HUMAN	P03062 homo sapien
24	442.5	58.1	129	1 KV3H HUMAN	P04207 homo sapien
25	442	58.1	108	1 KV1A HUMAN	P01593 homo sapien
26	441	58.0	108	1 KV1K HUMAN	P01603 homo sapien
27	437	57.4	130	1 KV5G MOUSE	P01639 mus musculus
28	435	57.2	128	1 KV3K HUMAN	P06311 homo sapien
29	432	56.8	108	1 KV1Q HUMAN	P01609 homo sapien
30	430	56.5	115	1 KV5F MOUSE	P01638 mus musculus
31	422	55.5	134	1 KV4C HUMAN	P06314 homo sapien
32	414	54.4	115	1 KV3I HUMAN	P04433 homo sapien
33	413.5	54.3	109	1 KV1T HUMAN	P01612 homo sapien
34	410	53.9	108	1 KV5K MOUSE	P01644 mus musculus
35	407	53.5	132	1 KV3F MOUSE	P01658 mus musculus
36	406	53.4	131	1 KV3I MOUSE	P01661 mus musculus
37	405	53.2	108	1 KV5L MOUSE	P01645 mus musculus
38	405	53.2	108	1 KV5O MOUSE	P01648 mus musculus
39	405	53.2	108	1 KV5P MOUSE	P01649 mus musculus
40	404.5	53.2	133	1 KV4B HUMAN	P06313 homo sapien
41	404	53.1	115	1 KV5D MOUSE	P01635 mus musculus
42	402	52.8	108	1 KV5C MOUSE	P01636 mus musculus
43	401.5	52.8	116	1 KV3J HUMAN	P04434 homo sapien
44	400	52.6	108	1 KV5M MOUSE	P01646 mus musculus
45	398.5	52.4	109	1 KV3D HUMAN	P01622 homo sapien

ALIGNMENTS

RESULT 1

ID	KV1W HUMAN	STANDARD;	PRT;	129 AA.
AC	P04431			
DT	13-AUG-1987 (Rel. 05, Created)			
DE	13-AUG-1987 (Rel. 05, Last sequence update)			
DE	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig kappa chain V-I region Walker precursor.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85014148; PubMed=6091049;			
RA	Klobeck H.G., Combrato G., Zachau H.G.;			
RT	"Immunoglobulin genes of the kappa light chain type from two human			
RT	lymphoid cell lines are closely related.";			
RL	Nucleic Acids Res. 12:6995-7006(1984).			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; X00965; CAA25477.1; ALT_TERM.			
DR	PIR; A01883; KIHUWK.			
DR	HSSP; P01607; IREI.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; ig; 1.			
DR	SMART; SM00406; IGV; 1.			
KW	Immunoglobulin V region; Signal.			
FT	SIGNAL 1 22			
FT	CHAIN 23 129			
FT	DOMAIN 23 45			
FT	DOMAIN 45 56			
FT	DOMAIN 57 71			
FT	DOMAIN 72 78			

DR	EMBL; J00245; AAA59087.1; -.
DR	EMBL; Z00001; CAA77292.1; -.
DR	PIR; A01882; KIHU12.
DR	HSSP; P01607; IREI.
DR	New; HGNC:5741; IGKV1-5.
DR	InterPro; IPR003006; IG_MHC.
DR	InterPro; IPR003596; IG_V.
DR	Fram; FR00047; Ig; 1.
DR	SMART; SM00406; IGV; 1.
KW	Immunoglobulin V region; Signal.
FT	SIGNAL 1 22
FT	CHAIN 23 >117
FT	DOMAIN 23 45
FT	DOMAIN 46 56
FT	DOMAIN 57 71
FT	DOMAIN 72 78
FT	DOMAIN 79 110
FT	DOMAIN 111 >117
FT	DISULFID 45 110
FT	NON_TER 117 117
SQ	SEQUENCE 117 AA; 12768 MW; ADLDF3A40AFIA49B CRC64;

Alignment Scores:

Pred. No.:	6.58e-48	Length:	117
Score:	531.00	Matches:	100
Percent Similarity:	94.74%	Conservative:	8
Best Local Similarity:	87.72%	Mismatches:	6
Query Match:	69.78%	Indels:	0
DB:	1	Gaps:	0

US-08-728-463B-220 (1-420) x KV1J_HUMAN (1-117)

QY	13	ATGATGGTCCACAGTCACCTCCTCGGTCTCTCTGCTGCTCTGGTTCCAGGTTCCAGATGC	72
Db	3	MetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuProGlyAlaLysCys	22
QY	73	GACATCCAGATGACCAGTCCTCCATCTTCCGCTGTCTCATCTGTAGGAGACAGAGTCACC	132
Db	23	AspIleGlnMetThrGlnSerProSerThrLeuSerAlaSerValGlyAspArgValThr	42
QY	133	ATCACTTCTCGGCGAGTCAGATATTAGCAGCTGGTAGCTGGATTCAGCATAAACCA	192
Db	43	IleThrCysArgAlaSerGlnSerIleSerSerTrpLeuAlaTrpTrpGlnGlnLysPro	62
QY	193	GGTAAGCACCTAAAGCTCCTCATCTATGCTGCATCCAGTTTGCAAAGTGGTGTCCCATCA	252
Db	63	GlyLysAlaProLysLeuLeuIleTyAspAlaSerSerLeuGluSerGlyValProSer	82
QY	253	AGGTTACCGGAAGTGATCTGGAGACAGATTACTCTCAACATCAGCAGCCTGCACGCT	312
Db	83	ArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeuGlnPro	102
QY	313	GAAGATTTTGCAACTTACTATTGTCAACAGCGCTAATAGTTTC	354
Db	103	AspAspPheAlaThrTyThrCysGlnGlnTyAsnSerTyr	116

RESULT 3.

ID	KV1J_HUMAN	STANDARD;	PRT;	117 AA.
DT	21-JUL-1986	(Rel. 01, Created)		
DT	21-JUL-1986	(Rel. 01, Last sequence update)		
DT	15-JUL-1999	(Rel. 38, Last annotation update)		
DE	Ig kappa chain V-I region HK101 precursor (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TaxID=9606;				
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81098966; PubMed=6779204;			
RT	Bentley D.L., Rabbitts T.H.;			
RT	"Human immunoglobulin variable region genes -- DNA sequences of two V			

US-08-728-463B-220 (1-420) x KVID_HUMAN (1-107)

QY	73	GACATCCAGATGACCCAGCTCTCCATCTTCGCTGTCTGATCTGTAGGAGACAGAGTCACC	132
Db	1	AspIleGlnMeThrGlnSerProSerThrLeuSerAlaSerValGlyAspGValAla	20
QY	133	ATCACTTGTTCGGCGGAGTCAGGATATAGCAGCTGGTGTAGCTCGTATCAGCATAAACCA	192
Db	21	IleThrCysArgAlaSerGlnAsnIleSerSerTrpLeuAlaTPTyrGlnGlnIysPro	40
QY	193	GGTAAGACACCTAAGCTCTGATCTATCTGCTGCATCCAGCTTTGCAAGATGGTGTCCCATCA	252
Db	41	GlyLysAlaProLysValLeuIleTyrLysSerSerLeuGluSerGlyValProSer	60
QY	253	AGGTTTCAGCGGAAGTGGATCTGGGACAGATTTCACTCTCACCATCACGACCTGCACGCTT	312
Db	61	ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu***pro	80
QY	313	GAAGATTTTGCACACTTACTATTGTCAACAGAGCTAATAGTTTCCGCTACACTTTTGGTCAG	372
Db	81	*****PheAlaThrTyr-Tyr-CysGlnGlnTyrAsnThrPhe---PheThrPheGlyPro	99
QY	373	GGAACACAGCTGGAGATCAAAACGA	396
Db	100	GlyThrLysValAspIleLysArg	107

RESULT 8

KVID_HUMAN

ID	KVID_HUMAN	STANDARD;	PRT;	108 AA.
AC	P01600;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig kappa chain V-I region Hau.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI	TaxID=9606;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=71032830; PubMed=4097974;			
RA	Watanabe S., Hilschmann N.;			
RT	"The primary structure of a monoclonal kappa-type immunoglobulin L-			
RT	chain of subgroup I (Bence-Jones Protein Hau): subdivision within			
RT	subgroups."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295 (1970).			
CC	-I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.			
CC	-I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.			
DR	PIR; A01868; K1HUHU.			
DR	HSSP; P80362; 1WTU.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF00047; Ig; 1.			
DR	SMART; SM00406; IGV; 1.			
KW	Immunoglobulin V region; Bence-Jones protein.			
FT	DOMAIN 1 23			
FT	DOMAIN 24 34			
FT	DOMAIN 35 49			
FT	DOMAIN 50 56			
FT	DOMAIN 57 88			
FT	DOMAIN 89 97			
FT	DOMAIN 98 107			
FT	DISULFID 23 88			
FT	NON_TER 108 108			
SQ	SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;			

Alignment Scores:

Pred. No.:	1,02e-41	Length:	108
Score:	472.00	Matches:	92
Percent Similarity:	92.59%	Conservative:	8
Best Local Similarity:	85.19%	Mismatches:	8
Query Match:	62.02%	Indels:	0

QY 73 GACATCCAGATGACCCAGTCTCCATCTTCGGTCTGTCATCTGTAGGAGACAGAGTCACC 132
 DB 1 AspileGlnMetThrGlnSerProSerThrGlnProAlaSerValGlyAspArgValThr 20
 QY 133 ATCACTTGTCCGGCGAGTCCAGATATTAGCAGCTGGTTAGCCCTGGTATCAGCATAAACCA 192
 DB 21 IleThrCysArgAlaSerGlnSerIleAsnIleThrLeuAlaThrPyrGlnGlnLysPro 40
 QY 193 GGTAAAGCACCTAAGCTCTGATCTATGTCGATCCAGTTTGCAAGTGGTGTCCCATCA 252
 DB 41 GluLysAlaProLysLeuLeuIleThrLysAlaSerThrLeuGluThrGlyValProSer 60
 QY 253 AGCTTCAGCGAGTGGATCGGACAGATTTCACTCTCACCATCAGCAGCCCTGCAGCCT 312
 DB 61 ArgPheSerGlySerGlyThrGluPheThrLeuThrIleAsnSerLeuGlnPro 80
 QY 313 GAAGATTTTGCACCTTACTATTCTCAACAGGCTTAATGTTTCCCGTACACTTTTGTGTGAG 372
 DB 81 AspAspPheAlaThrTyThrCysGlnGlnTyThrSerArgTyThrPheGlyGln 100
 QY 373 GGAACCAAGCTGGAGATCAACGA 396
 DB 101 GlyThrLysLeuAspileLysArg 108

RESULT 11

KVIF_HUMAN
 ID KVIF_HUMAN STANDARD; PRT; 108 AA.
 AC P01598;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region EU.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=71064023; PubMed=5489770;
 RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
 RT acid sequence of the light chain."
 RL Biochemistry 9:3155-3161(1970).
 RN [2]
 RP DISULFIDE BOND.
 RX MEDLINE=71064027; PubMed=4923144;
 RA Gall W.E., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. X.
 RT Intrachain disulfide bonds."
 RL Biochemistry 9:3188-3196(1970).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PUR; A01866; KIHUEU.
 DR HSP; P01607; IREI.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D8823 CRC64;

Alignment Scores:

Pred. No.: 7.05e-41 Length: 108

Score: 464.00 Matches: 88
 Percent Similarity: 91.59% Conservative: 10
 Best Local Similarity: 82.24% Mismatches: 9
 Query Match: 60.97% Indels: 0
 DB: 1 Gaps: 0
 US-08-728-463B-220 (1-420) x KVIF_HUMAN (1-108)
 QY 73 GACATCCAGATCACCAGTCTCCATCTTCGGTCTGTCATCTGTAGGAGACAGAGTCACC 132
 DB 1 AspileGlnMetThrGlnSerProSerThrLeuSerAlaSerValGlyAspArgValThr 20
 QY 133 ATCACTTGTCCGGCGAGTCCAGATATTAGCAGCTGGTTAGCCCTGGTATCAGCATAAACCA 192
 DB 21 IleThrCysArgAlaSerGlnSerIleAsnIleThrLeuAlaThrPyrGlnGlnLysPro 40
 QY 193 GGTAAAGCACCTAAGCTCTGATCTATGTCGATCCAGTTTGCAAGTGGTGTCCCATCA 252
 DB 41 GlyLysAlaProLysLeuLeuMetTyThrLysAlaSerSerLeuGluSerGlyValProSer 60
 QY 253 AGCTTCAGCGAGTGGATCTGGACAGATTTCACTCTCACCATCAGCAGCCCTGCAGCCT 312
 DB 61 ArgPheIleGlySerGlyThrGluPheThrLeuThrIleSerSerLeuGlnPro 80
 QY 313 GAAGATTTTGCACCTTACTATTCTCAACAGGCTTAATGTTTCCCGTACACTTTTGTGTGAG 372
 DB 81 AspAspPheAlaThrTyThrCysGlnGlnTyThrAsnSerAspSerLysMetPheGlyGln 100
 QY 373 GGAACCAAGCTGGAGATCAACGA 393
 DB 101 GlyThrLysValGluValLys 107
 RESULT 12
 KV10_HUMAN
 ID KV10_HUMAN STANDARD; PRT; 108 AA.
 AC P01607;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Rei.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76023758; PubMed=809329;
 RA Palm W., Hilschmann N.;
 RT "The primary structure of a crystalline monoclonal immunoglobulin
 RT kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
 RT and characterization of the tryptic peptides; the complete amino acid
 RT sequence of the protein; a contribution to the elucidation of the
 RT three-dimensional structure of antibodies, in particular their
 RT combining site."
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=76039968; PubMed=1182131;
 RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
 RT "The molecular structure of a dimer composed of the variable portions
 RT of the Bence-Jones protein Rei refined at 2.0-A resolution."
 RL Biochemistry 14:4943-4952(1975).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
 CC MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR FIR; A01873; KIHURE.
 DR PDB; IREI; 17-FEB-84.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 FT DOMAIN 1 23
 FT FRAMEWORK-1.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=75059122; PubMed=4215718;
 RA Laure C.J., Watanabe S., Hilschmann N.;
 RT "The primary structure of a monoclonal IgM-immunoglobulin
 (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
 RT kappa-type, subgroup I.";
 RL Hoppe-Sevler's Z. Physiol. Chem. 354:1503-1504 (1973).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 CC MACROGLOBULIN.
 DR PIR; A01867; KIHUGL.
 DR HSP; P01607; IREI.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin v region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; CIAD3CB0F600FF73 CRC64;
 Alignment Scores:
 Pred. No.: 1,14e-40 Length: 108
 Score: 462.00 Matches: 90
 Percent Similarity: 90.74% Conservative: 8
 Best Local Similarity: 83.33% Mismatches: 10
 Query Match: 60.71% Indels: 0
 DB: 1 Gaps: 0
 US-08-728-463b-220 (1-420) x KV1G_HUMAN (1-108)
 QY 73 GACATCCAGATGACCCAGTCTCCATCTCCGTCTGTCATCTGTAGGAGACAGATCACC 132
 Db 1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
 QY 133 ATCACTTGTCGGCGAGTCAGGATATTAGCAGCTGGTGTAGCCTGGTATCAGCATAAACCA 192
 Db 21 IleIleCysArgAlaSerGlnGlyIleArgAsnAspLeuThrTrpTyrGlnGlnLysPro 40
 QY 193 GGTAAAGACCACTTAAGCTCTGATCTATGCTGTCATCCAGTTTGCATAAGTGGTGCCCATCA 252
 Db 41 GlyLysAlaProLysGluLeuLeuIleTyrAlaAlaSerAsnLeuGlnSerGlyValProSer 60
 QY 253 AGGTTCCAGCGAAGTGGATCTGGACAGATTTCACTCTACCATCAGACGCTGCAGCCT 312
 Db 61 ArgPheSerGlySerGlyAlaGlyThrGluPheThrLeuThrIleSerLeuGlnPro 80
 QY 313 GRAGATTTTGCACTTACTTCTCAACAGGCTTAATAGTTTCCGTCACACTTTTGTCTCAG 372
 Db 81 GluAspPheAlaThrTyrTyrCysLeuGlnGlnAsnSerTyrProArgSerPheGlyGln 100
 QY 373 GGAACCAAGCTGGAGATCAACCA 396
 Db 101 GlyThrLysValGluLeuLysArg 108
 RESULT 15
 KV1B_HUMAN
 ID KV1B_HUMAN STANDARD; PRT; 108 AA.
 AC P01594;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region AU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72189444; PubMed=5028201;
 RA Schlecht H., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
 RT protein Au).";
 RL Hoppe-Sevler's Z. Physiol. Chem. 353:345-370 (1972).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=77022433; PubMed=1234024;
 RA Fehlgammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
 RA Schwager P., Steigemann W., Schramm H.J.;
 RT "The structure determination of the variable portion of the
 RT Bence-Jones protein Au.";
 RL Biophys. Struct. Mech. 1:139-146 (1975).
 CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
 CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
 CC REGION OF THE KAPPA CHAIN REI.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 DR PIR; A01862; KIHUAU.
 DR HSP; P01607; IREI.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin v region; Bence-Jones protein.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11939 MW; E8011187B56F6B9 CRC64;
 Alignment Scores:
 Pred. No.: 3,01e-40 Length: 108
 Score: 458.00 Matches: 88
 Percent Similarity: 88.89% Conservative: 8
 Best Local Similarity: 81.48% Mismatches: 12
 Query Match: 60.18% Indels: 0
 DB: 1 Gaps: 0
 US-08-728-463b-220 (1-420) x KV1B_HUMAN (1-108)
 QY 73 GACATCCAGATGACCCAGTCTCCATCTCCGTCTGTCATCTGTAGGAGACAGATCACC 132
 Db 1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
 QY 133 ATCACTTGTCGGCGAGTCAGGATATTAGCAGCTGGTGTAGCCTGGTATCAGCATAAACCA 192
 Db 21 IleThrCysGlnAlaSerGlnAspIleSerAspTyrLeuAsnTrpTyrGlnGlnLysPro 40
 QY 193 GGTAAAGACCACTTAAGCTCTGATCTATGCTGTCATCCAGTTTGCATAAGTGGTGCCCATCA 252
 Db 41 GlyLysAlaProLysLeuLeuLeuIleTyrAspAlaSerAsnLeuGlnSerGlyValProSer 60
 QY 253 AGGTTCCAGCGAAGTGGATCTGGGACAGATTTCACTCTCACCATCAGACGCTGCAGCCT 312
 Db 61 ArgPheSerGlyGlySerGlyAlaHisPheThrPheThrIleSerSerLeuGlnPro 80
 QY 313 GAAGATTTTGCACTTACTTATTGTGTCACAGGCTAATAGTTTCCCGTACACTTTTGTCTCAG 372
 DB: 11939 MW; E8011187B56F6B9 CRC64;

Db . 81 GluAspIleAlaThrTyrTyrCysGlnGlnTyrAspTyrLeuProTyrThrPheGlyGln 100
QY 373 GGAACCAAGCTGGAGATCAACGA 396
Db 101 GlyThrLysValGluIleLysArg 108

Search completed: June 3, 2003, 09:04:11
Job time : 9.96662 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 37.2838 Seconds
(without alignments)
4642.224 Million cell updates/sec

Title: US-08-728-463B-220
Perfect score: 761
Sequence: 1 AAGCTTGCCACCATGATGTT.....TGGCTGCACCATCTGCTTC 420

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1343160

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-Q=/cgn2_1/USPTO.spool/US08728463/runat_03062003_085614_16815/app_query.fasta_1.3690
-DB=SPTREMBL_21 -QFMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US08728463 @CGN_1.1_380 @runat_03062003_085614_16815 -NCPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

SPTREMBL_21:.*
1: sp_archaea:.*
2: sp_bacteria:.*
3: sp_fungi:.*
4: sp_human:.*
5: sp_invertebrate:.*
6: sp_mammal:.*
7: sp_mhc:.*
8: sp_organelle:.*
9: sp_phase:.*
10: sp_plant:.*
11: sp_rodent:.*
12: sp_virus:.*
13: sp_vertebrate:.*
14: sp_unclassified:.*
15: sp_rvirus:.*
16: sp_bacteriap:.*
17: sp_archaeap:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	492	64.7	234	11	Q8R062

	2	486	63.9	108	4	Q9UL77	Q9UL77 homo sapien
	3	485	63.7	234	11	Q9LWF8	Q9LWF8 mus musculus
	4	484	63.6	234	11	Q8VCP0	Q8VCP0 mus musculus
	5	478	62.8	108	4	Q9UL70	Q9UL70 homo sapien
	6	475.5	62.5	107	4	Q96SA9	Q96SA9 homo sapien
	7	461	60.6	108	4	Q9UL79	Q9UL79 homo sapien
	8	457	60.1	116	4	Q96PF6	Q96PF6 homo sapien
	9	453	59.5	233	11	Q9LWS9	Q9LWS9 mus musculus
	10	450.5	59.2	107	4	Q9UL81	Q9UL81 homo sapien
	11	439	57.7	127	11	Q925S9	Q925S9 mus musculus
	12	426.5	56.0	239	4	Q8TCD0	Q8TCD0 homo sapien
	13	424	55.7	214	11	Q9RIA5	Q9RIA5 mus musculus
	14	403	53.0	298	11	Q9QYF0	Q9QYF0 mus musculus
	15	400	52.6	238	11	Q9NM37	Q9NM37 mus musculus
	16	399	52.4	108	4	Q9UL83	Q9UL83 homo sapien
	17	398	52.3	109	11	Q920E6	Q920E6 mus musculus
	18	395	51.9	108	11	Q8VIJ0	Q8VIJ0 mus musculus
	19	387.5	50.9	109	4	Q9UL78	Q9UL78 homo sapien
	20	384.5	50.5	109	4	Q9UL85	Q9UL85 homo sapien
	21	384	50.5	238	11	Q8VC16	Q8VC16 mus musculus
	22	383	50.3	107	11	Q9JL84	Q9JL84 mus musculus
	23	377	49.5	111	11	Q920E9	Q920E9 mus musculus
	24	372.5	48.9	239	11	Q8VC55	Q8VC55 mus musculus
	25	370.5	48.7	134	11	Q8VDD0	Q8VDD0 mus musculus
	26	369.5	48.6	109	4	Q9UL86	Q9UL86 homo sapien
	27	362.5	47.6	241	11	Q921A6	Q921A6 mus musculus
	28	362	47.6	234	11	Q8R028	Q8R028 mus musculus
	29	347	45.6	107	11	Q9ERZ9	Q9ERZ9 mus musculus
	30	342.5	45.0	106	5	Q9U410	Q9U410 schistosoma
	31	342.5	45.0	235	11	Q9LW12	Q9LW12 mus musculus
	32	337	44.3	99	11	Q9UL74	Q9UL74 mus musculus
	33	334	43.9	101	11	Q9JL78	Q9JL78 mus musculus
	34	327	43.0	103	11	Q9JL80	Q9JL80 mus musculus
	35	318	41.8	97	11	Q9JL76	Q9JL76 mus musculus
	36	309	40.6	114	4	Q9UL80	Q9UL80 homo sapien
	37	305.5	40.1	104	11	Q9JL82	Q9JL82 mus musculus
	38	294	38.6	109	6	Q9N0W5	Q9N0W5 oryctolagus
	39	271	35.6	233	4	Q8TBC9	Q8TBC9 homo sapien
	40	265.5	34.9	130	4	Q9NP29	Q9NP29 homo sapien
	41	259	34.0	237	4	Q8WTU6	Q8WTU6 homo sapien
	42	255	33.5	237	4	Q8WUK4	Q8WUK4 homo sapien
	43	231	30.4	107	4	Q9UL82	Q9UL82 homo sapien
	44	230.5	30.3	107	4	Q9NSD6	Q9NSD6 homo sapien
	45	225	29.6	218	11	Q925S1	Q925S1 mus musculus

ALIGNMENTS

RESULT 1

ID	Q8R062	PRELIMINARY;	PRT;	234	AA.
AC	Q8R062;				
DT	01-JUN-2002 (TrEMBLrel. 21, Created)				
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)				
DE	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)				
DE	Hypothetical 25.9 kDa protein.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_TaxID=10090;					
NCBI	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=COLON;				
RA	Strausberg R.;				
RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC027418; AAH27418.1; -				
KW	Hypothetical protein.				
SQ	SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;				

Alignment Scores:

Pred. No.:	7.64e-47	Length:	234
Score:	492.00	Matches:	97
Percent Similarity:	82.22%	Conservative:	14

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US-08-728-463B-220 (1-420) x Q9UL77 (1-108)

QY 73 GACATCCAGATGACCCAGCTCCATCTTCGGTCTCTGCATCTCTAGGAGCAGAGTCACC 132
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 133 ATCACTTGTTCGGCGGAGTCAGGATATTAGCAGCTGGTTAGCCCTGGTATCAGCATAAACCA 192
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 21 IleThrCysArgAlaSerGlnSerIleSerSerTyrlleuAsnTrpTyrlGlnLysPro 40
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 193 GCTAAGACGACCTTAGCTCTCATCTATGCTGCATCCAGTTTGCAAAAGTGGTGTCCCATCA 252
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 41 GlyLysAlaProAsnLeuLeuIleTyrlAlaAlaSerSerLeuGlnSerGlyValProSer 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 253 AGGTTTCAGCGGAAGTGGATCTGGGACAGATTTCACTCTCAACATCAGCAGCCTGCAGCCT 312
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 313 GAAGATTTTGCNACTTACTATTGTCAACAGGCTAATAGTTTCCGCTACACTTTTGTGTGAC 372
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 81 GluAspPheAlaThrTyrlTyrlCysGlnGlnSerTyrlSerThrSerTrpThrPheGlyGlu 100
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 373 GGAACCAAGCTCGAGATCAAAACGA 396
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 101 GlyThrLysValGluIleLysArg 108
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 3
Q91WF8 PRELIMINARY; PRT; 234 AA.
ID Q91WF8
AC Q91WF8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

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DE	Hypothetical 25.9 kDa protein.
DS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX	NCBI_TaxID=10090;
[1]	
RN	SEQUENCE FROM N.A.
RP	
RC	TISSUE=COLON;
RA	Straussberg R.;
RL	Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; BC015292; AAH15292.1; -.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR001865; Ribosomal_S2.
DR	Pfam; PF00047; ig; 2.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR	PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
KW	Hypothetical protein.
SQ	SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;

Alignment Scores:	
Pred. No.:	4.72e-46
Score:	485.00
Percent Similarity:	82.22%
Best Local Similarity:	70.37%
Query Match:	63.73%
DB:	11
	Gaps:
	Length: 234
	Matches: 95
	Conservative: 16
	Mismatches: 24
	Indels: 0
	Gaps: 0

US-08-728-463B-220 (1-420) x Q91WF8 (1-234)

QY	13	ATGATGGTCCAGCTTCAGCTCCTCGGTCTCTCGTCTCTGCCAGTTCCAGATGC	72

[illegible]

DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035035; AAD56271.1; -
DR HSP; P01607; IREI.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Alignment Scores:
Pred. No.: 2,156-43 Length: 108
Score: 461.00 Matches: 91
Percent Similarity: 89.81% Conservative: 6
Best Local Similarity: 84.26% Mismatches: 11
Query Match: 60.58% Indels: 0
DB: 4 Gaps: 0

US-08-728-463B-220 (1-420) x Q9JUL79 (1-108)

Qy 73 GACATCCAGATGACCCAGCTCTCCATCTTCGGTCTGCACTCTGTAGGACACAGAGT
Db 1 AspIleValMetThrGlnSerProSerLeuLeuSerAlaSerThrGlyAspArgVa
Qy 133 ATCACTCTGCGGGCAGTCAGGATATTAGCAGCTGGTGTAGCTCGGTATCAGCATTA
Db 21 IleSerCysArgMetSerGlnGlyIleSerSerTyLeuAlaTrpTyGlnGlnLy
Qy 193 GGTAAAGCACCTAAGCTCTGATCTATGCTGCATCCAGTTGCAAAAGTGGTGTCCC
Db 41 GlyLysAlaProGluLeuLeuIleTyAlaAlaSerThrLeuGlnSerGlyValPr
Qy 253 AGGTTTCACGGAACTGATCTGGACAGATTTCCTCACCATCAGCAGCGCTGCA
Db 61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerCysLeuG
Qy 313 GAAGAATTTTGCACTACTATTGTCACAGCGCTAATAGTTTCCCGCTACACATTTTGG
Db 81 GluaspPheAlaThrTyTyTyCysGlnGlnTyTySerPheProThrPheGln
Qy 373 GSAACCAAGCTGGAGATCAACCA 396
Db 101 GlyThrLysValGluIleLysArg 108

RESULT 8
Q96PF6 PRELIMINARY; PRT; 116 AA.
ID Q96PF6
AC Q96PF6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Kappa 1 light chain variable region (Fragment).
GN SDNK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.


```

RX MEDLINE-21361171; PubMed=11468171;
RA Comenzó R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RT "The tropism of organ involvement in primary systemic amyloidosis:
RT contributions of Ig V(L) germ line gene use and clonal plasma cell
RT burden.";
RL Blood 98:714-720(2001).
DR EMBL; AF361758; AAK51465.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 1 1
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;

Alignment Scores:
Pred. No.: 6.18e-43 Length: 116
Score: 457.00 Matches: 87
Percent Similarity: 86.21% Conservatve: 13
Best Local Similarity: 75.00% Mismatches: 16
Query Match: 60.05% Indels: 0
DB: 4 Gaps: 0

US-08-728-463B-220 (1-420) x Q96PF6 (1-116)
QY 73 GACATCCAGATGACCCAGTCTCCATCTCCGTCTCTGTCATCTGTAGGACAGAGTCACC 132
Db 1 AspilleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
QY 133 ATCACTTGTGGCGAGTCCAGGATATTAGCATTAGCAGTGTAGCTGGTATCAGCATAAACA 192
Db 21 PheileCysGlnAlaSerGlnAspIleAlaAenHisLeuAsnTrpYrGlnIlyslsPro 40
QY 193 GGTAAAGCACTTAAGTCTCTGATCTAGTGTGATGTCAGTTCAGTTCAGTTCAGTTCAGTTC 252
Db 41 GlyGluAlaProIlyslsPheLeuIlyleTyAspGlySerPheLeuIlyslsThrGlyValPro 60
QY 253 AGTTCAGCGGAGTGGATCTGGAGCAGATTCACATCTCCATCAGCAGCCTGAGCCT 312
Db 61 ArgPheSerGlyGlyGlySerAlaThrAsnPhenThrValThrIleSerSerLeuGlnPro 80
QY 313 GAAGATTTTGCACCTTACTATTGTCACAGGCTAATGTTCCCGTACACTTTTGGTCAG 372
Db 81 GluAspPheAlaThrTyTyCysGlnGlnTyHisLeuProPhenThrPheGlyPro 100
QY 373 GGAAACAGCTGGAGATCAACAGCACTGTGGTGGCACCATCTGCTCTTC 420
Db 101 GlyThrLysValAspPheLysArgThrValAlaAlaProSerValPhe 116

RESULT 9
Q91WS9 PRELIMINARY; PRT; 233 AA.
AC Q91WS9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 25.8 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013496; AAH13496.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
FT NON_TER 1 1
FT NON_TER 116 116
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Alignment Scores:
Pred. No.: 3.31e-42 Length: 107
Score: 450.50 Matches: 90
Percent Similarity: 89.81% Conservatve: 7
Best Local Similarity: 83.33% Mismatches: 10

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Pred. No.: 1.95e-42 Length: 233
Score: 453.00 Matches: 89
Percent Similarity: 81.60% Conservatve: 13
Best Local Similarity: 71.20% Mismatches: 23
Query Match: 59.53% Indels: 0
DB: 11 Gaps: 0

US-08-728-463B-220 (1-420) x Q91WS9 (1-233)
QY 43 CTGCTGCTCTGTTCCAGATGTCAGATCCAGATGACCCAGTCTCCATCTTCC 102
Db 10 LeuLeuLeuCysPheGlnGlySerArgCysAspIleGlnMetThrGlnThrThrSerSer 29
QY 103 GTGCTGCTGTTAGGACAGAGTCCATCATCTTGTGGCGGAGTCCAGATATTATG 162
Db 30 LeuSerAlaSerLeuGlyAspArgValThrIleSerCysSerGlySerGlnGlyIleAla 49
QY 163 AGCTGTTAGCTGTATCAGCATTAACCCAGGTAAAGCACCTAAAGCTCTGATCTATGCT 222
Db 50 AsnTyrLeuAsnTrpYrGlnGlnIlyslsProAspGlyThrValIlyslsLeuIlyleTy 69
QY 223 GCATCCAGTTTCAAAAGTGGTCTCCATCAAGTTTCAGCGGAAGTGGATCTGGACAGAT 282
Db 70 ThrSerSerLeuHisSerGlyValProSerArgPheSerGlySerGlyThrAsp 89
QY 283 TTCATCTCACCATCAGCAGCTGAGCTGAGGCTGAAGATTTTGCACCTTACTATTGTCACAG 342
Db 90 TyrSerLeuThrIleSerAsnLeuGluProGluAspIleAlaThrTyTyCysGlnGln 109
QY 343 GCTAATAGTTTCCCTACACTTTTGGTCAGGGAACCAAGCTGAGATCAACCAAGTCTG 402
Db 110 TyrArgTyrLeuProTrpThrPheGlyGlyThrLysLeuGluIlyslsArgAlaAsp 129
QY 403 GCTGACCATCTGTC 417
Db 130 AlaAlaProThrVal 134

RESULT 10
Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; RAD56269.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
FT NON_TER 1 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Alignment Scores:
Pred. No.: 3.31e-42 Length: 107
Score: 450.50 Matches: 90
Percent Similarity: 89.81% Conservatve: 7
Best Local Similarity: 83.33% Mismatches: 10

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Query Match: 59.20% Indels: 1
DB: 4 Gaps: 1
US-08-728-463B-220 (1-420) x Q9UL81 (1-107)

QY 73 GACATCCAGATGACCCAGTCTCCATCTTCGCGTCTGCATCTGTAGGACAGAGTCACC 132
DB 1 AspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThr 20
QY 133 ATCACTTGTCCGGCGAGTCAGATATTAGCAGCTGGTGTAGCTGTATCAGCATAAACCA 192
DB 21 IleThrCysArgAlaSerGlnSerIleSerAsnTyrLeuAsnTyrGlnGlnLysPro 40
QY 193 GGTAAAGCACCTTAAGCTCTGATCTATGTCATCCAGTTCGAAAGTGGTGTCCCATCA 252
DB 61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerGlyLeuGlnAla 80
QY 313 GAAGATTTTGCACCTTACTATTGTCAACAGGCTAATAGTTCCCGTACACTTTTGGTCAG 372
DB 81 GluAspPheAlaThrTyrCysGlnGlnSerTyrSer---AlaLeuThrPheGlyPro 99
QY 373 GGAACCAAGCTGGAGATCAACGA 396
DB 100 GlyThrLysValAspIleArgArg 107

RESULT 11
ID Q925S9 PRELIMINARY; PRT; 127 AA.
AC Q925S9;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Immunoglobulin light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA MEDLINE=93308687; PubMed=10380019;
RA Tripathi P.K., Qin H., Bhattacharya-Chatterjee M., Ceriani R.L.,
RA Foon K.A., Chatterjee S.K.;
RT "Construction and characterization of a chimeric fusion protein
RT consisting of an anti-idiotypic antibody mimicking a breast cancer-
RL Hybridoma 18.193-202(1999).
DR EMBL; AF124721; AA55120.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
FT NON TER 127 127
SQ SEQUENCE 127 AA; 13794 MW; 13F61BEBB981FA5 CRC64;

Alignment Scores:
Pred. No.: 6,77e-41 Length: 127
Score: 439.00 Matches: 88
Percent Similarity: 77.95% Conservative: 11
Best Local Similarity: 69.29% Mismatches: 28
Query Match: 57.69% Indels: 0
DB: 11 Gaps: 0

US-08-728-463B-220 (1-420) x Q925S9 (1-127)
QY 13 ATGATGTCCAGCTCAGCTCTCGGTCTCCTGCTGCTGTGTTCCAGTTCAGATGC 72
DB 1 MetArgAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCys 20
QY 73 GACATCCAGATGACCCAGTCTCCATCTTCGCTGTGCATCTGTAGGACAGAGTCACC 132
DB 21 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 40
QY 133 ATCACTTGTCCGGCGAGTCAG-----GATATTAGCAGCTGGTTCAGCTGG 177
DB 41 IleSerCysArgSerThrGlnSerLeuValTyrSerAspGlyAsnThrTyrLeuAsnTrp 60
QY 178 TATCAGCATAAACAGGTAAGCACCTTAAGCTCTGATCTATGCTGCATCCAGTTTCGAA 237
DB 61 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLysValSerAsnArgAsp 80
QY 238 AGTGGTGTCCCATCAAGGTTTCAGCGGAAGTGGATCTCGGACAGAGATTTCACTCTCCACATC 297
DB 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 100

RESULT 12
ID Q8TCD0 PRELIMINARY; PRT; 239 AA.
AC Q8TCD0;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical 26.2 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022362; AAH22362.1; -.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; FAGEDC3A3B03871D CRC64;

Alignment Scores:
Pred. No.: 1.93e-39 Length: 239
Score: 426.50 Matches: 81
Percent Similarity: 74.47% Conservative: 24
Best Local Similarity: 57.45% Mismatches: 31
Query Match: 56.04% Indels: 5
DB: 4 Gaps: 1

US-08-728-463B-220 (1-420) x Q8TCD0 (1-239)
QY 13 ATGATGTCCAGCTCAGCTCTCGGTCTCCTGCTGTGTTCCAGTTCAGATGC 72
DB 1 MetArgLeuProAlaGlnLeuLeuGlyLeuLeuMetLeuTrpValProGlySerSerGly 20
QY 73 GACATCCAGATGACCCAGTCTCCATCTTCGCTGTGCATCTGTAGGACAGAGTCACC 132
DB 21 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 40
QY 133 ATCACTTGTCCGGCGAGTCAG-----GATATTAGCAGCTGGTTCAGCTGG 177
DB 41 IleSerCysArgSerThrGlnSerLeuValTyrSerAspGlyAsnThrTyrLeuAsnTrp 60
QY 178 TATCAGCATAAACAGGTAAGCACCTTAAGCTCTGATCTATGCTGCATCCAGTTTCGAA 237
DB 61 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLysValSerAsnArgAsp 80
QY 238 AGTGGTGTCCCATCAAGGTTTCAGCGGAAGTGGATCTCGGACAGAGATTTCACTCTCCACATC 297
DB 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 100

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QY 298 AGCAGCTGCAGCTGAAGATTGTCACCTACTATGTCACAGGCTAATAGTTCCCG 357
Db : : : : :
101 ThrArgValGlnIleGlnValGlyValTyrPheCysMetClnGlnIleThrHisTyrPro 120
QY 358 TACACTTTGTGACGAGGACCAAGCTGAGATCAACAGCACTGTGCTGACCATCTGTC 417
Db : : : : :
121 SerThrPheGlnGlnIleGlnIleValSerGlnIleValSerGlnIleValSerGlnIleVal 140
QY 418 TTC 420
Db 141 Phe 141

RESULT 13

Q9RIAS

ID Q9RIAS PRELIMINARY; PRT; 214 AA.

AC Q9RIAS; 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Kappa light chain of Mab7 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN (1)
RP SEQUENCE FROM N.A.
RA Wille K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv)."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152371; AAD40242.1; -
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003600; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_1like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1 214
FT NON_TER 1 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Alignment Scores:

Pred. No.: 3,63e-39 Length: 214
Score: 424.00 Matches: 80
Percent Similarity: 84.35% Conservative: 17
Best Local Similarity: 69.57% Mismatches: 18
Query Match: 55.72% Indels: 0
DB: 11 Gaps: 0

US-08-728-463b-220 (1-420) x Q9RIAS (1-214)

QY 73 GACATCCAGATGACCCAGTCTTCATCTTCGTCGTCATCTGAGAGACAGATCACC 132
Db : : : : :
1 AsplIleGlnLeuThrGlnSerProSerSerMetCylAlaSerLeuGlnIleValThr 20
QY 133 ATCACTGTGGGGGAGATCAGATATTAAGAGCTGTTAGCTGTATACAGATAACCA 192
Db : : : : :
21 IleThrCysValAlaSerGlnAspIleAsnSerTyrLeuSerTyrPheGlnGlnIleValThr 40
QY 193 GGTAAAGACCTAAGCTCTGATCTATGTCATCAAGTTGCAAGTGTGTCCCATCA 252
Db : : : : :
41 GlyLysSerProLysThrIleLeuTyrGlnAlaAsnArgLeuValAspGlyValProSer 60
QY 253 AGTTTCAGCGGAGATGATGAGACAGATTTCATCTCAGATCAGAGCTGAGAGCT 312
Db : : : : :
61 ArgPheSerTyrSerGlySerGlyGlnAspTyrSerLeuThrIleSerSerLeuGlnIleVal 80
QY 313 GAAGATTTTGCACTACTATGTCACAGGCTAATAGTTCCGTCACCTTTGGTCAG 372
Db : : : : :
81 GluAspMetCylIleTyrTyrCysLeuGlnIleValSerGlnIleValProPheThrPheGlySer 100

QY 373 GAACCAAGCTGAGATCAACAGCACTGTGCTGACCATCTGTC 417
Db : : : : :
101 GlyThrLysLeuGlnIleValSerGlnIleValSerGlnIleValSerGlnIleVal 115

RESULT 14

Q9QYF0

ID Q9QYF0 PRELIMINARY; PRT; 298 AA.

AC Q9QYF0; 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CN 8 scFv.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=SPLEEN;
RX MEDLINE=20183931; PubMed=10706631;
RA Shinohara N., Demura T., Fukuda H.;
RT "Isolation of a vascular cell wall-specific monoclonal antibody
RT recognizing a cell polarity by using a phage display subtraction
RT method".
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590 (2000).
DR EMBL; AB036341; BAAB8633.1; -
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IGV; 2.
DR SMART; SM00406; IGV; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Alignment Scores:

Pred. No.: 9e-37 Length: 298
Score: 403.00 Matches: 77
Percent Similarity: 78.99% Conservative: 17
Best Local Similarity: 64.71% Mismatches: 25
Query Match: 52.96% Indels: 0
DB: 11 Gaps: 0

US-08-728-463b-220 (1-420) x Q9QYF0 (1-298)

QY 61 GGTTCAGATGAGATGACATGACCCAGTCTTCATCTTCGTCGATCTGTAGA 120
Db : : : : :
169 GlyGlyGlySerAspIleGlnLeuThrGlnSerProLysSerLeuSerAlaSerValGly 188
QY 121 GACAGAGTCAACATCACTTGTGGGCGAGTCAGATATTAAGCACTGTGATAGCTGTAT 180
Db : : : : :
189 GluThrValThrIleThrCysArgAlaSerCylAsnIleHisAsnTyrLeuAlaTyr 208
QY 181 CAGCTAAACAGGTAAGCACTAAGCTCTGATCTATGTCGATCAGATTTGCAAGT 240
Db : : : : :
209 GlnGlnLysGlnGlySerProGlnLeuValTyrAsnAlaLysThrLeuAlaAsp 228
QY 241 GGTGCCATCAAGTTCAGCGAAGTGAAGTCTTGGGACAGATTTCACTCAGCATCAGC 300
Db : : : : :
229 GlyValProSerArgPheSerGlySerGlySerCylThrGlnTyrSerLeuLysIleAsn 248
QY 301 AGCTGAGCTGAAGATTTTGCACTTACTATGTCACAGGCTAATAGTTCCCGTAC 360
Db : : : : :
249 SerLeuGlnProGlnAspPheGlySerTyrCylGlnHisPheThrPheThrProTyr 268
QY 361 ACTTTGTCAGGAACCAAGCTGAGATCAACAGCACTGTGCTGACCATCTGTC 417
Db : : : : :
269 ThrPheGlyGlyThrLysLeuGlnIleValSerGlnIleValAlaAlaGlyAlaProVal 287

RESULT 15

Q99M37

ID Q99M37 PRELIMINARY; PRT; 238 AA.

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 08:56:21 ; Search time 27.1662 Seconds
(without alignments)
4120.219 Million cell updates/sec

Title: US-08-728-463B-220

Perfect score: 761
Sequence: 1 AACCTTGCCACCATGATGCT.....TGGCTGCACCATCTGCTTC 420

Scoring table:
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 908470 segs, 133250620 residues

Total number of hits satisfying chosen parameters: 1816540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0 %
Maximum Match 100 %

Listing first 45 summaries

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-NO MAMP -LARGEJOINT -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MAAN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	656	86.2	236	23 AAU74297	Anti-human ALLIM m
2	621.5	81.7	241	22 AAB82912	Human immune respo
3	610.5	80.2	234	14 AAR38162	Sequence of the Ka
4	610.5	80.2	237	21 AAY96298	Human IGFBP-10 imm
5	606.5	79.7	237	21 AAY96289	Human IGFBP-1 immu
6	606.5	79.7	237	21 AAY96301	Human IGFBP-13 imm
7	602	79.1	139	23 ABA31557	Human ovarian anti
8	601	79.0	260	23 ABA41164	Human ovarian anti
9	599	78.7	234	13 AAR20058	Light chain of 3D6
10	597	78.4	146	22 AAB99115	Human protein SEQ
11	591	77.7	234	18 AAM11638	Human anti-RSV mon
12	588	77.3	236	21 AAY96297	Human anti-RSV mon
13	585.5	76.9	237	21 AAB15546	Human immune syste
14	585	76.9	236	14 AAR42065	Human anti-HBs 1lg
15	582	76.5	130	16 AAR75394	Anti-interleukin-1
16	578	76.0	128	17 AAM01527	Monoclonal antibod
17	578	76.0	128	18 AAM24990	Monoclonal antibod
18	578	76.0	130	21 AAY56737	Amino acid sequenc
19	577	75.8	236	21 AAY96293	Human IGFBP-5 immu
20	574	75.4	132	18 AAW22842	Human anti-tumour
21	568	74.6	124	21 AAY56723	Amino acid sequenc
22	567	74.5	236	16 AAR77614	Humanised 5G1.1 VL
23	567	74.5	236	23 AAB51696	5G1.1 light chain
24	565	74.2	134	23 AAM47645	Human protein sequ
25	564	74.1	129	19 AAM70379	Anti-human CD23 5E
26	562	73.9	129	21 AAY56722	Amino acid sequenc
27	561	73.7	234	18 AAM10233	Thrombopoietin ago
28	560	73.6	129	23 AAB35326	Human anti-RSV mon
29	558.5	73.4	235	18 AAM11640	Human anti-RSV mon
30	557	73.2	129	16 AAR65018	93K99 anti-Varicel
31	557	73.2	133	17 AAR87057	CDR grafted anti-1
32	550	72.3	233	17 AAB03713	Immunoglobulin kap
33	546	71.7	129	15 AAR57482	Humanised anti-Pas
34	546	71.7	129	17 AAR92085	Humanised antibody
35	543.5	71.4	128	21 AAY56717	Amino acid sequenc
36	543	71.4	234	12 AAR13050	CD4-specific CDR-g
37	543	71.4	238	21 AAM90930	Humanised anti-Pas
38	543	71.4	238	21 AAB74899	Humanised anti-Pas
39	542	71.2	129	21 AAY56724	Amino acid sequenc
40	542	71.2	232	22 AAB18767	Novel human diagno
41	542	71.2	238	21 AAW90932	Humanised anti-Pas
42	542	71.2	238	23 AAB74901	Humanised anti-Pas
43	541	71.1	235	21 AAB03684	Immunoglobulin kap
44	539	70.8	128	15 AAR54053	Sequence of the VL
45	539	70.8	238	21 AAW90931	Humanised anti-Pas

ALIGNMENTS

RESULT 1
AAU74297
AAU74297 standard; Protein; 236 AA.

AC AAU74297;
DT 12-MAR-2002 (first entry)

XX Anti-human ALLIM monoclonal antibody clone Unab-136, light chain.

XX Human, antineumatic; antiarthritic; antiabiotic; antiposiatric;
XX antiallergic; antitumor; neuroprotective; antithyroid; vasotrophic;
XX immunosuppressive; dermatologic; antidiarrheal; hepatotropic;
XX activation inducible lymphocyte immunomodulatory molecule; ALLIM;
XX monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;
XX multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;
XX allergic contact-type dermatitis; chronic inflammatory dermatosis;
XX systemic lupus erythematosus; autoimmune disorder; inflammation;
XX graft versus host reaction; immune rejection; intestinal immunity;

XX	ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.
XX	
OS	Homo sapiens.
XX	
PN	WO200187981-A2.
XX	
XX	
PD	22-NOV-2001.
XX	
PF	15-MAY-2001; 2001WO-JP04035.
XX	
PR	18-MAY-2000; 2000JP-0147116.
PR	30-MAR-2001; 2001JP-0099508.
XX	
XX	
PA	(NISB) JAPAN TOBACCO INC.
XX	
PI	Tsujii T, Tezuka K, Hori N,
XX	
DR	WPI; 2002-075113/10.
DR	N-PSDB; AAS99473.
XX	
XX	
PT	New human monoclonal antibody that binds to activation inducible
PT	lymphocyte immunomodulatory molecule, useful for treating rheumatoid
PT	arthritis, multiple sclerosis and inflammation -
XX	
PS	Claim 30; Page 2-271; 300pp; English.
XX	

The invention relates to a novel human antibody (I), preferably a human monoclonal antibody which binds to an activation inducible lymphocyte immunomodulatory molecule (Allim). (I) is useful for modulating signal transduction into a cell mediated by Allim, for modulating proliferation of Allim-expressing cells, for modulating production of a cytokine from Allim-expressing cells, and for inducing antibody-dependent cytotoxicity against Allim-expressing cells and/or immune cytotoxic or apoptosis of Allim-expressing cells. (I) is useful for treating, preventing or prophylaxis of delayed type allergy. (I) is useful for treating and preventing various diseases associated with Allim-mediated costimulatory transduction, and for inhibiting the onset and/or advancement of the diseases. (I) is useful for suppression, prevention and/or treatment of rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis, allergic conjunctivitis, multiple chronic inflammatory dermatosis, systemic lupus erythematosus, insulin-dependent diabetes mellitus, psoriasis, autoimmune or allergic disorders, inflammation, graft versus host reaction, graft versus host disease, immune rejection, disorders caused by abnormal intestinal immunity, specifically inflammatory intestinal disorders such as ulcerative colitis, pneumonia, hepatitis, nephritis, vasculitis, and pancreatitis. (I) induces no serious immunorejection due to antigenicity to human, i.e., human anti-mouse immunoreactivity (HAMA) in a host. ANU74296-ANU74301 represent anti-human Allim monoclonal antibody amino acid sequences of the invention.

SQ Sequence 236 AA;

Alignment Scores:	
Pred. No.:	1,06e-61
Score:	656.00
Percent Similarity:	95.59%
Best Local Similarity:	94.12%
Query Match:	86.20%
DB:	23
Length:	236
Matches:	128
Conservative:	2
Mismatches:	6
Indels:	0
Gaps:	0

US-08-728-463B-220 (1-420) X AAU74297 (1-236)

QY 13 ATATGSGTCCAGCTAGCTCCTCGGTCTTCGCTGCTCTGTGTTCCAGGTTCCAGATGC 72
|||
Db 3 MeaArgValProIaGlnLeuLeuGlyLeuLeuLeuLeuTrpPheProGlySerArgCys 22

QY 73 GACATCCAGATGACCAGCTCTCCATCTTCGCTGTGCATCTGAGAGAGACAGAGTACC 132
|||
Db 23 AspIleGlnMetThrGlnSerProSerSerValSerIleAspValGlyAspArgValThr 42

QY 133 ATACCTTGTCCGGCCAGTACGATATTAGACGCTGGTTAGCGCTGGTATCAGCATAAACA 192
|||

D _b	43	IleThrCysArgAlaSerGlnGlyIleSerArgLeuLeuAlaTrpTyrGlnGlnLysPro	62
Q _y	139	GSTAAAGCACTTAAGTCCTGATCTAATGTGCATCCAGTTTGCAAAGTGATGCCATCA	252
D _b	63	GlyValAlaProlYsLeuLeuIleTyrValAlaSerSerLeuGlnSerGlyValProSer	82
Q _y	253	AGGTTACCGGAATGGATCTGGAGACAATTACATCCACCATAGAGAGCTCACGCT	312
D _b	83	ArgPheSerGlySerGlySerGlyTrnHisPheTrnMetTrnIleSerSerLeuGlnPro	102
Q _y	313	GAAGATTTGGCACTTACTAATTGTCAACAGGCTAAATAGTTTCCCCTACACTTTTGCTCAG	372
D _b	103	GlnsppheaIatTrTyrTyrCysGlnGlnAlaIaSenSerPheProTrpTrnPheGlyGln	122
Q _y	373	GGAACCAAGCTGAGATCAAAAGCAATGAGGGCTGGACCATCTGCTTTC	420
D _b	123	GlyThrIysValGlnIleIysArgTrnValAlaAlaAlaProSerValPhe	138

RESULT 2	
AA82912	
ID	AA82912 standard; Protein; 241 AA.
XX	
AC	AA82912;
XX	
DT	26-NOV-2001 (first entry)

Human immune protein HIRP1.

KW Immuneresponse protein, HRP; human, immunologic disease;
KW cell proliferation; cancer; anti-HIV, antitumor;
KW antiasthma; antistaphylococcal; antistaphylococcal;
KW immunosuppressive; dermatologic; antidiabetic; antiinflammatory
KW neuroprotective; osteopathic; antineumatic; antiaortic;
KW antifungal; virulence; antibacterial; antifungal;
KW antihelminthic; vulnery; hepatotropic; cytoskeletal; therapy;
KW diagnosis; vaccine; immunoglobulin.

OS Homo, sapiens

FT	Key	Location/Qualifiers
FT	Peptide	1..22
FT		/label= Signal_peptide
FT	Protein	22..241
FT		/label= Mature_protein
FT	Modified-site	36
FT		/note= "O-phosphorylated"
FT	Modified-site	44
FT		/note= "O-phosphorylated"
FT	Modified-site	79
FT		/note= "O-phosphorylated"
FT	Modified-site	80
FT		/note= "O-phosphorylated"
FT	Modified-site	94
FT		/note= "O-phosphorylated"
FT	Modified-site	129
FT		/note= "O-phosphorylated"
FT	Modified-site	189
FT		/note= "O-phosphorylated"
FT	Modified-site	191
FT		/note= "O-phosphorylated"
FT	Modified-site	209
FT		/note= "O-phosphorylated"
FT	Domain	38..117
FT		/note= "immunoglobulin domain motif"
FT	Region	98..134
FT		/note= "T-cell glycoprotein CD8 motif"
FT	Region	123..240
FT		/note= "immunoglobulin kappa complex motif"
FT	Domain	154..223
FT		/note= "immunoglobulin domain motif"
FT	Region	219..225
FT		/note= "Ig MHC motif"
FT	Region	197..240

Db	83	ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro	102
Qy	313	GAAGATTTTGCACCTTACTATTGTCAACAGCCTAAATAGTTTC--CGSTACATTTTGGT	368
Db	103	GluAspPheMetAlaThrTyrTyrCysGlnGlnSerTyrSerThrProIleThrPheGly	122
Qy	370	CAGGAGACCAAGCTGGAGATCAAAAGAACTGGGTGGCCATCGTGTTC	420
Db	123	GlnGlyThrArgLeuGlnIleLysAspGlnValAlaAlaProSerValPhe	139

RESULT 5

ID	AAV96289	standard; protein; 237 AA.
XX		
AC	AAV96289;	
XX		
DT	16-AUG-2000	(first entry)
XX		
DE		Human IGFAM-1 immunoglobulin.
XX		
KW		Human; immunoglobulin; IGFAM-1; IGFAM; immune disorder; cancer; infection; inflammation; haematopoiesis; AIDS; allergy.
XX		
OS	Homo sapiens.	

FT	Key	Location/Qualifiers
FT	Peptide	1..22
FT		/label= signal_peptide
FT	Protein	23..237
FT		/label= IGPM-1
FT	Domain	38..112
FT		/label= Ig_domain
FT	Domain	150..219
FT		/label= Ig_domain
FT	Region	154..176
FT		/label= Ig_signature
FT	Domain	193..236
FT		/label= Ig_domain
FT	Region	215..232
FT		/label= Ig_signature
XX		
XX		

WO200029583-A2.

[illegible]

XX Immunoglobulin superfamily proteins, the agonist and antagonist of the
PT protein is useful for preventing and treating disorders associated with
PT altered levels of the protein such as cancer, immune system disorders
PT _
XX
XX Claim 1, Page 77-78, 105pp, English.

The present sequence is the human immunoglobulin superfamily protein IGMAM-1. Its gene was isolated from a cDNA library of synovial membrane tissue. It is expressed in reproductive, gastrointestinal and cardiovascular tissue, where cancer and inflammation are common. The gene, protein, its antibodies, agonists and antagonists are suitable for diagnosing and treating many diseases, including cancer, immune system

CC disorders (such as inflammation, AIDS, allergies, anaemia, .
CC arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
CC disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,
CC systemic sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
CC multiple sclerosis, erythema multiforme and ulcerative colitis), complications of
CC cancer, haemodialysis and extracorporeal circulation, trauma and
CC haematopoietic cancer (such as leukaemia) and infections caused by
CC bacteria, viruses, fungi or parasites.

Alignment Scores:

Pred. No.:	2,35-56	Length:	23
Score:	606.50	Matches:	12
Percent Similarity:	91.97%	Conservative:	5
Best Local Similarity:	88.32%	Mismatches:	10
Query Match:	79.70%	Indels:	1
DB:	21	Gaps:	1

US-08-728-463B-220 (1-420) x AAY96289 (1-237)

Qy	73	GACATCCAGATGACCCAGTCTTCATCTTCCTGTCGATCTGTAGAGACAGAGTCACC	132
		:::	
Db	23	AspIIeGImerThrGlnserProserSerleuSerIaIaIaValGlyAspArgValThr	42
Qy	133	ATACCTTGTCCGGCCAGTCCAGATATTTCAGCTGGTTCAGCTGTATCAGCATTAACCA	197
		:::	
Db	43	IleThrCysArgIaIaIaGlnserIleSerIeSerIeIleuAenTPYrGlnGlnIaIaPro	62
Qy	193	GGTAAAGACACCTAAAGCTCCTGATCTATCTGTCGATCCAGTTTGGCAAGNGGTGCCCATCA	255
Db	63	GlyIuYalaIaProIuSerIeIuIeIuIeIeYrIaIaIaSerSerIeIuGlnSerGlyIaIaProSer	82
Qy	253	AGGTTCCAGCGGAAGTGATCTTGCGACAGATTTTCATCTCACCATCAGCAGCCTTCAGCCT	312
Db	83	ArgPheSerGlySerGlySerGlyIynhrAspPheThrIleuThrIleSerSerIeGlnPro	102
Qy	313	GAAGATTTTGGCACTTACTATTGTGCACAGCCTAAATAGTTCC---CCGTACACTTTTGGT	365
		:::	
Db	103	GluAspPheAlaThrTyIeTyIeCysGlnGlnIeIeIeTyIeSerThrProPheIleThrPheGly	122
Qy	370	CAGGAGCAACAGCTGGAGATCAAAAGCACTGTGGCTGGACCATCTGTCTTC	420
		:::	
Db	123	GlnGlyIThrArgIeIuIeIleYsrIghrIaIaIaIaIaProSerValPhe	139

RESULT 6

AAV96301
ID AAV96301 standard; protein; 237 AA.

AC AAY96301;

DT 16-AUG-2000 (first entry)

Human IGFAM-13 immunoglobulin

KM Human, immunoglobulin, IGFAM-13; IGFAM; immune disorder; cancer
KM infection; inflammation; haematopoiesis; AIDS; allergy.

OS Homo sapiens

Key	Location/Qualifiers
FT	1..22
FT	/label= signal_peptide
FT	22..237
FT	/label= IGFPM-13
FT	38..112
FT	/label= Ig_domain
FT	150..219
FT	/label= Ig_domain

FT	Domain	193..236
FT	/label=Ig_domain	
XX		
XX	WO200029583-A2.	
PX		
PD	25-MAY-2000.	
PF		
XX	19-NOV-1999;	99MO-US27566.
PR	19-NOV-1998;	99US-0113635.
PR	22-DEC-1998;	98US-0113635.
PR	07-APR-1999;	99US-0128194.
XX	(INCY-) INCYTE PHARM INC.	
XX		
PI	Yue H, Tang YT, Corley NC, Guegler KI, Gorgone GA, Baughn MR,	
PI	Lu DM, Lai P, Hillman JL, Yang J;	
XX		
DR	WPI; 2000-387796/33.	
DR	N-PSTDB; AAA27393.	
XX		
PT	Immunoglobulin superfamily proteins, the agonist and antagonist of the	
PT	protein is useful for preventing and treating disorders associated with	
PT	altered levels of the protein such as cancer, immune system disorders	
PT	-	
XX		
PS	Claim 1; Page 87-88; 105pp; English.	
XX		
CC	The present sequence is the human immunoglobulin superfamily protein	
CC	IGPM-13. Its gene was isolated from a cDNA library of lung tumour	
CC	tissue. It is expressed in reproductive, gastrointestinal and	
CC	cardiovascular tissue, where cancer and inflammation are common. The	
CC	gene, protein, its antibodies, agonists and antagonists are suitable for	
CC	diagnosing and treating many diseases, including cancer, immune system	
CC	disorders (such as inflammation, AIDS, allergies, anaemia,	
CC	arteriosclerosis, asthma, atherosclerosis, cholelithiasis, Crohn's	
CC	disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,	
CC	multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,	
CC	systemic lupus erythematosus and ulcerative colitis), complications of	
CC	cancer, hemodialysis and extracorporeal circulation, trauma and	
CC	bacteriostatic cancer (such as leukaemia) and infections caused by	
CC	bacteria, viruses, fungi or parasites.	
XX		
SQ	Sequence 237 AA;	
<hr/>		
Alignment Scores:		
<hr/>		
Pred. No.:	2,13e-56	Length: 237
Score:	606.50	Matches: 119
Percent Similarity:	93.43%	Conservative: 9
Best Local Similarity:	86.86%	Mismatches: 8
Query Match:	79.70%	Indels: 1
DB:	21	Gaps: 1
<hr/>		
US-08-728-463B-220 (1-420) x AAY96301 (1-237)		
QY	13 ATGATGGTCCAGTCAGTCCTCGGTCTGCCTGCTGTTCCAGATTCCAGATGC	72
Db	3 MetarhyalprohaemulinleucunglyleuleuleuleutripLeuargilyAlaryGys	22
QY	73 GACATCCAGATGAACCAAGTCTCATTTCCGTGTGCAATCTGTAGAGAGACAGATCAC	133
Db	23 AsplilegmethrghinserrProserSerleuleraserValGlyAsparigValthr	42
QY	133 ATCAGTGTGGGGCGAGTGACGATATTATACACTGGTTAAGCTGGTATACATPAACA	195
Db	43 MethrhyalarhyalaserginseriliserThrTyrlaasentriptyrGlInglalyBro	62
QY	193 GTTAAGACACTTAGCTCTGTATCTATAGCTGCATCAGATTGCAAAAGGNGTCCATCA	255
Db	63 GlyLylalABrolyserleulenilerTyrlalaaserSerleuinserGlyValproser	82
QY	253 AGGTTCAGGGGAAGTGATCTGGGACAGATTTCATCTTCACCATGACAGCTTGACCTT	312

Db	83	ArgpheeerGtYserGtYserGtYthAspPheThrLeuThrIleSerSerLeuGlnPro	102
Qy	313	GAGATTTCGCACTTACTTATTTGTCACAGAGCT---ATAAGTTTCCCGTACACTTTGGT	369
Db	103	GluAspPheAlaThrTrpTrpCysGlnGlnSerPheAsnThrHISmetTrpThrPheGly	1222
Qy	370	CAGGAACCAAGCGGAGATCAACCAACACTGTGGCTGCACCACTGTCTTC	420
Db	123	GlnGlyThrArgLeuGlnMetCysArgTrpValAlaAlaProSerValPhe	139
RESULT 7			
ABP43157	ID	ABP43157 standard; Protein; 139 AA.	
XX	AC	ABP43157;	
XX	DT	22-AUG-2002 (first entry)	
XX	DE	Human ovarian antigen HVC150, SEQ ID NO:4289.	
XX	KM	Human: ovarian antigen; ovary; ovarian; breast; cancer; tumour;	
XX	KM	ovarian cancer; breast cancer; tumour; reproductive system disorder;	
XX	KM	infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;	
XX	KM	PCOS; ovarian cysts; dysmenorrhoea; endocrine disorder; infection;	
XX	KM	inflammatory condition; immune disorder; blood disorder;	
XX	KM	cardiovascular disorder; respiratory disorder; neurological disorder;	
XX	KM	gastrointestinal disorder; urinary system disorder; drug screening;	
XX	KM	gene therapy; chromosome mapping; forensic analysis;	
XX	KM	antibody preparation; cytostatic; immunomodulatory; neuroprotective;	
XX	KM	antiinflammatory; gynaecological; reproductive.	
OS		Homo sapiens.	
PN		WO200200677-A1.	
XX	PD	03-JUN-2002.	
XX	PF	07-JUN-2001; 2001WO-US18569.	
XX	PR	07-JUN-2000; 2000US-209467P.	
PA		(HUMA-) HUMAN GENOME SCI INC.	
PI		Birce CE, Rosen CA;	
XX	DR	WPI; 2002-147878/19.	
XX	DR	N-PsDB; AB056234.	
XX	PT	Isolated nucleic acid molecules encoding novel ovarian polypeptides,	
XX	PT	useful in the prevention, treatment and diagnosis of cancer (e.g.	
XX	PT	ovarian cancer), immune disorders, cardiovascular disorders and	
XX	PT	neurological diseases -	
XX	PS	Claim 11; SEQ ID No 4289; 29222pp; English.	
XX			
CC		The invention relates to 2175 novel human ovarian antigens (ABP41054-	
CC		ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also	
CC		encompasses polypeptides 90% identical and polynucleotides 95% identical	
CC		to the sequences of the invention. The invention additionally relates to	
CC		recombinant vectors and host cells comprising human ovarian antigen	
CC		polynucleotides, antibodies against human ovarian antigen, and the use	
CC		of ovarian antigen polynucleotides and polypeptides in diagnosing,	
CC		treating, prognosing or preventing various ovary and/or breast-related	
CC		disorders. Such conditions include ovarian cancer and breast cancer, and	
CC		metastatic tumours of ovarian or breast origin, reproductive system	
CC		disorders (e.g., infertility, disorders of pregnancy, anovulation,	
CC		polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine	
CC		disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic	
CC		shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and	
CC		vaginitis), immune disorders (e.g., congenital and acquired	
CC		immunodeficiencies, autoimmune oophoritis), systemic lupus erythematosus),	
CC		blood-related disorders (e.g., anaemia), cardiovascular disorders,	
CC		respiratory disorders, neurological disorders, gastrointestinal disorders	

XX AAB15546;
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE Human immune system molecule from Incyte clone 1666486.
 XX
 KM Anti-inflammatory; keratolytic; anti-HIV; anti-allergic; antianaemic;
 KM antiarteriosclerotic; antischmatic; antidiabetic; nephrotoxic; cancer
 KM antitumor; dermatological; antithyroid; vitaminic; hepatotropic; antibody
 KM immunosuppressive; cyostatic; fungicide; protozoal; antidiabetic;
 KM gene therapy; diagnostic; immunological disorder; viral infection;
 KM bacterial infection; fungal infection; parasitic infection; immunogen.
 XX
 OS Homo sapiens.
 PN WO200060080-A2.
 XX
 PD 12-OCT-2000.
 XX
 PF 04-APR-2000; 2000WO-US09072.
 XX
 PR 05-APR-1999; 99US-0127852.
 PR 05-MAY-1999; 99US-0132647.
 XX
 PA (INCY-) INCYTE PHARM INC.
 PI Yue H, Lai P, Tang YT, Baughn MR, Azimzai Y, Lu DM;
 DR WPI: 2000-665005/64.
 DR N-PSDB; AAB95785.
 XX
 PT New human immune system molecules 1-15 and polynucleotides encoding
 PT them useful for diagnosing, treating or preventing e.g. immunological
 PT disorders, infections, cell proliferative disorders, microbial
 PT infections
 XX
 PS Claim 1; Page 83-84; 95pp; English.
 XX
 CC This sequence represents a human immune system molecule (IMOL) encoded
 CC by the CDNA isolated as clone 1666486 from the Incyte BMANOT03 library.
 CC The human IMOLs (AAB15536-815550) and their encoding polynucleotides
 CC (AAB95775-495789), and compositions comprising them are useful for the
 CC diagnosis, treatment or prevention of immunological disorders,
 CC infections and cell proliferative disorders, including cancer. The IMOL
 CC may be used to treat or prevent disorders associated with decreased
 CC expression or activity of IMOL, such as immunological disorders
 CC (e.g. inflammation, actinic keratosis, AIDS, Addison's disease),
 CC haematopoietic cancer, infections caused by virus (e.g. adenovirus,
 CC parvovirus, coronavirus), bacteria (e.g. Staphylococcus, Streptococcus,
 CC Shigella), fungi (e.g. Aspergillus, Blastomycetes), parasites (e.g.
 CC Plasmodium, Trypanosoma, intestinal protozoal), parasites (e.g.
 CC disorders (e.g. actinic keratosis, arteriosclerosis, psoriasis), and
 CC cancers (e.g. leukemia, melanoma, sarcoma). The peptides are also
 CC useful as immunogens for the development of antibodies that
 CC specifically recognize these peptides. The polynucleotides may be used
 CC to detect and quantify gene expression in biopsied tissues in which
 CC expression of IMOL may be correlated with the disease, as targets in a
 CC microarray, to detect differences in gene sequences among normal,
 CC carrier and affected individuals, and for screening libraries of
 CC compounds in drug screening techniques. Antibodies which specifically
 CC bind to IMOL may be used for the diagnosis of disorders characterized
 CC by expression of IMOL, or in assays to monitor patients being treated
 CC with IMOL or agonists, antagonists, or inhibitors of IMOL.

Alignment Scores:	
Pred. No.:	3,78e-54
Score:	585.50
Percent Similarity:	93.43%
Best Local Similarity:	80.29%
Query Match:	76.94%
Length:	237
Matches:	110
Conservative:	18
Mismatches:	8
Indels:	1

DB:		21	Gaps:	1
US-08-728-463B-220 (1-420) x AAB15546 (1-237)				
OY	13	ATGATAGTCCAGCTCAGCTCTCGTGCTGTGGTTCCAGTTCAGATGC	72	
Dd	3	MetArgValProIaGlnLeuLeuGlYneuleuLeutPleuProGIAlaIalysCyS	22	
OY	73	GACATCCAGATGCCAGTCTTCATTCTCCGTGTCTGCATCTGTAGAGACAGTCAACC	13	
Dd	23	AspIleuLeuutrGlnserProSerThrValSerIaservAlglYAspargValthr	42	
OY	133	ATCACTTGTCGGGGCATGATATTAGCAGCTGGTAGCTGGTATCACATPAACA	19	
Dd	43	IlethrCysargIatrnGlnserIleGlYserTrpAlaIatrPrYrGlnGlnlysePro	62	
OY	193	GGTAACACACTTAAGCTCTGATTTANAGCTGCATCCAGTTTGCAAAGTGTGTCATCA	25	
Dd	63	GlyylvalabProGlnLeuLeuIleYrlylalaSerSerleuGlnserGlyValProser	82	
OY	253	AGGTTACGGGAAGTGCATCTGGGACAGATTTCCTCACCCATCAGAGCTCAGCCT	31	
Dd	83	ArgPheSerIlyserGlyserGlyThnGluPheThrIeuserIleasnSerleuGlnpro	10	
OY	313	GAAGATTTGCCAATTACTATTGTCCAAGCTAAATAATTGCCG--TACACTTTGGT	36	
Dd	103	AspAspPhealathrTyrrPheCysGlnGlnIntyAsphrTyrrProthrTrpserPheGly	12	
OY	370	CAGGSAACCAAGCTGAGATCAACGAACTGTGGCTGCACCATCTGTCTTC	420	
Dd	123	GlnGlyThrlyleuGlnIleIlysArgThrValAlaIalabProservAlaphe	139	
RESULT 14				
AAR42065				
ID	AAR42065	standard; Protein; 236 AA.		
XX				
AC	AAR42065;			
XX				
DT	29-APR-1994	(first entry)		
XX				
DE	Human anti-HBs light chain.			
XX				
KM	Antibody; Ab; light; heavy; chain; hepatitis B;			
XX	HB; surface antigen.			
OS	Homo sapiens.			
XX				
FH	Key	Location/Qualifiers		
FT	Peptide	1..22		
FT	Protein	/label= sig_peptide		
FT		23..236		
FT		/label= mat_protein		
XX				
PN	WO9320205-A.			
XX				
PD	14-OCT-1993.			
XX				
PF	30-MAR-1993;	93WO-JP00396.		
XX				
PR	30-MAR-1992;	92JP-0074678.		
XX				
PA	(SUNR) SUNTORI LTD.			
XX				
PI	Arima K, Kurihara T, Matsuura S, Nishihara T, Teurucka N;			
XX				
DR	WPI; 1993-336913/42.			
XX	N-Psdb; AAQ49943.			
XX				
PT	Human anti-hepatitis B surface antigen antibody gene - can be			
XX	used to produce L and H chains of the antibody in large quantity			
XX				
S8	Disclosure; Fig 4-5; 46pp; Japanese.			
XX				

human anti-hepatitis B surface antigen antibody gene - can be
used to produce L and H chains of the antibody in large quantity
PS Disclosure; Fig 4-5; 46pp; Japanese.
XX
XX

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Tue Jun 3 09:41:15 2003

us-08-728-463b-220.rag

Page 13

Db 123 GlyThrIysValGluHisLysArg 130

Search completed: June 3, 2003, 09:02:30
Job time : 29.3328 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 09:04:15 ; Search time 17.8452 Seconds
(without alignments)
4764.744 Million cell updates/sec

Title: US-08-728-463B-220

Perfect score: 761

Sequence: 1 AAGCTTGCCACCATGATGCT.....TGGCTGCACCATCTGCTTC 420

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 383519 segs, 101223694 residues

Total number of hits satisfying chosen parameters: 767038

Minimum DB seg length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ n2p.model -DEV=xip
-O=/cgn2_1/USPTO.spool/US08728463/runat_03062003_085618_16959/app.query.fasta.1.3690
-DB=published.Applications_AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blomsun62
-TRANS=human40.caf -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US08728463 @CGN 1.1 51 @runat_03062003_085618_16959
-NCPU=6 -ICPU=3 -NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep:*\n2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep:*\n3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep:*\n4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep:*\n5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep:*\n6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep:*\n7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep:*\n8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep:*\n9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep:*\n10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep:*\n11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep:*\n12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep:*\n13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep:*\n14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	656	86.2	236	US-09-859-053-30 Sequence 30, Appl
2	591	77.7	234	US-09-740-002-24 Sequence 24, Appl
3	567	74.5	236	US-10-006-593-69 Sequence 69, Appl
4	558.5	73.4	234	US-09-740-002-26 Sequence 26, Appl

5	548	72.0	128	US-09-855-271-26 Sequence 26, Appl
6	534	70.2	234	US-09-800-729-150 Sequence 150, App
7	529	69.5	214	US-10-153-382-19 Sequence 19, Appl
8	526.5	69.2	109	US-09-798-058-4 Sequence 4, Appl
9	524	68.9	127	US-10-283-349-71 Sequence 71, Appl
10	522.5	68.7	235	US-09-800-729-152 Sequence 152, App
11	520	68.3	214	US-09-940-166A-2 Sequence 2, Appl
12	520	68.3	214	US-09-811-384-11 Sequence 11, Appl
13	520	68.3	237	US-10-227-694-1 Sequence 1, Appl
14	520	68.3	237	US-09-940-166A-6 Sequence 6, Appl
15	518	68.1	244	US-09-880-748-1881 Sequence 1881, Ap
16	514	67.5	109	US-09-811-123-6 Sequence 6, Appl
17	514	67.5	218	US-09-917-410-2 Sequence 2, Appl
18	514	67.5	237	US-10-020-786-10 Sequence 10, Appl
19	514	67.5	237	US-09-056-160B-100 Sequence 100, App
20	514	67.5	491	US-10-011-125-2 Sequence 2, Appl
21	512	67.3	218	US-09-925-179-9 Sequence 9, Appl
22	512	67.3	218	US-09-802-077-9 Sequence 9, Appl
23	512	67.3	218	US-09-802-096-9 Sequence 9, Appl
24	512	67.3	218	US-09-920-171-13 Sequence 13, Appl
25	509	66.9	108	US-09-056-160B-12 Sequence 12, Appl
26	509	66.9	127	US-10-283-349-88 Sequence 88, Appl
27	509	66.9	218	US-09-920-171-15 Sequence 15, Appl
28	509	66.9	218	US-09-920-171-17 Sequence 17, Appl
29	509	66.9	218	US-09-920-171-19 Sequence 19, Appl
30	509	66.9	218	US-09-920-171-24 Sequence 24, Appl
31	504	66.2	107	US-10-268-501-5 Sequence 5, Appl
32	504	66.2	212	US-10-011-125-5 Sequence 5, Appl
33	503	66.1	218	US-10-253-366-1 Sequence 1, Appl
34	503	66.1	218	US-09-925-179-67 Sequence 67, Appl
35	502	66.0	214	US-09-875-221A-18 Sequence 128, App
36	502	66.0	214	US-09-949-559-128 Sequence 128, App
37	502	66.0	240	US-09-968-561A-2 Sequence 2, Appl
38	502	66.0	240	US-09-192-854-2 Sequence 2, Appl
39	501	65.8	237	US-10-020-786-8 Sequence 8, Appl
40	501	65.8	237	US-10-227-694-4 Sequence 4, Appl
41	499	65.6	106	US-10-027-725A-12 Sequence 12, Appl
42	498	65.4	127	US-10-283-349-92 Sequence 92, Appl
43	498	65.4	128	US-09-992-524-6 Sequence 6, Appl
44	498	65.4	245	US-09-797-941A-6 Sequence 6, Appl
45	497	65.3	107	US-09-848-798-40 Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-09-859-053-30
; Sequence 30, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND
; FILE REFERENCE: PHARMACEUTICAL USE THEREOF
; CURRENT APPLICATION NUMBER: 06501-079001
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-30
Alignment Scores: 3.82e-49 Length: 236
Pred. No.:


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Db 43 ILeThrcYseGlYAlaSerGIuaenILeTYrGIYAlaLeuansnIPYrGIInGInLysPro 62
QY 193 GGTAAAGCACCTAAGCTCTGATCTATGTCATGCATGCTTGGCAAGTGGTGTCCTCA 252
Db 63 GILYsAlaProLYsLeuLeuILeTYrGIYAlaThrnsnLeuAlaapGIYAlaProSer 82
QY 253 AGGTTACGGGAAGTGATCTGGAGACGATTTCACCTCACTCCATCAGACCTGGACCT 312
Db 83 ArgPheSerGIYserGIYserGIYThrAspPheThrLeuThrILeSerSerLeuGInPro 102
QY 313 GAAGATTTTGCACTTCTATTGTGCAACAGCTTAATGTTCCGTACCTTTTGGTCAG 372
Db 103 GluAspPheAlaThrTYrTYrCYsGInAsnValLeuansnThrProLeuThrPheGIn 122
QY 373 GGAACCAAGCTGGAGATCAACAGCACTGGGCTGCACCATCTGCTTC 420
Db 123 GILYThrLYsValGInILeLYsArgThrValAlaAlaProSerValPhe 138

RESULT 4
US-09-740-002-26
; Sequence 26, Application US/09740002
; Patent No. US20020001798A1
; GENERAL INFORMATION:
; APPLICANT: BRAMS, PETER
; APPLICANT: MORROW, PHILLIP
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
; TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
; FILE REFERENCE: 037003-0275759
; CURRENT APPLICATION NUMBER: US/09/740,002
; PRIORITY FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/335,697
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/488,376
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 234
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-740-002-26

Alignment Scores:
Pred. No.: 1,11e-40 Length: 234
Score: 558.50 Matches: 109
Percent Similarity: 91.91% Conservative: 16
Best Local Similarity: 80.15% Mismatches: 10
Query Match: 73.39% Indels: 1
DB: 10 Gaps: 1

US-08-728-463b-220 (1-420) x US-09-740-002-26 (1-234)
QY 13 ATGATGGTCCAGCTCAGCTCTCGTCTCTGCTGCTGCTGCTCCAGGTTCCAGATGC 72
Db 3 MetArgValProAlaGInLeuLeuGlyLeuLeuLeuLeuThrLeuArgGlyAlaArgCys 22
QY 73 GACATCCAGATGACCCAGCTCTCCATCTTCGCTGCTGCTGATCTGTAGAGACAGATCA 132
Db 23 AspILeGInMetThrGInSerProSerSerLeuSerValGlyAspArgValThr 42
QY 133 ATCCTTGTGGGGGAGATCAGATATTAGACGCTGGTATGAGCTGTATCCAGCAATAACA 192
Db 43 ILeThrcYsAlaProLYsLeuLeuILeTYrGIYAlaThrnsnIPYrGIInGInLysPro 62
QY 193 GGTAAAGCACCTAAGCTCTGATCTATGTCATGCATGCTTGGCAAGTGGTGTCCTCA 252
Db 63 GILYsAlaProLYsValLeuILePheAlaSerAlaasnLeuValserGIYAlaProSer 82
QY 253 AGGTTACGGGAAGTGATCTGGAGACGATTTCACCTCACTCCATCAGACCTGGACCT 312
Db 83 ArgPheSerGIYserGIYserGIYThrValPheThrLeuThrILeSerAsnLeuGInPro 102
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QY 313 GAAGATTTTGCACTTACTATTGTCAACAGGCTTAATGTTCCGTACCTTTTGGTCAG 372
Db 103 GluAspPheAlaThrTYrPheCYsGInGInSerTYrThr---AsnPheSerPheGIn 121
QY 373 GGAACCAAGCTGGAGATCAACAGCACTGGGCTGCACCATCTGCTTC 420
Db 122 GILYThrLYsLeuGInILeLYsArgThrValAlaAlaProSerValPhe 137

RESULT 5
US-09-855-271-26
; Sequence 26, Application US/09855271
; Patent No. US20020042089A1
; GENERAL INFORMATION:
; APPLICANT: Bodmer, Mark W
; APPLICANT: Achwal, Diljeet Singh
; APPLICANT: Emtage, John Spencer
; TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
; FILE REFERENCE: CARP-0088
; CURRENT APPLICATION NUMBER: US/09/855,271
; PRIORITY FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/347,061
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 128
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020042089A1el Sequence
US-09-855-271-26

Alignment Scores:
Pred. No.: 9.07e-40 Length: 128
Score: 548.00 Matches: 104
Percent Similarity: 89.84% Conservative: 11
Best Local Similarity: 81.25% Mismatches: 13
Query Match: 72.01% Indels: 0
DB: 10 Gaps: 0

US-08-728-463b-220 (1-420) x US-09-855-271-26 (1-128)
QY 13 ATGATGGTCCAGCTCAGCTCTCGTCTCTGCTGCTGCTGCTCCAGGTTCCAGATGC 72
Db 1 MetSerValProThrGInValLeuGlyLeuLeuLeuLeuThrLeuThrAspAlaArgCys 20
QY 73 GACATCCAGATGACCCAGCTCTCCATCTTCGCTGCTGCTGATCTGTAGAGACAGATCACC 132
Db 21 AspILeGInMetThrGInSerProSerSerLeuSerAlaSerValGlyAspArgValThr 40
QY 133 ATCCTTGTGGGGGAGATCAGATATTAGACGCTGGTATGAGCTGTATCCAGCAATAACA 192
Db 41 ILeThrcYsLeuAlaSerGInGlyILeSerSerTYrLeuAlaTrPYrGIInGInLysPro 60
QY 193 GGTAAAGCACCTAAGCTCTGATCTATGTCATGCATGCTTGGCAAGTGGTGTCCTCA 252
Db 61 GILYsAlaProLYsLeuLeuILeTYrGIYAlaAsnSerLeuGInThrGlyAlaProSer 80
QY 253 AGGTTACGGGAAGTGATCTGGAGACGATTTCACCTCACTCCATCAGACCTGGACCT 312
Db 81 ArgPheSerGIYserGIYserAlaThrAspTYrThrLeuThrILeSerSerLeuGInPro 100
QY 313 GAAGATTTTGCACTTACTATTGTCAACAGGCTTAATGTTCCGTACCTTTTGGTCAG 372
Db 101 GluAspPheAlaThrTYrTYrCYsGInGInSerTYrLYsPheProAsnThrPheGIn 120
QY 373 GGAACCAAGCTGGAGATCAACAGCA 396
Db 121 GILYThrLYsValGInValLYsArg 128

RESULT 6
US-09-800-729-150
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Alignment Scores:	
Pred. No.:	1,49e-78
Score:	534.00
Percent Similarity:	86.03%
Best Local Similarity:	74.26%
Query Match:	70.17%
DB:	10
Gaps:	0
Indels:	0
Mismatches:	19
Conservative:	101
Matches:	234
length:	

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; PRIOR FILING DATE:2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 214
; TYPE: PRt
; ORGANISM: Homo sapiens
US-10-153-382-19
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Alignment Scores:	
Pred. No.:	4,05e-38
Score:	529.00
Percent Similarity:	93.97%
Best Local Similarity:	89.66%
Query Match:	69.51%
GB:	9
Gaps:	0
Length:	21
Matches:	10
Conservative:	5
Mismatches:	7
Indels:	0
Gaps:	0

US-08-728-463B-220 (1-420) X US-10-153-382-19 (1-214)

QY	73	SACATCCAGATGAGACCCAGTCCATCTTCGCTGCGCATCTGTAGAGACAAGCAC	132
Db	1	AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr	20
QY	133	ATCACTTGTCCGGGAGTCAAGATATTACAGAGCTGGTTCAGCTGTATCAGATAACCA	192
Db	21	IleThrCysaGlaAlaSerGlnSerIleAlaSerTyrLeuAspThrPyrGlnGlnLysPro	40
QY	193	GGTAAGACACCTAAGCTCCGTGATCTATGTCGATCCAGTTCGAAAGTGGTGCCATCA	252
Db	41	GlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyAlaProSer	60
QY	253	AGGTTTCAGCGGAATGGATCTGGGACAGATTTACTCTCAACATCAGACCTCGACGCT	312
Db	61	ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro	80
QY	313	GAAGATTTTGCATTCTACTATTGTCAACAGGGCTAATAGTTCCCGGACATTTGGTGAG	372
Db	81	GlnAspPheAlaThrTyrTyrGlnGlnGlnTyrTyrSerThrProPheThrPheGlyPro	100
QY	373	GGAAACCAAGCTGGAGATCAAGCAACTGTGGCTGACCACTGTGTCTTC	420
Db	101	GlyThrLysValGlnIleLysArgThrValAlaAlaProSerValPhe	116

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RESULT 8
US-09-798-058-4
: Sequence 4, Application US/09798058
: Patent NO. US20020098523A1
: GENERAL INFORMATION:
: APPLICANT: Vaughan, Tristram John
: APPLICANT: Wilton, Alison Jane
: APPLICANT: Smith, Stephen
: APPLICANT: Main, Sarah Helen
: TITLE OF INVENTION: Human antibodies against ectoxin and their use
: FILE REFERENCE: 84632-000100
: CURRENT APPLICATION NUMBER: US/09/798,058
: CURRENT FILING DATE: 2001-08-29
: PRIOR APPLICATION NUMBER: US 60/187,246
: PRIOR FILING DATE: 2000-03-03
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 4
: LENGTH: 109
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-798-058-4

Alignment Scores:
Pred. No.:
Score:
Sequence Similarity:
Best Local Similarity:
Query Match:

6.67e-38
526.50
97.25%
95.41%
69.19%

Length: 109
Matches: 104
Conservative: 2
Mismatch: 2
Indels: 1
Gaps: 1

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US-08-728-463b-220 (1-420) x US-09-798-058-4 (1-109)

QY 73 GACATCCAGATGACCCAGTCTCCATCTCCGTCGTGATCTGTAGAGACAGATCACC 132
 1 AapleGlmeThrGlnSerProSerSerValSerAlaSerValGlyAspArgValThr 20

QY 133 ATCACTTGTCGGCGAGTCAGATATTAGCAGCTGTGATCCCTGTATCAGCATAAACA 192
 21 IIEthrCysArgAlaSerGlnAspIleSerSerTrpLeuAlaTrpYrGlnGlnLysPro 40

QY 193 GGTAAAGCACCTTAAGTCTCGATCTGATCTGATCCAGTTCGAAAGTGTGTCCATCA 252
 41 GlyValAlaProLysLeuLeuIleYrAlaAlaSerSerLeuLysGlyValProSer 60

QY 253 AGGTTGAGCGAAGTGGATCTGGAGCAGATTTCCTCAGCATCAGCAGCTGAGCCT 312
 61 ArgPheSerGlySerGlySerGlyTrpAspPheThrLeuThrIleSerSerLeuGlnPro 80

QY 313 GAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCG--TACACTTTTGGT 369
 81 GluAspPheAlaThrYrYrYrCysGlnGlnAlaSerSerPheProSerIleThrPheGly 100

QY 370 CAGGGAACCAAGCTGGAGATCAACCA 396
 101 GlnGlyThrArgLeuGlnIleLysArg 109

Db 101 GlnGlyThrArgLeuGlnIleLysArg 109

RESULT 9
 US-10-283-349-71
 Sequence 71, Application US/10283349
 Publication No. US2003096977A1
 GENERAL INFORMATION:
 APPLICANT: KOIKE, Masaamichi
 FURUYA, Akiko
 NAKAMURA, Kazuyasu
 IIDA, Akihito
 ANAZAWA, Hideharu
 HANAI, No. US2003096977A1uo
 TAKATSU, Kiyoshi
 TITLE OF INVENTION: Antibody Against Human Interleukin-5
 Receptor Alpha Chain
 NUMBER OF SEQUENCES: 106
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/283,349
 FILING DATE: 29-Oct-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/836,561
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: JP 232384/95
 FILING DATE: 11-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Lawrence, III, Stanton T
 REGISTRATION NUMBER: 25,736
 REFERENCE/DOCKET NUMBER: 7005-115-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-790-9090
 TELEFAX: 212-869-9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 71:
 SEQUENCE CHARACTERISTICS:

LENGTH: 127 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 71:
 US-10-283-349-71

Alignment Scores:
 Pred. No.: 1,1e-37 Length: 127
 Score: 524.00 Matches: 103
 Percent Similarity: 85.83% Conservative: 6
 Best Local Similarity: 81.10% Mismatches: 18
 Query Match: 68.86% Indels: 0
 DB: 9 Gaps: 0

US-08-728-463b-220 (1-420) x US-10-283-349-71 (1-127)

QY 13 ATGATGTCCTCCAGCTCAGCTCCTCGGTCTGCTGCTGCTGCTGCTCCAGGTTCCAGATGC 72
 1 MetMetSerSerIleGlnPheLeuGlyLeuLeuLeuLeuCysPheGlnAspIleArgCys 20

QY 73 GACATCCAGATGACCCAGTCTCCATCTCCGTCGTGATCTGTAGAGACAGATCACC 132
 21 AapleGlmeThrGlnSerProSerSerValSerAlaSerValGlyAspArgValThr 40

QY 133 ATCACTTGTCGGCGAGTCAGATATTAGCAGCTGTGATCCCTGTATCAGCATAAACA 192
 41 IIEthrCysGlyThrSerGlnAspIleIleAsnYrLeuAsnTrpYrGlnGlnLysPro 60

QY 193 GGTAAAGCACCTTAAGTCTCGATCTGATCTGATCCAGTTCGAAAGTGTGTCCATCA 252
 61 GlyValAlaProLysLeuLeuIleYrAlaAlaSerSerLeuLysGlyValProSer 80

QY 253 AGGTTGAGCGAAGTGGATCTGGAGCAGATTTCCTCAGCATCAGCAGCTGAGCCT 312
 81 ArgPheSerGlySerGlySerGlyTrpAspPheThrLeuThrIleSerSerLeuGlnPro 100

QY 313 GAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCGTCATCACTTTTGGTCA 372
 101 GluAspPheAlaThrYrYrYrCysGlnGlnAlaSerSerPheProSerIleThrPheGlyGln 120

QY 373 GGAACCAAGCTGGAGATCAAC 393
 121 GlyThrLysValGlnIleLys 127

Db 121 GlyThrLysValGlnIleLys 127

RESULT 10
 US-09-800-729-152
 Sequence 152, Application US/09800729
 Patent No. US20020068319A1
 GENERAL INFORMATION:
 APPLICANT: NI et al.
 TITLE OF INVENTION: 32 Human secreted proteins
 FILE REFERENCE: P2044P1
 CURRENT APPLICATION NUMBER: US/09/800,729
 CURRENT FILING DATE: 2001-03-08
 PRIOR APPLICATION NUMBER: PCT/US00/26013
 PRIOR FILING DATE: 2000-09-22
 PRIOR APPLICATION NUMBER: 60/155,709
 PRIOR FILING DATE: 1999-09-24
 NUMBER OF SEQ ID NOS: 217
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 152
 LENGTH: 235
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-800-729-152

Alignment Scores:
 Pred. No.: 1,48e-37 Length: 235
 Score: 522.50 Matches: 105
 Percent Similarity: 83.82% Conservative: 9
 Best Local Similarity: 77.21% Mismatches: 21
 Query Match: 68.66% Indels: 1

REFERENCE/DOCKET NUMBER: P1729C1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5530

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 214 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-811-384-11

Alignment Scores:

Pred. No.: 2,45e-37 Length: 214

Score: 520.00 Matches: 100

Percent Similarity: 93.10% Conservative: 8

Best Local Similarity: 86.21% Mismatches: 8

Query Match: 68.33% Indels: 0

DB: 10 Gaps: 0

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QY 73 GACATCCAGATGAGCCAGTCTTCATCTTCGCTGTCATCTGTAGAGAGAGATGACC 132

DB 1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20

QY 133 ATCACTTGCGGGCGAGTCAAGATATTAGAGCTGTAGCTGTAGCTGTAGCAATTAACA 192

DB 21 IleThrCysArgAlaSerGlnAspIleAsnAsnTrpLeuSerGlnGlnPro 40

QY 193 GGTAAAGCACTTAAGCTCTGATCTATGTCATCCAGTTCAGCAAGTGTGTCATCA 252

DB 41 GlyValAlaProLeuLeuIleTrpThrSerThrLeuHisSerGlyValProSer 60

QY 253 AGGTTCAGCGGAGTGTATGTCAGATTTCACTTCACCATCAGACCTGTCACCT 312

DB 61 ArgPheSerGlySerGlySerGlyThrAspTrpThrLeuThrIleSerSerLeuGlnPro 80

QY 313 GAAGATTGTCACCTTACTATTGTCAACAGGCTATAGTTCCGTCACCTTTGTGTCAG 372

DB 81 GluAspPheAlaThrTrpTrpCysGlnGlnGlyAsnThrLeuProProthrpheGlyGln 100

QY 373 GGAACCAAGCTGAGATCAACGAAGCTGCTGACCATCTGCTTC 420

DB 101 GlyThrValGluIleLeuArgThrValAlaAlaProSerValPhe 116

RESULT 13

US-10-227-694-1

Sequence 1, Application US/10227694

Publication No. US2003007739A1

GENERAL INFORMATION:

APPLICANT: Simmons, Laura

TITLE OF INVENTION: A SYSTEM FOR ANTIBODY EXPRESSION AND ASSEMBLY

FILE REFERENCE: P1867R1

CURRENT APPLICATION NUMBER: US/10/227,694

CURRENT FILING DATE: 2002-08-26

PRIOR APPLICATION NUMBER: US 60/315,209

PRIOR FILING DATE: 2001-08-27

NUMBER OF SEQ ID NOS: 6

SEQ ID NO 1

LENGTH: 237

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: Synthetic

US-10-227-694-1

Alignment Scores:

Pred. No.: 2,45e-37 Length: 237

Score: 520.00 Matches: 100

Percent Similarity: 93.10% Conservative: 8

Best Local Similarity: 86.21% Mismatches: 8

Query Match: 68.33%

DB: 9 Indels: 0

Gaps: 0

US-08-728-463b-220 (1-420) x US-10-227-694-1 (1-237)

QY 73 GACATCCAGATGAGCCAGTCTTCATCTTCGCTGTCATCTGTAGAGAGAGATGACC 132

DB 24 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 43

QY 133 ATCACTTGCGGGCGAGTCAAGATATTAGAGCTGTAGCTGTAGCTGTAGCAATTAACA 192

DB 44 IleThrCysArgAlaSerGlnAspIleAsnAsnTrpLeuSerGlnGlnPro 63

QY 193 GGTAAAGCACTTAAGCTCTGATCTATGTCATCCAGTTCAGCAAGTGTGTCATCA 252

DB 64 GlyValAlaProLeuLeuIleTrpThrSerThrLeuHisSerGlyValProSer 83

QY 253 AGGTTCAGCGGAGTGTATGTCAGATTTCACTTCACCATCAGACCTGTCACCT 312

DB 84 ArgPheSerGlySerGlySerGlyThrAspTrpThrLeuThrIleSerSerLeuGlnPro 103

QY 313 GAAGATTGTCACCTTACTATTGTCAACAGGCTATAGTTCCGTCACCTTTGTGTCAG 372

DB 104 GluAspPheAlaThrTrpTrpCysGlnGlnGlyAsnThrLeuProProthrpheGlyGln 123

QY 373 GGAACCAAGCTGAGATCAACGAAGCTGCTGACCATCTGCTTC 420

DB 124 GlyThrValGluIleLeuArgThrValAlaAlaProSerValPhe 139

RESULT 14

US-09-940-166A-6

Sequence 6, Application US/09940166A

Patent No. US20020058324A1

GENERAL INFORMATION:

APPLICANT: Blank, Gregory S.

Narindray, Daljit S.

Zapata, Gerardo A.

TITLE OF INVENTION: Protein Recovery

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/940,166A

FILING DATE: 27-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/097,309

FILING DATE: 13-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Schwartz, Timothy R.

REGISTRATION NUMBER: 32171

REFERENCE/DOCKET NUMBER: P1105R1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-7467

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 237 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-940-166A-6

Alignment Scores:

Pred. No.: 2,45e-37 Length: 237
 Score: 520.00 Matches: 100
 Percent Similarity: 93.10% Conservative: 8
 Best Local Similarity: 86.21% Mismatches: 8
 Query Match: 68.33% Indels: 0
 DB: 10 Gaps: 0

US-08-728-463B-220 (1-420) x US-09-940-166A-6 (1-237)

QY 73 GATATCCAGATGACCCAGTCTCCATCTTCGCTGTCATCTGTMAGAGACAGAGTACC 132
 DB 24 AsplIGImethrInserProSerSerLeuSerAlaSerValGlyAspArgValThr 43
 QY 133 ATCACTTGTGCGGCGAGTACGATATTACAGAGTGGTGGTGGATACAGATTAACA 192
 DB 44 IetHrCyArgAlaSerGlnAspIleAsnMetTyrLeuAsnTrpTyrGlnGlnPro 63
 QY 193 GGTAAAGCACTTACCTGATCTATGCTGCATCCAGTTTGCAAAAGTGTGCCATCA 252
 DB 64 GlyValAlaProLeuLeuLeuIleTyrTyrThrSerThrLeuHisSerGlyValProSer 83
 QY 253 AGGTTAGCGGAGTGGATCTGGGACAGATTTCACCTTCACATCAGACGCTGACGCT 312
 DB 84 ArgPheSerGlySerGlySerGlyThrAspTyrThrLeuThrIleSerSerLeuGlnPro 103
 QY 313 GAAGATTTTGCACTTACTATTGTCAACAGGCTTAATAGTTTCCGTACACTTTGGTAC 372
 DB 104 GluAspPheAlaThrTyrTyrCysGlnGlnGlnAsnThrLeuProThrPheGlyGln 123
 QY 373 GGAACCAAGCTGAGATCAAGAACTGGCTGCACCACTGTCTTC 420
 DB 124 GlyThrIleValGluIleValArgThrValAlaAlaProSerValPhe 139

RESULT 15

US-09-880-748-1881
 ; Sequence 1881, Application US/09880748
 ; Publication No. US20030059937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PFS23
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1881
 ; LENGTH: 244
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-880-748-1881

Alignment Scores:

Pred. No.: 3.65e-37 Length: 244
 Score: 518.00 Matches: 101
 Percent Similarity: 92.86% Conservative: 3
 Best Local Similarity: 90.18% Mismatches: 8
 Query Match: 68.07% Indels: 0
 DB: 9 Gaps: 0

US-08-728-463B-220 (1-420) x US-09-880-748-1881 (1-244)

QY 61 GGTTCAGATGCGACATCCAGATGACCCAGTCTCCATCTTCGATGCTGATGATGAGGA 120

DB 133 GlyIleGlySerAspIleValMetThrGlnSerProSerThrLeuSerAlaSerValGly 152
 QY 121 GACAGAGTACACATCACTTGTGCGGCGAGTACAGATATTAGACAGCTGTAGCTGGTAT 180
 DB 153 AspArgValThrIleThrCyArgAlaSerGlnIlyIleSerSerTrpLeuAlaTrpTyr 172
 QY 181 CAGCATTAACCAAGTAAAGCACTTACCTCTGATCTTANGCTGCATCCAGTTTGCAAGT 240
 DB 173 GlnGlnIlySProgIlyValAlaProLeuLeuIleTyrAlaAlaSerSerLeuGlnSer 192
 QY 241 GGTGTCCCATCAAGGTTACAGGGAAGGATCTGGGACAGATTTCACCTTCACATCAGC 300
 DB 193 GlyValProSerArgPheSerGlySerGlyThrAspPheThrLeuThrIleSer 212
 QY 301 AGCTGACGCTGGAAGATTTTGCACTTACTATTGTCAACAGGCTTAATAGTTTCCGTAC 360
 DB 213 SerLeuGlnProGluAspPheAlaThrTyrTyrCysGlnGlnIleAsnSerPheProLeu 232
 QY 361 ACTTTGTGAGGGAACCAAGCTGAGATCAACA 396
 DB 233 ThrPheGlyIleGlyThrIlyValGluIleValArg 244

Search completed: June 3, 2003, 09:51:26
 Job time : 19.8452 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_nzp model

Run on: June 3, 2003, 09:02:35 ; Search time 9.55994 Seconds
(without alignments)
2585.294 Million cell updates/sec

Title: US-08-728-463B-220

Perfect score: 761
Sequence: 1 AAGCTTGCCACCATGATGCT.....TGGCTGCACCATCTGCTTC 420

Scoring table: BLOSUM62 Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 525148

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNIT=bits -START=1 -END=1 -MATRIX=blonum62 -TRANS=human40.cdi
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Issued Patents.AA.*

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- 2: /cg2_6/ptodata/1/iaa/5B.COMB.pep.*
- 3: /cg2_6/ptodata/1/iaa/6A.COMB.pep.*
- 4: /cg2_6/ptodata/1/iaa/6B.COMB.pep.*
- 5: /cg2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
- 6: /cg2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	585	76.9	236	1 US-08-157-101A-5	Sequence 5, Appl1
2	578	76.0	128	1 US-08-259-372A-14	Sequence 14, Appl1
3	578	76.0	128	1 US-08-468-671-14	Sequence 14, Appl1
4	562	73.9	129	1 US-08-217-918-2	Sequence 2, Appl1
5	550	72.3	233	3 US-08-812-586-45	Sequence 45, Appl1
6	548	72.0	128	2 US-08-470-139-26	Sequence 26, Appl1
7	548	72.0	128	4 US-09-347-061-26	Sequence 26, Appl1
8	541	71.1	235	3 US-08-812-586-16	Sequence 16, Appl1
9	534	70.2	128	4 US-08-569-147-80	Sequence 80, Appl1
10	528	69.4	117	4 US-09-042-353-48	Sequence 48, Appl1
11	528	69.4	117	4 US-08-758-417A-313	Sequence 313, Appl1
12	527	69.3	109	2 US-07-934-373C-3	Sequence 3, Appl1

13	527	69.3	109	3 US-08-437-642B-3	Sequence 3, Appl1
14	527	69.3	109	4 US-08-146-206C-3	Sequence 3, Appl1
15	527	69.3	109	5 PCT-US93-07832-3	Sequence 3, Appl1
16	526	69.1	127	2 US-08-621-751A-6	Sequence 6, Appl1
17	524	68.9	127	3 US-08-836-561-71	Sequence 71, Appl1
18	523	68.7	223	2 US-07-934-373C-25	Sequence 25, Appl1
19	523	68.7	223	3 US-08-437-642B-25	Sequence 25, Appl1
20	523	68.7	223	4 US-08-146-206C-25	Sequence 25, Appl1
21	523	68.7	223	5 PCT-US93-07832-25	Sequence 25, Appl1
22	522	68.6	214	2 US-07-934-373C-39	Sequence 39, Appl1
23	522	68.6	214	3 US-08-437-642B-39	Sequence 39, Appl1
24	522	68.6	214	5 PCT-US93-07832-39	Sequence 39, Appl1
25	521	68.5	116	1 US-08-053-131-185	Sequence 185, Appl1
26	521	68.5	116	2 US-08-096-762-185	Sequence 185, Appl1
27	520	68.3	214	2 US-07-934-373C-40	Sequence 40, Appl1
28	520	68.3	214	2 US-08-788-800-11	Sequence 11, Appl1
29	520	68.3	214	3 US-08-437-642B-40	Sequence 40, Appl1
30	520	68.3	214	3 US-09-097-309-2	Sequence 2, Appl1
31	520	68.3	214	4 US-09-097-171A-2	Sequence 2, Appl1
32	520	68.3	214	4 US-09-460-587-2	Sequence 2, Appl1
33	520	68.3	214	5 PCT-US93-07832-40	Sequence 40, Appl1
34	520	68.3	237	3 US-09-097-309-6	Sequence 6, Appl1
35	520	68.3	237	4 US-09-422-112B-10	Sequence 10, Appl1
36	520	68.3	237	4 US-09-607-756-2	Sequence 2, Appl1
37	520	68.3	237	4 US-09-607-756-2	Sequence 2, Appl1
38	520	68.3	237	4 US-09-460-587-6	Sequence 6, Appl1
39	517	67.9	127	4 US-09-136-315-8	Sequence 8, Appl1
40	517	67.9	128	4 US-08-569-147-78	Sequence 78, Appl1
41	514	67.5	218	5 PCT-US96-13152-2	Sequence 2, Appl1
42	513	67.4	131	4 US-08-579-378A-18	Sequence 18, Appl1
43	513	67.4	133	1 US-08-461-284-2	Sequence 2, Appl1
44	513	67.4	133	1 US-08-462-939-2	Sequence 2, Appl1
45	513	67.4	133	1 US-08-253-877C-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-157-101A-5
; Sequence 5, Application US/08157101A
; Patent No. 5808032
; GENERAL INFORMATION:
; APPLICANT: KURIHARA, TATSUYA
; APPLICANT: MATSUKURA, SHIGERAZU
; APPLICANT: TSURUOKA, NOBUO
; APPLICANT: ARIMA, KENJI
; APPLICANT: NISHIHARA, TATSURO
; TITLE OF INVENTION: ANTI-HBs ANTIBODY GENES AND EXPRESSION
; TITLE OF INVENTION: PLASMIDS THEREFOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/157,101A
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: TITUS, MARIANA K
; REGISTRATION NUMBER: 35843
; REFERENCE/DOCKET NUMBER: 9437/204199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944

QY	13	ATATGGTCCACCTAGCAGCTCCGTGGATCTTCGAGTCTGGATTCACGATTCACAGATGC	72
Db	3	MeArgValProIaGlnLeuLeuGlyLeuLeuLeuLeuTrrPleuProGlyAlaIaIaScys	22
QY	73	GACATCCAGATGACCCAGTCTCCATCTTCGATGCTGCATCTGTAGAGAGACAGATCAC	132
Db	23	AspIleGlnMetThrGlnSerProSerThrLeuSerAlaIaSerValGlyAspArgValThr	42
QY	133	ATCACTGTGTGGGGCAGTCAAGATATTATACAGCTGTTTAGCTGGTATCAGATTAACCA	192
Db	43	IleThrTySarArgIaIaSerGlnThrIleSerThrTrpLeuAlaTrpGlyGlnThrPro	62
QY	193	GGTAAACACCACTAAGCTCCGTGATCTATGCTGCATCCAGTTGGCAAGAGTGGTCCCATCA	252
Db	63	ArgIlyAlaIaProIaScyLeuMetIleIrrTyIyAlaIaSerIleLeuGlnAsnGlyValProSer	82
QY	253	AGGTTCAAGCGAAGTGGATCTGGACACGATTTTCACCTTCACCATCAGCAGCTCGAGCCT	312
Db	83	ArgPheSerGlySerGlySerGlyThrGlnPheThrLeuThrIleSerSerLeuGlnPro	102
QY	313	GAAGATTTTGCACTTACTATTGTCAACAGGCTAATAGTTTCCGTACACTTTGGTAG	372
Db	103	GlnAspPheAlaThrTyIrrTyCysGlnGlnTyIySerTyPrrIrrPheIleGln	122
QY	373	GGAACCAAGCTGGAGATCAAA	393
Db	123	GlyThrIySarGlnIleIyS	129

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RESULT 5
US-08-812-586-45
: Sequence 45, Application US/08812586
: Patent No. 6048704
:
: GENERAL INFORMATION:
: APPLICANT: Martin David Tilson
: TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
: TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSM (AAA)
: TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
: NUMBER OF SEQUENCES: 61
:
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooper & Dunham LLP
: STREET: 1185 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/812,586
: FILING DATE: 07-MAR-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: White, John P.
: REGISTRATION NUMBER: 28,678
: REFERENCE/DOCKET NUMBER: 0575/53862-A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 278-0400
: TELEFAX: (212) 391-0525
: INFORMATION FOR SEQ ID NO: 45:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 233 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
US-08-812-586-45

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Percent Similarity:	97.374	Conservative:	5
Best Local Similarity:	92.988	Mismatches:	13
Query Match:	72.274	Indels:	0
DB:	3	Gaps:	0

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 Db 23 GlnuethrGlnserProserSerValSerIalaserValGlysbaphValthrIleThr 42
 Oy 139 TGTGGGCGAGTCAGGATATTATGCAAGCTGTAGCTGTATCAGCATAAACAGGTAA 198
 43 CysArgIalaserGlnGlyIleSerSerThrPheuAlaTrpYrGlnGlnIlyProGlyLys 62
 Db 43 CysArgIalaserGlnGlyIleSerSerThrPheuAlaTrpYrGlnGlnIlyProGlyLys 62
 Oy 199 GCACTTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAGGTGGTGTCCATCAAGTTTC 255
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 Db 63 AlaProIlyseuIeuIleThrIySerIalaserSerIeuGlnSerGlyValProSerArgPhe 82
 Oy 259 AGCGGAAGTGGATCTGGGACAGATTTCATCTGCACCATCAGCAGCTGCACCTCGAAGAT 318
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 Db 83 SerGlySerGlySerGlyThrAspPheSerIeuThrIleSerSerIeuGlnProGlnAsp 107
 Oy 319 TTTCGAACCTACATTGTCGAACAGGCTAATAGTTCCCGTACACTTTGGTCAGAGGAACC 378
 : : : : :
 Db 103 SerAlaThrIyTrpYrCysGlnGlnIalAsnSerPheProIyThrPheGlyGlnGlyThr 122
 Oy 379 AACCTGGAGATCAACGAACCTGTGGCTGCACATCTGTCTTTC 420
 : : : : :
 Db 123 LysValGlnIleLysArgThrValAlaAlaProSerValPhe 136

```

RESULT 6
US-08-470-139-26
: Sequence 26, Application US/08470139
: Patent No. 599585
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Interleukin-5 specific recombinant antibodies
: NUMBER OF SEQUENCES: 28
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/470,139
: FILING DATE: 06 JUNE-1995
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: TRUITILO, DOREN YAKO
: REGISTRATION NUMBER: 35,719
: REFERENCE/DOCKET NUMBER: CAP-0044
: INFORMATION FOR SEQ ID NO: 26:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 128 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-470-139-26

Alignment Scores:
Pred. No.: 3 55e-52
Score: 548.00
Percent Similarity: 89.84%
Best Local Similarity: 81.25%
Query Match: 72.01%
DB: 2

US-08-728-463B-220 (1-420) x US-08-470-139-26 (1-128)

Length: 128
Matches: 104
Conservative: 11
Mismatches: 13
Indels: 0
Gaps: 0

13 ATGATGCTCCAGCTCAGCTCTCTGCTCTCTCTCTCTGTTCCAGATTCAGATTC

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: Sequence 1 Application US/08468671
: Patent No. 5648077
: GENERAL INFORMATION:
: APPLICANT: Ostberg, Lars G.
: TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
: TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
: NUMBER OF SEQUENCES: 16
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/468,671
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/259,372
: FILING DATE: 14-JUN-1994
: APPLICATION NUMBER: US 07/871,426
: FILING DATE: 21-APR-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/676,036
: FILING DATE: 27-MAR-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/538,796
: FILING DATE: 15-JUN-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/192,754
: FILING DATE: 11-MAY-1988
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 06/925,196
: FILING DATE: 31-OCT-1986
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 06/904,517
: FILING DATE: 05-SEP-1986
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M.
: REGISTRATION NUMBER: 30,223
: REFERENCE/DOCKET NUMBER: 11823-50-7
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 128 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-468-671-14

Alignment Scores:
Pred. No.: 1 83e-55 Length: 128
Score: 578.00 Matches: 110
Percent Similarity: 94.35% Conservative: 7
Best Local Similarity: 88.71% Mismatches: 7
Query Match: 75.95% Indels: 0
DB: 1 Gaps: 0

US-08-728-463B-220 (1-420) x US-08-468-671-14 (1-128)
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85 ACCCAAGCTTCATCTTCGCTGCTGTGCATCTGTAGAGACAGATCAACCATCATCTTTCGG 144

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Db 25 ThGInserProserSerValSerAlaSerValGlyAbaArgValThrValThCysArg 44
145 GCGAGTCAGGANTTAGCAGCTGGTTAGCTGGTATCAGCATAAACGAGTAAAGCACT 204
Db 45 AlSerGInGlyLeSerSerTrpLeuAlaTrpIYrGInGInLysProGlyLysAlaPro 64
Qy 205 AAACCTCGATTCANAGTCATCCAGTCAGATTGGCAAAAGTGATGCCATCAAGGTTACGCGGA 264
Db 65 LysLeuLeuLeuLeuAlaAlaSerSerLeuGInSerGlyValProSerArgPheIleIy 84
Qy 265 AGGAGACTGGGACACATTTCACTCTCAACATACAGACAGCCGACCGAAGATTTTGCA 324
Db 85 SerGlySerGlyThrAspPheThrIleuThrIleuTrsSerLeuGInAlaGluAspPheAla 104
Qy 325 ACTTACTATTGTCAACAGGCTAAATGTTTCCCGTACACTTTTGGTCAGGGAACCAAGCTG 384
Db 105 ThrTyrTyrCysGInGInAlaAspSerLeuProPheTrpPheGlyGlyIYrThyLeuVal 124
Qy 385 GAGATCAACGA 396
Db 125 AspPheLysArg 128

```

RESULT 4
US-08-217-918-2
; Sequence 2, Application US/08217918
; Patent No. 5506132
; GENERAL INFORMATION:
; APPLICANT: LAKE, PHILIP
; APPLICANT: OSTBERG, LARS
; TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
; TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Knourie and Cre
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,918
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-217-918-2

Alignment Scores:
Pred. No.: 1.04e-53
Score: 562.00
Percent Similarity: 92.13%
Best Local Similarity: 82.68%
Query Match: 73.85%

Length: 129
Matches: 105
Conservative: 12
Mismatches: 10
Indels: 0
Gaps: 0
US-08-728-463B-220 (1-420) x US-08-217-918-2 (1-129)

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Db 1 MetSerValProThrGlnValLeuGlyLeuLeuLeuLeuThrAspAlaArgCys 20
QY 73 GACATCCAGATGACCCAGTCTCCATCTTCCGTCTGCATCTGTAGAGACAGATCACC 132
Db 21 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 40
QY 133 ATCACTTGCGGGGAGATCAGATATTAAGCAGCTGTGTTAGCTGTATCAGATAAACA 192
Db 41 IleThrCysLeuAlaSerGlnGlyIleSerSerCysLeuAlaTrpYrGlnGlnLysPro 60
QY 193 GGTAAAGCACCTAAGTCTCGATCTATGCTATGCTGAGTTGCAAGGNGGTCCCACTCA 252
Db 61 GlyValAlaProLysLeuLeuIleTyrGlyAlaAsnSerLeuGlnThrGlyValProSer 80
QY 253 AGTTGACCGAGATGATCTGGAGACAGATTTCACTCTACCATCAGACAGCTTGACCT 312
Db 81 ArgPheSerGlySerGlySerAlaThrAspTyrThrLeuThrIleSerSerLeuGlnPro 100
QY 313 GAAGATTTTGCACTTACTATTTGTCACACAGGCTAATAGTTCCGTACACTTTTGTGAC 372
Db 101 GluAspPheAlaThrTyrTyrCysGlnGlnSerTyrLysPheProAsnThrPheGlyGln 120
QY 373 GGAACCAAGCTGGAGATCAACAGA 396
Db 121 GlyThrLysValGlnValLysArg 128
RESULT 7
US-09-347-061-26
Sequence 26, Application US/09347061
Patent No. 6316227
GENERAL INFORMATION:
APPLICANT: Bodmer, Mark
APPLICANT: Achwal, Diljeet Singh
APPLICANT: Emtage, John Spencer
TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
FILE REFERENCE: CARP-0071
CURRENT APPLICATION NUMBER: US/09/347,061
CURRENT FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.0
SEQ ID NO 26
LENGTH: 128
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: No. 6316227el Sequence
US-09-347-061-26
Alignment Scores:
Pred. No.: 3,55e-52 Length: 128
Score: 548.00 Matches: 104
Percent Similarity: 89.84% Conservative: 11
Best Local Similarity: 81.25% Mismatches: 13
Query Match: 72.01% Indels: 0
Gaps: 4
US-08-728-463b-220 (1-420) x US-09-347-061-26 (1-128)
QY 13 ATGATGTCCTCCACTCAGCTCTCGGTCTCTGCTGCTGTTCCAGGTTCCAGATGC 72
Db 1 MetSerValProThrGlnValLeuGlyLeuLeuLeuLeuThrAspAlaArgCys 20
QY 73 GACATCCAGATGACCCAGTCTCCATCTTCCGTCTGCATCTGTAGAGACAGATCACC 132
Db 21 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 40
QY 133 ATCACTTGCGGGGAGATCAGATATTAAGCAGCTGTGTTAGCTGTATCAGATAAACA 192
Db 41 IleThrCysLeuAlaSerGlnGlyIleSerSerCysLeuAlaTrpYrGlnGlnLysPro 60
QY 193 GGTAAAGCACCTAAGTCTCGATCTATGCTATGCTGAGTTGCAAGGNGGTCCCACTCA 252

Db 61 GlyValAlaProLysLeuLeuIleTyrGlyAlaAsnSerLeuGlnThrGlyValProSer 80
QY 253 AGTTGACCGAGATGATCTGGAGACAGATTTCACTCTACCATCAGACAGCTTGACCT 312
Db 81 ArgPheSerGlySerGlySerAlaThrAspTyrThrLeuThrIleSerSerLeuGlnPro 100
QY 313 GAAGATTTTGCACTTACTATTTGTCACACAGGCTAATAGTTCCGTACACTTTTGTGAC 372
Db 101 GluAspPheAlaThrTyrTyrCysGlnGlnSerTyrLysPheProAsnThrPheGlyGln 120
QY 373 GGAACCAAGCTGGAGATCAACAGA 396
Db 121 GlyThrLysValGlnValLysArg 128
RESULT 8
US-08-812-586-16
Sequence 16, Application US/08812586
Patent No. 6048704
GENERAL INFORMATION:
APPLICANT: Martin David Tilsen
TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSM (AAA)
TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,586
FILING DATE: 07-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/53862-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-812-586-16
Alignment Scores:
Pred. No.: 2,46e-51 Length: 235
Score: 541.00 Matches: 105
Percent Similarity: 86.03% Conservative: 12
Best Local Similarity: 77.21% Mismatches: 19
Query Match: 71.09% Indels: 0
Gaps: 3
US-08-728-463b-220 (1-420) x US-08-812-586-16 (1-235)
QY 13 ATGATGTCCTCCACTCAGCTCTCGGTCTCTGCTGCTGTTCCAGGTTCCAGATGC 72
Db 3 MetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuThrProGlyAlaArgCys 22
QY 73 GACATCCAGATGACCCAGTCTCCATCTTCCGTCTGCTGATCTGTAGAGACAGATCACC 132
Db 23 AlaIleArgIleAlaGlnSerProSerSerLeuSerAlaSerThrGlyAspArgValThr 42


```

PRIORITY APPLICATION DATA: US 08/164,739
APPLICATION NUMBER: US 08/164,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-042-353-48

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Alignment Scores:	
Pred. No.:	5,38e-50
Score:	117
Percent Similarity:	528.00
Best Local Similarity:	93.04%
Best Local Similarity:	90.43%
Query Match:	69.38%
DB:	4
	Gaps: 0

Oy	1	ATGATGGTCCACACTAGAGTCCCTGGGTCTCCTGAGCTCTGGTATCCAGATTCCAGATG	72
Oy	13	ATGATGGTCCACACTAGAGTCCCTGGGTCTCCTGAGCTCTGGTATCCAGATTCCAGATG	72
Db	3	MetArgValIleuAlaGlnIleuLeuGlyIleuLeuLeuCysPheProGlyAlaArgCys	22
Oy	73	GACATCCAGATGACCCAGTCTCCATCTTCGCTGTCATCTGTAAGGAGACAGTACC	132
Db	23	AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr	42
Oy	133	ATCATCTGTGGGGCGAGTACAGATATTAGAGGTGGTATGCTGGTATCCAGATTAACA	192
Oy	43	IleMetCysArgAlaSerGlnGlyIleSerSerTyrPheAlaIleTyrGlnGlnIlePhePro	62
Oy	193	GGTAAAGCACCTTAAGTCTCTGATCTATGCTGCATCCAGTTTGCAAAAGTGtGCCATCA	252
Db	63	GluIysAlaProIysSerIleuIleTyrAlaIleSerSerLeuGlnIleSerGlyValProSer	82
Oy	253	AGGTTTCAGCGAAGTGGATCTGGGACAGATTTCACTCAGCATAGCAGCTCGAGCCT	312
Db	83	ArgPheSerGlySerGlySerGlyIleThrAspMetIleuThrIleIleSerSerLeuGlnPro	102
Oy	313	GAAGATTTTGCACTTAATGTCACAGGCTAATAATGTTCCCG	357

Db 103 Gluspspreall
RESULT 11
US-08-758-417A-313
Sequence 313, Application US/
Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
Kay, Robert M.
TITLE OF INVENTION: Transgenic
Producing He-300129-Human Animals for
Antibodies
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: Two Embarcadero Center, El
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIA TYPE: Floppy disk

? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patentin Release #1.0, Version #1.3G
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/758,412A
 ? FILING DATE: 02-Dec-1996
 ? CLASSIFICATION: <Unknown>
 ? PRIOR APPLICATION DATA: US 08/738,463

ERROR APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992

ATTORNEY/AGENT INFORMATION:
NAME: Serattin, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 313:
SEQUENCE CHARACTERISTICS:

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      TYPE: amino acid
      TOPOLOGY: linear
      MOLECULE TYPE: protein
      SEQUENCE DESCRIPTION: SEQ ID NO: 313
US-08-758-417A-313

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Alignment Scores:	
Pred. No.:	5.38e-50
Score:	528.00
Percent Similarity:	93.04%
Best Local Similarity:	90.43%
Query Match:	69.38%
DB:	4
	Gaps: 0
	Length: 117
	Matches: 104
	Conservative: 3
	Mismatches: 8
	Indels: 0
	Gaps: 0

US-08-728-463B-220 (1-420) X US-08-758-417A-313 (1-117)

QY	121	TGGCGTCTCAATGGTGGGTCCTTCATGGTGTACTACTGAGGTGATCCGGCAGGCCCA	180
Db	41	CysAlaValAlaValIleValSerPheSerGlyTyrTyrTbSerTbIleArgInProPro	60
QY	181	GGTAAAGGGCTGAGTGAGATTGGGGAATCAATCATATGTGAAAGCACCACCACTAACCCG	240
Db	61	GlyIleGlyIleuGluTbPbIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnPro	80
QY	241	TTCCTCAAGGTGAGTGCACCATATAGTCGACAGTCCCAAGAACCACTTCCCTGAAG	300
Db	81	SerIleuSerSerArgAlaIleIleSerValaPbPbMetSerLysAsnGlnPheSerIleuLys	100
QY	301	CTGAGCTCTGTGACCCGCCGCGACACAGCGCTGTGTATTACTGTGCAGA-----	348
Db	101	LeuSerSerValThrIleAlaIlePbThrIleAlaValTyrTyrCysAlaIleArgIleGlyPheAla	120
QY	349	-----GTATTATATTGGTTCGACCCCTGGGGCGCAGGAAACCTGTGACCGTCCCTCA	400
Db	121	AlaThrIleValAlaGluSerPheMetPbTyrTbGlyGlnGlyThrIleValaIleThrValSerSer	140

RESULT 2

Ig heavy chain precursor V-D-J region (clone MAB 63V4) - human (fragment)
 CSpecies: Homo sapiens (man)
 CDate: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
 CAccession: S78052, S23717
 R:Harindranath, N
 submitted to the EMBL Data Library, August 1990
 A:Reference number: S78051

A;Reference number: S78051

A;Molecule type: mRNA

A;Residues: 1-140 <HAR>

R:Harindranath, N.: Goldfarb, I.S.: Ikematsu, H.: Burastero, S.E.: Wilder

Int. Immunol. 3, 865-875, 1991

A/Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and high-affinity anti-*Salmonella typhimurium* antibodies

patient:
A:Reference number: S23716: MUID:92031262: PMID:1718404

A;Accession: S23717

A;Molecule type: mRNA

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A;Cross=references: EMBL:X54441
A;Residues: 15-111 <HAW>
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C; Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

F1-15-140/Product	IC heavy chain (fragment)	#status predicted <SIG>
F1-15-140/Product	IC heavy chain (fragment)	#status predicted <SIG>

F:29-111/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	1.55e-49	Length:	140
Score:	639.50	Matches:	12
Percent Similarity:	90.00%	Conservative:	2
Best Local Similarity:	88.57%	Mismatches:	11
Query Match:	86.07%	Indels:	3
DB:	2	Gaps:	2

US-08-728-463B-205 (1-403) x S78052 (1-140)

[illegible]

Oy	256	GTACACATATTCAGTGCACACGTCACAAAGACAGGTTCTCCCTGAAGCTGAGCTGTGATACC	315
Db	81	ValThrIleSerValAspHisSerIleSerAsnGlnPheSerLeuValSleuSerSerValThr	1000
Oy	316	GCCGCGGACACGCGCTGTATTACTGTACG-----AGAGTATTAAAT	357
Db	101	AlaAlaIAspThrAlaValIleTyrIleArgIleValSerValIleuArgPheIleuGlu	1200
Oy	358	TGG-----TTTCAGCCCTGGGGGCCAGGAAACCTGATCACCCTCTCTCA	402
Db	121	TrpIleuLeuTyrProAlaPheAspIleTyrIleGlnGlyThrIleuValThrValSerSer	1400

RESULT 3
137782

15/102
Ig variable region (VDJ) (clone T23-9) - human (fragment)

C:\Species: Homo sapiens (man)

C:\Date: 16-Feb-1996 #sequence_ revision 13-Mar-1997 #text_change 23-Jul-1998
C:\Accession: 137783: S25476

R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M
C/Accession: 13/02/ 2021/0

Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994

A/Title: Somatic diversification in the heavy chain variable region of immunoglobulin genes in the murine B cell repertoire

A: Accession: T37782
H: Reference Number: A56676; MUID: 34113917; PMID: 8230336

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-140 <RES>
A;Cross-references: EMBL.X67906. PTD.G33582. PTD.CAA48104.1: PTD.G33583

C; Superfamily: immunoglobulin V region; immunoglobulin homology

F;46-128/Domain: immunoglobulin homology <IMM>

Alignment Scores:

freq. no.:	2,354,46	length:	149
Score:	603.00	Matches:	119
Percent Similarity:	87.86%	Conservative:	4
Best Local Similarity:	85.00%	Mismatches:	11
Query Match:	81.16%	Indels:	6
DB:	2	Gaps:	2

US-08-148-463B-205 (1-403) X 13/82 (1-140)

QY	ATGAAACACCTGTGGTTCTTCTCTCCCTCGTGGAGAGCTCCAGATGGGTCTGTCCAG	60
Db	1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaIaProArgTrpValLeuSerGln	20
QY	61 GTGAGAGTATAGACAGTGGGGCCGACGACCTGTGAAGCCCTTGAGACCCCTCCCTAC	120
Db	21 ValGlnLeuMetIleuSerGlyProGlyLeuValIleProSerGluThrLeuSerLeuThr	40
QY	121 TGCCTGTCTATAGTGGGTCTTCAGTGGTTACTACTGAGCTGGATCCGCCACCCCA	180
Db	41 CysThrValSerGlyIleSerIleSerSerTrpTrpSerTrpIleArgGlnProPro	60
QY	181 GGTAGAGGGCTGAGAGTGGATTTGGGGAAATCATCATATGAGAGGACCAACTACAA	240
Db	61 GlyAlaSerLeuMetIleuTrpIleGlyTrpIleTrpTrpSerGlySerThrAsnTrpAsnPro	80
QY	241 TCCCTCAAGATCGAGTACCATATCAGTCGACACGTCACAGAACCAAGTCTCCCTGA	300
Db	81 SerLeuLysSerArgValThrIleSerValIaAspTrnSerLysAsnGlnPheSerLeuLys	100
QY	301 CTGAGGCTCTGTGACCGCCGGGGACACGGGTGTGTTACTGTGGCGAGA-----GT	355
Db	101 LeuSerSerValThrIaAlaAspThrAlaValIleTrpCysAlaIaArgHisAsnSerSer	120
QY	355 AATTGG-----TTGACCCCTTGGGGCCACGGAAACCTGGTGCACCGTCTCTCA	407
Db	121 SerTrpTrpGlyArgTrpPheAspTrpTrpGlyGlnGlyThrLeuValThrValSerSer	140

RESULT 4

Ig heavy chain V4.21-UniqueD-J5 region - human
C/Species: Homo sapiens (man)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OW nucleic - protein search, using frame_plus_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 17.0465 Seconds
(without alignments)
4545.477 Million cell updates/sec

Title: US-08-728-463B-205

Perfect score: 743
Sequence: 1 ATGAACACCTGCTGTTCTT.....CTGTGACCGTCTCTCAG 403

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 566448

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame_n2p.model -DEV=xlp
-Q=/cgrn2/USFTO.spool/US08728463.rnac.03062003.085615.16827/app_query.fasta_1.3690
-DB=PIR-73 -QMT=faetan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=us08728463@cgrn 1.1.177 @rnac.03062003.085615.16827 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR-73: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	679	91.4	140	2 A49045	Ig heavy chain V r
2	639.5	86.1	140	2 S78052	Ig heavy chain pre
3	603	81.2	140	2 I37782	Ig variable region
4	593.5	79.9	126	2 S47010	Ig heavy chain V4.
5	590	79.4	147	2 S13519	Ig heavy chain V r
6	581.5	78.3	137	2 S31676	Ig heavy chain V r
7	579	77.9	146	2 S31586	Ig heavy chain V r
8	578	77.8	146	1 G1H0H2	Ig heavy chain pre
9	577	77.7	133	2 S31511	Ig heavy chain - h
10	576	77.5	133	2 PS0341	Ig heavy chain V-D
11	573	77.1	155	2 S31512	Ig heavy chain - h
12	573	76.6	139	2 S31656	Ig heavy chain V r
13	569.5	74.6	145	2 S78055	Ig heavy chain pre
14	554	74.6	146	2 S09711	Ig heavy chain V r

15	550	74.0	116	2 B26340	Ig heavy chain pre
16	550	74.0	143	2 B49028	Ig heavy chain V-I
17	542	72.9	140	2 A24770	hypothetical hybrid
18	541	72.8	146	2 S09710	Ig heavy chain V r
19	539	72.5	118	2 A26340	Ig heavy chain pre
20	538	72.4	116	2 S18557	Ig heavy chain V r
21	536.5	72.2	231	2 B23746	Ig Fab region IV-J
22	530	71.3	122	2 J10047	Ig heavy chain V r
23	525.5	70.7	130	2 S31673	Ig heavy chain V r
24	525	70.7	130	2 S31690	Ig heavy chain V r
25	519	69.9	124	2 S31684	Ig heavy chain V r
26	518	69.7	97	2 S26898	Ig heavy chain V r
27	516.5	69.5	137	2 S31585	Ig heavy chain V r
28	516	69.4	135	2 S78051	Ig heavy chain pre
29	512.5	69.0	139	2 A41287	Ig heavy chain pre
30	510.5	68.7	143	2 B41287	Ig heavy chain pre
31	509	68.5	97	2 S14474	Ig heavy chain V r
32	508	68.4	97	2 G34964	Ig heavy chain V-I
33	500	67.3	114	2 I72667	cold agglutinin FS
34	497.5	67.0	117	2 E34964	Ig heavy chain pre
35	490	65.9	97	2 S26805	Ig heavy chain V r
36	485	65.9	123	2 S30530	Ig heavy chain V r
37	485	65.3	135	2 S31604	Ig heavy chain V r
38	483	65.0	97	2 S26806	Ig heavy chain V r
39	483	65.0	97	2 JH0428	Ig gamma chain V r
40	475	63.9	123	2 S30529	Ig heavy chain V r
41	472	63.5	97	2 S26808	Ig heavy chain V r
42	470.5	63.3	120	2 PT0370	Ig mu chain precut
43	466.5	62.8	130	2 S30534	Ig heavy chain V r
44	465	62.6	109	2 PH1673	Ig heavy chain V r
45	464.5	62.5	129	2 S44114	Ig heavy chain V r

ALIGNMENTS

RESULT 1
A49045
Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C/Accession: A49045
R/Gilliot-Courvalin, C.; Brouet, J.C.; Pillier, F.; Rassegni, L.Z.; Labaume, S.; Silverm
Eur. J. Immunol. 22, 1781-1788, 1992
A/Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes I b
A/Reference number: A49045, PMID:92334290, PMID:1623923
A/Accession: A49045
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-140 <GRI>
A/Cross-references: GB:S39381, NID:G250899, PIDN:AAB22441.1, PID:G250900
A/Note: sequence extracted from NCBI backbone (NCBIN:108088, NCBI:P.108089)
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/34-116/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
1	679.00	93.57%	92.14%	91.39%	140	129	2	3	6	1

US-08-728-463B-205 (1-403) x A49045 (1-140)

QY 1 ATGAACACCTGCTGTTCTTCTCTCTGTCGACGCTCCAGATGGCTCTGCTCCAG 60
DB 1 MetlyHhIeIeUrphrPheLeuLeuValAlaAlaProArgTrpValIleuSerGln 20
QY 61 GTGCACCTACAGAGAGGCGGCGAGACACTGTAAGCTTCGGAGACCCGCTCCAC 120
DB 21 ValGlnLeuGlnInTrpGlyAlaGlyLeuLeuLysProSerGlnIuThrLeuSerLeuThr 40

QY 121 TGGCTGTCTATGATGGGTCCTTCAAGTGTACTAGTGAAGCTGATCCGACCCCA 180
DB 41 CytThrValSerGlySerIleSerSerTyrtTyrTrpSerTrpIleArgGlnProAla 60
QY 181 GGTAAAGGGCTGAGATGGATTTGGGAATCAATCATATGTGGAAGCAACCAATCAACCCG 240
DB 61 GlySerGlyLeuGlnTrpIleGlyArgIleTyrThrSerGlySerThrAsnPro 80
QY 241 TCCTCAAGAGTGGAGTACCATATATGATGACACCGCCAAAGACGATCTCCCTGAAG 300
DB 81 SerLeuSerSerArgValThrMetSerValAspThrSerGlySerGlnPheSerLeu 100
QY 301 CTGAGCTCTGACCCCGCGGACACGCGCTGTGATTAATCTGCGAGA-----GTA 351
DB 101 LeuSerSerValThrAlaAlaAspThrAlaValTyrTyrValAlaArgAlaProLeu 120
QY 352 ATTAATGTTTCACCCCTGGGCGCAGGAAACCTGTCAACCTCTCTCA 402
DB 121 MetTyrGlyMetAspValTyrGlyGlnGlyThrThrValThrValSerSer 137

RESULT 7

S31586
Ig heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31586
R/Cuiquier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31586
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-139 <CUI>
A/Cross-references: EMBL:Z14196; NID:G30978; PIDD:CAH78565.1; PID:G30979
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/3-4-116/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	2.5e-44	Length:	139
Score:	581.50	Matches:	115
Percent Similarity:	85.61%	Conservative:	4
Best Local Similarity:	82.73%	Mismatches:	15
Query Match:	78.26%	Indels:	5
DB:	2	Gaps:	1

US-08-728-463b-205 (1-403) x S31586 (1-139)

QY 1 ATGAACACCTGATGGTCTTCTCTCTGAGTGGAGCTCCAGATGGTCTGTCAG 60
DB 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProAlaGlyValLeuSerGln 20
QY 61 GTGAGCTACAGCAGTGGGCGCAGAGCTGTGAAGCTTCGAGACCTGTCCTCACC 120
DB 21 ValGlnLeuGlnIleSerGlyProGlyLeuValLysProSerGlnTrpIleArgGlnProAla 40
QY 121 TGGCTGTCTATGATGGGTCCTTCAAGTGTACTAGTGAAGCTGATCCGACCCCA 180
DB 41 CytThrValSerGlySerIleSerSerTyrtTyrTrpSerTrpIleArgGlnProAla 60
QY 181 GGTAAAGGGCTGAGATGGATTTGGGAATCAATCATATGTGGAAGCAACCAATCAACCCG 240
DB 61 GlySerGlyLeuGlnTrpIleGlyArgIleTyrThrSerGlySerThrAsnPro 80
QY 241 TCCTCAAGAGTGGAGTACCATATATGATGACACCGCCAAAGACGATCTCCCTGAAG 300
DB 81 SerLeuSerSerArgValThrMetSerValAspThrSerGlySerGlnPheSerLeu 100
QY 301 CTGAGCTCTGACCCCGCGGACACGCGCTGTGATTAATCTGCGAGA-----GTA 351
DB 101 LeuSerSerValThrAlaAlaAspThrAlaValTyrTyrValAlaArgAlaProLeu 120

QY 349 ---GTAATTAATGTTTCACCCCTGGGCGCAGGAAACCTGTGATCCCTCTCA 402
DB 121 IleArgArgGlyAlaAlaPheAspIleTrpGlyGlnGlyThrMetValThrValSerSer 139

RESULT 8

G1HMH2
Ig heavy chain precursor V-II region (ARR-77) - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 02-Sep-1997
C/Accession: A02101
R/Kudo, A.; Ishihara, T.; Nishimura, Y.; Watanabe, T.
Gene 33, 181-189, 1985
A/Title: A cloned human immunoglobulin heavy chain gene with a novel direct-repeat sequ
A/Reference number: A02101; MUID:85205332; PMID:3922855
A/Accession: A02101
A/Molecule type: mRNA
A/Residues: 1-146 <KUD>
A/Note: the sequence was determined from the differentiated gene
A/Note: the authors translated the codon GGG for residue 17 as Arg
C/Genetics:
A/Gene: GDB:IGHV@
A/Cross-references: GDB:128528; OMIM:147070
A/Map position: 14q32.33-14q32.33
A/Intons: 16/3
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-146/Product: Ig heavy chain V-II region (ARR-77) #status predicted <MAT>
F/35-117/Region: V segment
F/118-127/Region: D segment
F/128-146/Region: J segment
F/42-115/Distal bonds: #status predicted

Alignment Scores:

Pred. No.:	4.2e-44	Length:	146
Score:	579.00	Matches:	118
Percent Similarity:	83.67%	Conservative:	5
Best Local Similarity:	80.27%	Mismatches:	11
Query Match:	77.93%	Indels:	14
DB:	1	Gaps:	3

US-08-728-463b-205 (1-403) x G1HMH2 (1-146)

QY 1 ATGAACACCTGATGGTCTTCTCTCTGAGTGGAGCTCCAGATGG-----GTCTGTC 56
DB 1 MetLysHisLeuTrpPhePheLeuLeu-TyrCysGlnLeuProAspValGlyValLeuSe 20
QY 57 CCAGGTGACGTACAGCAGTGGGCGCAGAGTGTGAAGCTTCGAGACCTGTCCTCCT 116
DB 20 GlnValGlnLeuGlnGlnTrpGlyAlaGlyLeuValLysProSerGlnTrpIleArgGlnPro 40
QY 117 CACCTGCTGTATATGATGGGTCCTTCAAGTGTACTAGTGAAGCTGATCCGACCC 176
DB 40 uThrCysAlaValAlaPheGlyGlySerPheSerGlyTyrTyrTrpSerTrpIleArgGlnPro 60
QY 177 CCAGGTGAGGGCTGAGTGGATTTGGGGAATCAATCATATGTGGAAGCAACCAATCAAC 236
DB 60 oProGlyArgGlyLeuGlnTrpIleGlyGlnIleAsnHisSerGlySerThrAsnTyrLys 80
QY 237 CCCGTCCTCAAGAGTCAATCATATGATGATGATGATGATGATGATGATGATGATGATGAT 296
DB 80 sThrSerLeuLysSerArgValThrIleSerLeuAspThrSerLysAsnLeuPheSerLeu 100
QY 297 GAAGTGAAGCTGTGTGACCGCGGACACGCGCTGTGATTAATCTGCGAGATTAAT-- 354
DB 100 uLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgGlyLeuSe 120
QY 355 -----AATTGG-----TTGACACCCCTGGGCGCAGGGAAC 383
DB 120 uArgGlyGlyTyrTrpAsnAspValAspTyrTyrTyrGlyMetAspValTrpIleGlnGly 140

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C/Accession: S47010
R/Mahmoudi, M.; Gasyana, E.; Denonne, G.; Edwards, J.; Bell, D.; Cairns, E.
submitted to the EMBL Data Library, July 1994
A/Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody b1r
A/Reference number: S47009

A/Accession: S47010
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-126 <NMH>
A/Cross-references: EMBL:Z35492; NID:G517254; PIDN:CAA84625.1; PID:G517255
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	2,09e-45	Length:	126
Score:	593.50	Matches:	113
Percent Similarity:	89.68%	Conservative:	0
Best Local Similarity:	89.68%	Mismatches:	2
Query Match:	79.88%	Indels:	11
DB:	2	Gaps:	1

US-08-728-463b-205 (1-403) x S47010 (1-126)

```
QY 58 CAGGTGACGTACAGCAGTGGGCGCAGACCTGTGAAGCCTTCGAGACCTGCTCCCTC 117
Db 1 GlnValGlnLeuGlnGlnGlnTrrpGlyAlaGlyLeuLeuLeuProSerGlnThrLeuSerLeu 20
QY 118 ACTCGGCTGTCTAAGTGGGCTCTTCACTGCTTACTACTGAGCTGGATCCGCCAGCC 177
Db 21 ThCysAlaValAlaValrGlyGlySerPheSerGlyTyrTrpSerTrpPheArgGlnPro 40
QY 178 CCAGTAAGGGGCTGAGTGGATTGGGGAATCATCATAGTGAAGCACAATCAAC 237
Db 41 ProGlyLysGlyLeuGlnTrpIleGlyGlnIleHisSerGlySerThrAsnTrpAsn 60
QY 238 CCGTCCCTCAAGATCGAGTCACCATATCAGTCGACACGTCGAAGACAGATTCTCCCTG 297
Db 61 ProSerLeuLeuSerAlaValThrIleSerValAspThrSerLysAsnGlnPheSerLeu 80
QY 298 AACCTGAGCTCTGACCCCGCGGACACGGCTGTATTACTGTGGAGA----- 348
Db 81 LysLeuSerSerValThrAlaAlaSerThrAlaValTyrTrpCysAlaArgGlyGln 100
QY 349 -----GTAATTAATTGGTGCACCCCTGGGGCGAGGAGCC 384
Db 101 CysProLysAlaAlaSerCysTyrTrpLysAsnTrpPheAspProTrpGlyGlnGlyThr 120
QY 385 CTGGTCACCGCTCTCTCA 402
Db 121 LeuValThrValSerSer 126
```

RESULT 5

S13519

Ig heavy chain V region precursor - human

C/Species: Homo sapiens (man)

C/Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C/Accession: S13519

R/Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.

Nucleic Acids Res. 19, 673, 1991

A/Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked

A/Reference number: S13519; PMID:91187691; PMID:2011556

A/Accession: S13519

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-147 <NOR>

A/Cross-references: EMBL:X56158; NID:G37724; PIDN:CAA39626.1; PID:G37725

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/41-125/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	4.32e-45	Length:	147
Score:	590.00	Matches:	116
Percent Similarity:	86.43%	Conservative:	5
Best Local Similarity:	82.86%	Mismatches:	13
Query Match:	79.41%	Indels:	6
DB:	2	Gaps:	2

US-08-728-463b-205 (1-403) x S13519 (1-147)

```
QY 1 ATGAACACCTGTTCTTCTCTCTCTGAGTGGAGCTCCAGATGGGCTGTCCAG 60
Db 8 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 27
QY 61 GTGCAGCTACAGAGTGGGCGCAGAGCTGTGAAGCCTTCGAGACCTGTCTCCAC 120
Db 28 LeuGlnLeuGlnLeuSerGlyProGlyLeuValLysProSerGlnThrLeuSerLeuThr 47
QY 121 TGGCTGTCTAAGTGGGCTCTTC-----AGTGTACTACTGAGCTGATCCGCCAG 174
Db 48 CysThrValSerGlyGlySerIleSerSerSerTyrTrpGlyTrpIleArgGln 67
QY 175 CCCCCAGTAAGGGCTGAGTGGATTGGGGAATCATCATAGTGAAGCACAATCACTAC 234
Db 68 ProGlyLysGlyLeuGlnTrpIleGlySerIleTyrTrpSerGlySerThrTyr 87
QY 235 AACCCGTCCTCAAGATCGAGTCACCATATCAGTCGACACGTCGAAGACAGTCTCC 294
Db 88 AsnProSerLeuLeuSerAlaValThrIleSerValAspThrSerLysAsnGlnPheSer 107
QY 295 CTGAAGCTAGCTCTGTACCCCGCGGACACGGCTGTATTACTGTGGAGATTAAT 354
Db 108 LeuLysLeuSerSerValThrAlaAlaSerThrAlaValTyrTrpCysAlaArgProLeu 127
QY 355 AATTGG-----TTGCACCCCTGGGGCGAGGGAACCTGTGACCGTCTCTCA 402
Db 128 LeuTrpPheGlyGlnLeuPheAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 147
```

RESULT 6

S31676

Ig heavy chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C/Accession: S1676

R/Cuisinier, A.M.; Gauchier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

submitted to the EMBL Data Library, June 1992

A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Reference number: S31585

A/Accession: S31676

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-137 <CU1>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/34-116/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	2.5e-44	Length:	137
Score:	581.50	Matches:	114
Percent Similarity:	86.86%	Conservative:	5
Best Local Similarity:	83.21%	Mismatches:	15
Query Match:	78.26%	Indels:	3
DB:	2	Gaps:	1

US-08-728-463b-205 (1-403) x S31676 (1-137)

```
QY 1 ATGAACACCTGTTCTTCTCTCTCTGAGTGGAGCTCCAGATGGGCTGTCCAG 60
Db 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20
QY 61 GTGCAGCTACAGAGTGGGCGCAGAGCTGTGAAGCCTTCGAGACCTGTCTCCAC 120
Db 21 ValGlnLeuGlnLeuSerGlyProGlyLeuValLysProSerGlnThrLeuSerLeuThr 40
```

Percent Similarity: 84.51% Conservative: 9
 Best Local Similarity: 78.17% Matches: 14
 Query Match: 77.52% Indels: 8
 DB: 2 Gaps: 2

US-08-728-463B-205 (1-403) x S31512 (1-155)

QY 1 ATGAACACCTGTGTTCTTCTCTCTGCTGAGCCTCCAGATGGCTCTGCTCCAG 60
 DB 14 MetLysHisLeuThrPhePheLeuLeuValAlaIaIaProArgTrpValLeuSerGln 33
 QY 61 GTGACGCTACGACGATGGGGCGACGACTGTGAAGCTTTCGAGACCTGCTCCAC 120
 DB 34 ValGlnLeuGlnIleuSerGlyProGlyLeuValIleProSerGluThrLeuSerLeuThr 53
 QY 121 TGGCGCTGTATGCTGGCTCTTCACAGTGTACTACCTGAGACCTGAGCCGCCAGCCCA 180
 DB 54 CysThrValSerGlyGlySerIleSerSerTrpTrpSerTrpIleArgGlnProPro 73
 QY 181 GGTAAAGGGCTGAGATGGATTGGGAATCATCATAGTGAAGCAACCACTACCAACCG 240
 DB 74 GlyIleGlyLeuGlnIleuTrpIleGlyTrpIleTrpThrGlySerAlaThrTrpAsnPro 93
 QY 241 TCCCTCAAGATGAGTACCATATTCATGTCAGACGTCACAAACCACTTCTCCCTGAG 300
 DB 94 ProIleIleSerArgValThrIleSerValAspThrSerIleAsnGlnPheSerLeuLys 113
 QY 301 CTGACGCTGTGACCGCGCGGACAGCGCTGTATACCTGTGCGAGA-----GTA 351
 DB 114 ValSerSerValThrAlaIaIaAspThrAlaValTrpCysAlaArgGlyGlyIle 133
 QY 352 ATTAATTGGTTC-----GACCCCTGGGGCGACGGAACCTGTGTCACCGTC 396
 DB 134 SerSerTrpTrpValTrpValTrpGlyMetAlaAspValTrpValGlnGlnThrThrVal 153
 QY 397 TCCCTCA 402
 DB 154 SerSer 155

RESULT 12
 S31696
 Ig heavy chain V region - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S31696
 R:Chisnier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tommelle, C.
 Submitted to the EMBL Data Library, June 1992
 A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
 A:Reference number: S31585
 A:Accession: S31696
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-139 <CDI>
 A:Cross-references: EMBL:Z14194; NID:930975; PIDN:CA78563.1; PID:930976
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:34-116/Domain: immunoglobulin homology <IMM>

Alignment Scores:
 Pred. No.: 1.45e-43 Length: 139
 Score: 573.00 Matches: 114
 Percent Similarity: 83.57% Conservative: 3
 Best Local Similarity: 81.43% Mismatches: 16
 Query Match: 77.12% Indels: 7
 DB: 2 Gaps: 1

US-08-728-463B-205 (1-403) x S31696 (1-139)

QY 1 ATGAACACCTGTGTTCTTCTCTCTGCTGAGCCTCCAGATGGCTCTGCTCCAG 60
 DB 14 MetLysHisLeuThrPhePheLeuLeuValAlaIaIaProArgTrpValLeuSerGln 33
 QY 61 GTGACGCTACGACGATGGGGCGACGACTGTGAAGCTTTCGAGACCTGCTCCAC 120

DB 21 ValGlnLeuGlnIleuSerGlyProGlyLeuValIleProSerGluThrLeuSerLeuThr 40
 QY 121 TGGCGCTGTATGCTGGCTCTTCACAGTGTACTACCTGAGACCTGAGCCGCCAGCCCA 180
 DB 41 CysThrValSerGlyGlySerIleSerSerTrpTrpSerTrpIleArgGlnProPro 60
 QY 181 GGTAAAGGGCTGAGATGGATTGGGAATCATCATAGTGAAGCAACCACTACCAACCG 240
 DB 61 AlaIleGlyLeuGlnIleuTrpIleGlyArgIleTrpThrSerGlySerThrAsnTrpAsnPro 80
 QY 241 TCCCTCAAGATGAGTACCATATTCATGTCAGACGTCACAAACCACTTCTCCCTGAG 300
 DB 81 SerLeuLysSerArgValThrMetSerValAspThrSerIleAsnGlnPheSerLeuLys 100
 QY 301 CTGAGCTGTGACCGCGCGGACAGCGCTGTATACCTGTCGCGAGA-----GTA 348
 DB 101 LeuSerSerValThrAlaIaIaAspThrAlaValTrpCysAlaArgGlyLeuGly 120
 QY 349 -----GTAATTAAATTGGTTCGACCGCTGAGCGCGAGCAACCTGTCACCGTCTCT 400
 DB 121 LeuThrGlyAspLysTrpIleAspTrpTrpGlyGlnGlyThrLeu-SerProSerPro 139

RESULT 13
 S78055
 Ig heavy chain precursor V-D-J region (clone mAb 67VH) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
 C:Accession: S78055; S23720
 R:Harindranath, N.
 Submitted to the EMBL Data Library, August 1990
 A:Reference number: S78051
 A:Molecule type: mRNA
 A:Residues: 1-145 <HAR>
 A:Cross-references: EMBL:X54445; NID:937817; PIDN:CA38312.1; PID:937818
 R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Nockin
 Int. Immunol. 3, 865-875, 1991
 A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and
 patient.
 A:Reference number: S23716; MUID:92031262; PMID:1718404
 A:Accession: S23720
 A:Molecule type: mRNA
 A:Residues: 18-115 <HAM>
 A:Cross-references: EMBL:X54445
 A>Note: the authors translated the codon GCA for residue 67 as Arg
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:1-17/Domain: signal sequence (fragment) #status predicted <SIG>
 F:18-145/Product: Ig heavy chain (fragment) #status predicted <MAT>
 F:32-115/Domain: immunoglobulin homology <IMM>

Alignment Scores:
 Pred. No.: 2.99e-43 Length: 145
 Score: 569.50 Matches: 114
 Percent Similarity: 82.07% Conservative: 5
 Best Local Similarity: 78.62% Mismatches: 13
 Query Match: 76.65% Indels: 13
 DB: 2 Gaps: 2

US-08-728-463B-205 (1-403) x S78055 (1-145)

QY 7 CACCTGTGTTCTTCTCTCTGCTGAGCCTCCAGATGGCTCTGCTCCAGATGGCT 66
 DB 1 HisLeuThrPhePheLeuLeuValAlaIaIaProArgTrpValLeuSerGlnValGln 20
 QY 67 CTACAGCAGTGGGGCGACGACTGTGAAGCTTTCGAGACCTGCTCCCTGCTGCTGCT 126
 DB 21 LeuGlnIleuSerGlyProGlyLeuValIleProSerGlyThrLeuSerLeuThrCysAla 40
 QY 127 GTCTAGTGTGGGCTCTCTCTCTCTGCTGAGCCTGCTGAGCCTGCTGAGCCTGCT 183
 DB 41 ValSerGlyGlySerIleSerSerTrpTrpSerTrpValArgGlnProProGly 60

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QY 184 AAGGGCTGGAGTGGATTTGGGAAATCAATCATAGTGAAGACCAACTACACCCGCC 243
Db 61 LysGlyLeuGlnIurPrIleGlyGlnIleTyrlHisSerGlySerThrIleAsnProSer 80
QY 244 CTCAGAGTCGAGTCACCATATGATGACAGCTCCAGAACAGATTCTCCGAAAGCTG 303
Db 81 LeuLysSerAlaValThrIleSerValAspLysSerLysAsnGlnPheSerLeuLys 100
QY 304 AGCTCTGTGACCCCGGACAGCGGTGTATTACTGTGCGAGAGTAATTAAT----- 357
Db 101 SerSerValThrAlaAlaSerThrAlaValTyrlCysAlaArgValThrGlySerThr 120
QY 358 -----TGTTGACCCCTGGGGCGGAGAACCTG 387
Db 121 PheTrpSerGlyTyrlTyrlThrArgGlyTyrlTyrlPheAspTyrlTrpGlyGlnGlyThrLeu 140
QY 388 GTCACCGTCTCTCTCA 402
Db 141 ValThrValSerSer 145

RESULT 14

S09711
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C/Accession: S09711
R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Condwel, J.
B:Chem. J. 268, 135-140, 1990
A/Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains C
A/Reference number: S09710; MUID:90262535; PMID:2111699
A/Accession: S09711
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1146 <RUG>
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/34-118/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	7.38e-42	Length:	146
Score:	554.00	Matches:	110
Percent Similarity:	80.82%	Conservative:	8
Best Local Similarity:	75.34%	Mismatches:	16
Query Match:	74.56%	Indels:	12
DB:	2	Gaps:	2

US-08-728-463B-205 (1-403) x S09711 (1-146)

QY 1 ATGAACACCTGTGTTCTTCTCTCTCTGTCGAGCTCCAGATGGTCTGTCCAG 60
Db 1 MetLysHisLeuTrpPhePheLeuLeuValAlaArgAlaProArgTrpCysLeuSerGln 20
QY 61 GTGCACTACAGAGTGGGGCGAGACTGTTGAAGCTTGGAGACCTGTCTCCAC 120
Db 21 ValGlnLeuGlnIurSerGlyProGlyLeuValLysProSerGlyThrLeuSerValThr 40
QY 121 TGGGCTGTATAGTGGGCTCTTC-----AGTGTACTACTGAGCTGAGTCCGAG 174
Db 41 CysThrValSerGlyLysSerValSerSerSerGlyLeuTyrlTrpSerTrpIleArgGln 60
QY 175 CCCCCAGTGAAGGGCTGAGTGGATTTGGGAAATCAATCATAGTGAAGACCACTAC 234
Db 61 ProProGlyLysGlyProGlyIurPrIleGlyTyrlIleTyrlSerGlySerThrAsnTyrl 80
QY 235 AACCCGTCCTCAAGAGTCAGTACCAATCATAGTGAAGCTCCAGAACAGTTCTCC 294
Db 81 AsnProSerLeuArgSerArgValThrIleSerValAspThrSerLysAsnGlnPheSer 100
QY 295 CTGAAGCTGAGCTCTGAGACCGCGGAGACAGCGCTGTGATTAAGTGGAGAGTAAT 354
Db 101 LeuLysLeuGlySerValThrAlaAlaSerThrAlaValTyrlTyrlCysAlaArgValLeu 120

QY 355 -----AATGGTTCGACCCCTGGGGCCAGGAGACC 384
Db 121 ValSerArgThrSerIleSerGlnTyrlSerTyrlMetAlaSerValTrpGlyGlyThr 140
QY 385 CTGTCACCGTCTCTCTCA 402
Db 141 ThrValThrValSerSer 146

RESULT 15

B26340
Ig heavy chain precursor V-II region (71-4) - human
C/Species: Homo sapiens (man)
C/Date: 05-Jun-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
C/Accession: B26340
R:Kodaira, M.; Kinashi, T.; Umemura, I.; Matsuda, F.; Noma, T.; Ono, Y.; Honjo, T.
J. Mol. Biol. 190, 529-541, 1986
A/Title: Organization and evolution of variable region genes of the human immunoglobulin
A/Reference number: A26340; MUID:87061007; PMID:3097326
A/Accession: B26340
A/Molecule type: DNA
A/Residues: 1-116 <KOD>
A/Cross-references: GB:X05711; NID:G33602; PIDN:CAA29183.1; PID:9296660
A/Note: the authors translated the codon GAG for residue 25 as Gln
C/Genetics:
A/Intons: 16/1
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/1-19/Domain: signal sequence #status predicted <Sig>
F/20-116/Product: Ig heavy chain V region 71-4 #status predicted <MAT>
F/34-116/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	1.69e-41	Length:	116
Score:	550.00	Matches:	105
Percent Similarity:	93.10%	Conservative:	3
Best Local Similarity:	90.52%	Mismatches:	8
Query Match:	74.02%	Indels:	0
DB:	2	Gaps:	0

US-08-728-463B-205 (1-403) x B26340 (1-116)

QY 1 ATGAACACCTGTGTTCTTCTCTCTCTGTCGAGCTCCAGATGGTCTGTCCAG 60
Db 1 MetLysHisLeuTrpPhePheLeuLeuValAlaArgAlaProArgTrpValLeuSerGln 20
QY 61 GTGCACTACAGAGTGGGGCGAGACTGTTGAAGCTTGGAGACCTGTCTCCAC 120
Db 21 ValGlnLeuGlnIurSerGlyProGlyLeuValLysProSerGlyThrLeuSerValThr 40
QY 121 TGGGCTGTATAGTGGGCTCTTC-----AGTGTACTACTGAGCTGAGTCCGAG 180
Db 41 CysThrValSerGlyLysSerValSerSerSerGlyLeuTyrlTrpSerTrpIleArgGlnProPro 60
QY 181 GGTAAAGGGCTGAGTGGATTTGGGAAATCAATCATAGTGAAGACCACTACACCG 240
Db 61 GlyLysGlyLeuGlnIurPrIleGlyTyrlIleTyrlSerGlySerThrAsnTyrlAsnPro 80
QY 241 TCCCTCAAGTGTGAGTCCCATATGATGTCAGTGAAGCTCCAGAACAGATTCTCCGAG 300
Db 81 SerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeuLys 100
QY 301 CTGAGCTCTGACCCCGGAGACAGCGCTGTGATTAAGTGGAGAGTAAT 348
Db 101 LeuSerSerValThrAlaAlaSerThrAlaValTyrlTyrlCysAlaArgValLeu 116

Search completed: June 3, 2003, 09:07:51
Job time: 19.0465 secs